

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LLVVYPWTQRFFDSFGNLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG
1595	7092	A	1718	41	597	APSPRRPWVISQRRTKATITSLWKG \VNVE\DAGGETLGRLLVVPWT\ QRFFD\SFGNLSSASAIHGQPPKVQ GTWSKKVLTFLGEMP*KHL\DDLK GHLLPKPEVNLHC\DKPAMWDP\EN FKAPGEMLLVTRFWAIPFSAKEFHP WRLAGLPQKDG*LGVGQCPCSFQ IPLKPLGP*IQ\SFQG
1596	7093	A	1719	3	573	HSLFGTSEVINKLLVPDAHGSFHRG GPRLLSTSLWGKGECGKMLEEKPL GRLLVVPWTQRFFESFGNLVLLP SCPSMGQPPKVKAHGKRRRC*LSLG RCQ*STLDDL\KGTFCPSLKRNLHC* QACNVGS*RTSKLLGENVAG*PVFG QFHFRAKNFTPEGCKASWQKQKM AEDGDWSWPVPLFLPDYH
1597	7094	A	1720	676	1283	QRKILYTHNTTENKWEIINF*SFR IFLFFLRRSFTLVAQAGVQ\WDLGS LQPLPPRFKQFSCGLPSSWDYR/RC VPAHPANFCIF**RWGFTMLARLLS NS*PQGDPPASASQ\SAGITGVSA/H APVRASFFLSLTVSGVQWRDLGSLQ PLPSGFKGFSCLSLPSSWDYGCPPPS PANFCIFSRHGFSPCWSGWSQTPDL K
1598	7095	A	1721	41	669	APSSRRPWVISQRRTKATITSLWKG \VNVE\DAGGRKPLGKAPWLSTPWT \QRFFDSFGNLSSASA/LSMGKPPKS KAHGK\KVL\TSLGDA\TKHL\DDLK G\TFAQA*SATCTVDKLHV\DPGGT FKLLGENVAG*PVFGQFHFRAKNFT PGGCRASWQKQKMAEDGDWS\GQ CP\VLQIPLKLNCP*MQSFSRIRLLFL QAITNNKSISAKRSP
1599	7096	A	1722	2	307	TPYLVGVVAGAAQALQFESHAGH LGPQLFNKFALPYIRDVAQVKARL REAGLAPVPMIIFAKDGHFALEELA QAGYEVV/GDDFGPHRYIANLGHG LYPDM
1600	7097	A	1723	20	473	AVEFEANGLGPQGFPKNDIFL*A AWGEETDYTPVWCMRQAGRYLPE FRETRAQAQDFSTCRSPEACCELTL QPLRRFPLDAAIIFSDILVVPQWTLM TYMVEGGGSSTMAQAKRWLYQRP QASHQLLRILTDALVPYLVGVVVA GAQAL
1601	7098	A	1724	3	1170	CKHSLGHTCYSPRGSSYRQLTMEA NGLGPQGFPELKNDTFLRAAWGEE TDYTPVWCMRQAGRYLPEFRETRA AQDFSTCRSPEACCELTLQALGME VTMVPKGKPSFPEPLREEQDLERLR DPEVVASELGYVFQAITLTRQRLAG

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						RVPLIGFAGAPWTLMTYMVEGGGS STMAQAKRWLYQRPQASHQLLRIL TDALVPYLVGQVVAQAALQLFES HAGHLGPQLFNKFALPYIRDVAKQ VKARLAREAGLAPVPSIIFAKDGHF ALEELAQAGYEVVGLD\WTVAPKK ARECLGKTVTLQGNLDPCALYASE EEIGQLVKQNL\DTFGPHRYIANLG HGLYPDMDPEHVGAFVDAGHKHS RLV*QNMWGPLWMLGINTHVWFD KTECIPLSRTPNPDDWLFSGP
1602	7099	B	1725	92	846	IIFAMDGHFALEELAQAGYEVVGLD WTVAPKKARECVGKTVTLQGNLDP CALYASEEEIGQLVKHMLDDFGPH RYIANLGHGLYPDMDPQHVGAFVD AVHKHLRLV*
1603	7100	A	1726	1	804	
1604	7101	A	1727	178	1093	TFLLPACLLAALLPLRHHVRGRAW VQGSILNEGVG*ALKDLINEACWG Y*APAGVNLQSMGHRPTVSL\VQLT LRV*GASTPYRC\DRNLGHGR*NLT SMSKILKMAAGNED\ISLTLRAEDN AGYLGR*YFEGTKPGRKFSYEMK LMDLDVEQLGIPEQEVSCVVKMPS GEYA\RICRESQPILGDAVVISCA\K DGSENFASGELGNET\IKLSQTSNV DKEEEA\VPKMNPEVQPNFCH*GY LNFFTK\ATPLSSTVDTPVCSADGTP LVGRSIIAGYGDHLKYLLGLPKDP RIEEGSLGHS
1605	7102	A	1728	58	483	AARDRLHLRRTTEQHVPEVEVQVK RRRTASLSNQCQLYPRRSQQQVVP VVDFAELRQAFLAETPRGTVA AIAATASIAGAPTQYPPGRGT RRQTTPPPGIM\APPPGMRPPIG\PPPI GFPLARGTPI SMPPSGN
1606	7103	A	1729	292	531	FQAKTSLPLGFQKHQVLTVDIGFGG TAIMTVGKSSKMLQSLFPLQW/CFV KLCRVFVSFLPHFALIIANNKCIEQ KKKKK
1607	7104	B	1730	326	419	XRLTCKRSLARSIASLNAPQTDASGI SGGPDA*
1608	7105	A	1731	774	1763	GNPRSYLLSIAFPLGLQKAFKVFNC GTLDFGWNSNHDLFGKS SKLLQHI DYRMRCILQDGRIFIGTFKAFDKH MNLILCDCDEFKIK\PKNAKQPRA VEE/ESRVLGLVLLRG\ENLVSMTE GPPPKDT\GIARVPLAGAAEGPG\V GRAAGRGVPAG\VPISPGPLAGLAG PCSRGSLGGP/SPQQVMTSTGKEAL* AAAAVA\ATASIA GAPNTVPTQGT GTPAPTSGRATQP\PGIMAPPP\GM RPPMGP\PMGLRPARGTP\IGMPAG \MRPPPPG\IRGPPPP\GMRPHKTL SILFDPSQSLFPLQCVLVKLCRVSAELF CSLIIAIRC
1609	7106	A	1732	32	487	SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIM

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						GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG
1610	7107	A	1733	1	591	NFALEAKNSARAISLVPDAHGVIS QRRTKATITSLWGK\VNVE\ DAGGE TLGRLLVVYPWTQRFFDQLLANLS SASAHGQPPKVQGHMAKKVLTFL GEMPIKHLDDLKGHLLPKPEVNCT VDKPAMWDPENFKAPGEMLLVT/L FWAIPFSGKEFTP*RLQASWAERWV TWS\GQCPCSFQIPLKPLGP*IQ\SFQ G
1611	7108	A	1734	1	477	RRPSWLVA AVLNRNANMQIFVKLT GONHHPLRYETQ*HPLKNVQPKIS KNKGGYPHPD\QQRLDNLPGKQLE GWPALLSDYKHPRKESHAPWCLR LR\GGIIEPFSPGPLPKYYLRQR*SC RQVLCFAFNPPCLSTGRKK\KCGSH QTTLRPQEGRFK
1612	7109	C	1735	9	254	MEFHSCCPGWSAMARSQTAATAS QVQSDSPASASRVAGINRHALTHPA NFVFLVETRFLHVRQAGLELPPQPP KLLGLQV*
1613	7110	A	1736	5	290	FNLTHIESRPSRLKK/DEYE/FFTHLD KRSLPALTNIIKILRHDIGATVHEL RDKKKDTPVPWFPRTIQELDRFANQI LSYGAELDADHPVSPWPVG
1614	7111	A	1737	68	312	
1615	7112	A	1738	317	916	TSSPPSSLCFLSFS DICHELLGHVPLF SDRSFAQFSQEIGLASLGAPDEYIEK LATIYWFTVEFGLCKQGDSIKAYGA GLLSSFGELQYCLSEKPKLLPLELEK TGIONYTVTEFQPLYVAESINDAK EKVGNSAATIPRPF SVRYDPYTQRIE GLDNTQQAHDLG*FHLTVEIGILCS ALQKNKVKAMDRMVVCQAVE
1616	7113	A	1739	389	1881	NLQPHVLFANLPVPEALKSQRPHSR GASMSTAVLENPGLGRKLSDFGQAE TSY\EDNCNQKWVPISLDPPHLKER KLGALGPKYCALFAEENDVNLT\HIE S\RPSRLK\KDEYGFPPFGIKRSLPA LTNIIKILRHDIGATVHELSDKKKD TVPWFPRTIQ\ELDRFANQLSYGSG NWD\DHGPGFKDPVYRARRKQFAD IAYNYRHGQPIPRVEYMEEEKKTW GTVFKTLKSLYKTHACYEYNHIFPL LEKYCASHEDNIPQL\EDVSQFL\QT CTGFRLRPVAGLLSSRDFLGDLAFR VFHCTQYIRHGSKPMYTPEDICHE LLGHVPLFSDRSFAQFSQEIGLASLG APDESIEKLAPIYWFTVEFGLCKQG DSIKAYGAGLLSSFGFQYCLSEK KLLPL/ESLEKTAIQNYTVTEFQPLY YLAE\SFNDAQGEI*GTFAATIPRPF SVRHDPHTPQRIGGSWDNTQQLKI LADSI*Q*IGIPFAVALQNIK

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1617	7114	A	1740	1	191	MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWQLST/FQQMWISKQEY DESGPSIVHRKCF
1618	7115	A	1741	1	360	SGACPAFLVDRNLRRHHETTFNLIMK CDVDIRKDLYANTVLSGG\TTMYPG IADRMQKEITAL/APPSTLRFRIAPP/ ERRKYSVWIGG\SILASLSTFQQMC LGKQEYDESGPSIVQRKCF
1619	7116	A	1742	13	1277	INPPLSRRCLSHSVLPPLRRRVSL PVAMEEEIAALVIDNGSGMCKAGF AGDDAPRAVFPSIVGRPRHQGMV GHGPRTDSYVGDEA/QRSKRGITL KYPIDHIVTNWDDMEKIWHHTFY NELRVAPEKHPVL\LTEAPLNPKAN REKMTQ/ILCFETFNTPGHVPWPIQA VLSL*SLWAQPIGIVMDSG\DGVT TV\PILRGATTLLHANLRLGPLARD LTDYLMKILTERGYSFTTHGPGSKT FRNIKGEACATSPLDFEQEMGTAA SSSSLEKSYELPDGQVITIGNERFRC PEALFQPSFLGMESCGIHETTFNSIM KCDVDIRKDLYANTVLSGGTTMDP GVADKIAEGRSTALAAPAP*KIRVIA PP\ERK\YSVWIGGSILASLSTFPARF WISKQEYDESGPSIVHRKCF
1620	7117	A	1745	644	844	ELSPTTFMPFSEGAEHL\YLPQGPG* GSESPGGCPA/PPYSPYSAPPATPEP IEKSQPNPIRHRFP
1621	7118	A	1746	2	271	
1622	7119	A	1747	83	420	DSSNPSCQSPTQLSKANTLGWHVV CELALPDQSSGTSASRGGLE*THLL VA*ALEPIVL*SGAGLPGKL\GPVRP LG*AAVGPGAESLLPSVRSGSSLPQ RREGLSPDGPLP
1623	7120	A	1748	154	1030	SDISQAQLSCTGPPAIPGIPGTPG PDGQPG\TPGIKGEKGLPG\LAGDHG EF\GEKGDPIPG\N\PGKKFGPKGP MGPKGGPGAPGTPGP\KGDSGDYK ATQKIAFSATRTINVP/LLRRSQTNRF RPRCITNMNTN\YE\PRSGKFTLQGC PGLY*FNLSTPVSRGNLCVNLMRG RERAQKV\VTFCGLMAYNTFQ\VT GGHGSSAEE/GPQKEGGGKRPFF LQATDKN\SLTGAWEGANSVFSGL AFFQIWEGLTCGLASHTPAPPARN AHYTPNNNHMTKPNHNDRD
1624	7121	A	1749	3	607	FCPRGQEFGEKNLLSPRRPWVISQ RRTKAT\TSLWGK\VKCGKNAGKE ETPGKGS\LVV\HPWTPRGSEQLW QTCPSALCPSMGNPQSQGTMAKKV LTS\GRCP*STLD\DLKGHLLPKPEV NLHLLTSLHVG*SRTFKLPGEMLLV T/LFWAIPFSAKEFHPLKVAGFPQK DG*LGVGQCPCSFQIPLKPLGP*IQS FQG
1625	7122	A	1750	2	585	AAAAPAGGNPEQRLDYERAAALGG PDGRAWGGRSPLPPAP*AQGAPGP RWPPPRAGSPAPSPAGCGGGKGGG

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						LVTPGRGGPRAAGREL/RAVRCPCP VRPRPPSKPALGGSLPQPEPAAAPG PSIR/PVLPQTGSPWRRPKSLRPVL GTRVGRTPPLPPP/PDPAGPPPLPLPG P\HPSRPPPTGPWRPARADGRV
1626	7123	A	1751	25	1295	KLCATKDLSYLAAAASPTAFAYLG GLFSPKLPVTMAHRFPALTPEQKK ELSEIAQSIVANGKGILAADESVGT MGNRLQRIKV\ENT\EENRRQFR\EIL FLLWDSSIQPGGIGGC*FLFPRR/YPL TQKGTARGKLFPGNIPSREKGDWS VGNQV*DQGRFLFCREPNKGNNH FKGLDGLF\ERFVQYKKDGVDFGK WRAVLRIADS\CPSSLAIHENANAL ARYASICQQNGLVPIVEPQVIPDGD HDLEHCQYVTEKVLA\AVYKALND HHVYLEGTLLKPNMVTAGHACTK KYTPEQVGYGSP*QALHRTGPAAV PGVICFLSGGMSEEDATLNLNAYQTF A/TSTKSPWKLSFSYG\RGLQAQCTG LPWGGKAANKGGNPR\TAFMKRAH GLTCQAAQRDSMFTRVLLGAASHP SRLHHPCLYPT
1627	7124	A	1752	1	186	IFSRDGA\HRVTQDGLDLLTS*SARL SLPKCSDYSREPPRPAQTPIRHFH NSKHEKTME
1628	7125	A	1754	74	595	RGGQGLLSTSLWGK\VNVEDAGGE TPGKGSLLVYPMPGPQRFDSFGNL SSASAIHGQTPKVKA\HGGKADFP WDDAIKHL\DDLKGHLLPKPEVNLH C*QACNVGSLRTFKLPGENVAGLT VFGNPIFGKRISPLKVAGFPQKDG* LGVGQCPCSFQ\PLKPLGP*IQ\SFQ G
1629	7126	A	1755	21	457	NPRVRGALTMELSES\QKGFQMLA DPRSFDSNAFTLLLRAAFQSLLDAQ ADEAVL\DNKNSLEILLGSIGRSLPHI TDVSWRLEYQIKTNQLHRMYRPAY LVTL\SVQNTD\SPSYPEISSSCSMEQL QDLGGKLDASKSLGKSTQL
1630	7127	A	1756	1	455	
1631	7128	A	1757	3	468	
1632	7129	A	1758	50	895	THASDGALTMELSES\QKGFQMLA DPRSFDSNAFTLLLRAAFQSLLDAQ AD\EA\LDHP\DLKHIDPVVLKHC\ HAAA\ATYILEAGKHRA\DKSTLST YL\EDCKILTEKRIELFFAREYQ\NNK VNSLE\LLGKY*GRSLPSYNRVFSW ALWIIQVKDQSTFHRMYRPA\YLG DLKVVQNTGIPPSYPRELVFSCQPW NQL\QDL\VGETLKDASKKPWKRA SVVTLGKVNRSPSSRRKTQKPLP FSWNHRLCRA\GCPFSVEKNFSLNL YPFIHFGHFKNV
1633	7130	A	1759	470	737	RKSFFLAQTVLKWCCEKMSSPGKK LFPGEIWGVKGNKNKLWPLPDPSIR HRFERVPSHKRPLPGWVRWLTPIPS TLGGQSAVDHLRSGVRDQPGQHGE

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						TPSVLKI*KLGRGGRQL*SQLFGRL RQENCLNTGG\RGCEPRSHHCTPA WATE*NSWDYSCLPPRPANFYIFST DGVSPCWPGWSRTPDLK
1634	7131	A	1760	1	297	
1635	7132	A	1761	1	162	
1636	7133	A	1762	54	504	YTAIMSIMS YNGGAVMAMKGKNC VAIAADRRFGIQAQMVTTDFQKIFP MGDRLYIGLAGLATDVQTVARLK FRLNLYELKEGRQIKPYTLMSMVA NLLYEK/RDPDHLFETISQAMLNAV DRDAVSGMGVIVHIEKDKITRTL KARMD
1637	7134	A	1763	51	748	YTAIMSIMS YNGGAVMAMKGKNC VAIAADRRFGIQAARLLTTFQKIFP MGDRLYIGLGPASPLDVQTS/VAQR LQVSGLNLY*V*REG\RIQTFTILM EAWLANLFVMRKRF\GPLLTLRPVH LPGLGPERPFKALSIC/SL*DLIRVGP MGDLNDFCGSSGNLAPNQMLRECV ESLWGGPTWVPDSTVLKTIFPRPW NAVGPWGQCSGMGSSLFHIEKDKI TTRTLKARMD
1638	7135	A	1764	433	851	KPQPFILCSKYNQMILLHLRAPGHA DASTQKQQLWL*NLLTSLGQRLFN FFETESHVST*L/QCSGMISAYCNIC LPDSSNPPTSASRVAGTAKRQHHTQ LIFCIF/VVQTGFCHVGPGLGFTEAR AIHPPWV\PKVLGLQV
1639	7136	A	1765	213	617	KRFLV*KVASVLKGLHA\VVSDRD GSTLLLKWANDNAPEHAF/RGPGFL \STFALATDQKGQTWDFSKNKSINC LLTPYQGGFNFSFYLVWGEFS*A QAGSAQLQGLICSA*EKGTWFPLF* RN*GQVVEVSLI
1640	7137	A	1766	2	140	
1641	7138	A	1767	157	371	
1642	7139	A	1768	3	135	
1643	7140	A	1769	1	1431	MHKAGLLGLCARAWNSVRMASSG MTRRDPLANKVALVTASTDGIGFAI ARRLAQDGAHV\VVSSRKQQNVQDQ AVATLQGEGLSVTGTVCHVGKAED RERLVATAVKLHGGIDILVSNAAVN PFFGSIMDVTEEVWDKTLDINVKAP ALMTKAVVPEMEKRGGSVIVVSSI AAFSPSPGFSPYNVSKTALLGLNNT LAIELAPRNIRVNC/LAPGLIKTSFSR MLGEPEDCAGIVSFLCEDASYITG ETVVNLSVMFTGGGVCRAASWKE GGTGTPTPTPRESRQREPGETSSTD QENKVWNGLPANPQRPAAEGPVRR KTNKQKGIASTSAKDSINIRTKGDIH TKTPSIGHQHQRPKVDKTTKMERN QSKKAETSRNQNVSSLPKEYKSSPA REQNW MENKFDDLTDVSFRRSVIT NYTQLKEHVLTHCKEAKNLDKML NEWLTRMKNLEKSLNDLMELITTV

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						QELHEGYTSFNS
1644	7141	A	1770	53	582	RKETVSVSPQQSRHLIGVRSPKGLS EVALAGLIHAQGAATSVHCARAGK SVRLASSGMTRRDPLTNKVALVTA STD*ALHRLSLDLTTTQARQGLFSR SAVALAQIAGATSQGPT/CQ*GKTQT SQAPFLYWLPVDYQAAKPYGGIDIL SSKAVVNPLFEA*RVSPPEARLTL DIIG
1645	7142	A	1771	44	1059	AMHKTGLLGLCARAWNSVRMASS GMTRRDPLANKVALVTASTDGIGF AIARRLAQDGAHVVVSSRKQQNVD Q\AVATL\QGEGLSVTGTVCHVGKA EDRGAAW\PPAVKLHGGIDILVSN AAVNPFPGSIMDVTEEV\WDKTLDI\ NVKGPKP*MTKAVVPEMEKRGGGS \VVIGLSIAAPSPSPGFSLYNVSKPAL LGLAQTLPIEL\APRNIRVNCLAPG\ LIKTSF\SRML\WMDKEKEESMKE\T LRIKKV*ASPEDCAGUVSFLCEDAS LHSLGKTVVVGSGTPVASEGTGK TAQRPKVGLLSFLVLFPAIQPNWPF PTSCSTLLFHPHSNQFLPL
1646	7143	C	1772	1	174	MWIFIFNKYYQHVKSPMTSRTGKS ATCDGCGMAAHCSRCWGLSWGLG EALSYSKNVS*
1647	7144	A	1773	154	765	RAGLEELTAAVMVRLNLCIVAVSQ NMGIGKNGDLPWPPLKNEFIYFQR MTTSSVEGKQNLVIMGKKTW\FSI PE/RRNRPFKG*EFNLVLSRELQGNL PQGA\HFLFQKF*D/AMPLKLTEQPE LANKVDMVWIVGGSSVYKEAMN HLGHLKLFVTRIMQDFESDTFFSEID LEKYKLLPEYPGILSDVQEGKHIKY KFEVCEKDD
1648	7145	A	1774	1	676	DRPNSGRPRAALAAGSTFPVLACSS AMAPKGSSKQQSEEDLLLQDFSRN LSAKSSALFFGN\AFIVFAIPIWLYW RIWHMDLFKSAVLYSVMT*LSTYL VAFAYKNVKFVLKHKV\AQKEGK DAVSK\EVTRKLFWKLDY*ERCSRE GRKD\ERILWK\KNEV\ADYEATNIF PIFYNNTLFLVLVIVASFFILKNFQ PHSVSFSRNYILSISG\SSGLIALFTG SK
1649	7146	A	1775	99	362	
1650	7147	A	1776	3	403	
1651	7148	A	1777	184	360	
1652	7149	A	1778	1	885	EFGTRWDFSMVAFADLDLRAGSDL KALRGLV\ETA AHLGYSVVAINHIV DFKEKKQEIEKPVAVSELFTLPIVQ GKSRPIKILTRLTIIVSDP\SHCNFER QLLRGARLYDVVAVF\PKGQEKSLF HIA\CTHLGCGDLVCITVTEETTIFT SKRPPINVAIDRGLAFDLALIPLLSR TPTMRKVYNFPSAPPILMPNLAKGK NVNYYLGGWQERAFREIR\GP\YDV

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						GKS*ACLFGPFF*K*TPRVRVSTNCR AA\LLHGETRKTAFGHIISTVKKPRP\S EGDEDCLPASKKAKCEG
1653	7150	A	1779	175	534	DCSLPSVCHFPHLPSPTHPTTHPPWG /CPSGGPEGLPIT*RHQVGSCPTAPPP VPAPSRQSDCGAVHSQDENTVNALI GGFLVLLHIMCNVVALTFYATIYED LCCTCNKYIEKAHTSVW
1654	7151	A	1780	190	390	TKRGAGEGNSKVVLGLQVGCQSQR GNHQGMFTWA/CCGKDSGGACSCSCL GV*CSWGQKSIRVSLWGF
1655	7152	A	1781	805	1325	ASKLEGSPCGKGGVGLGGCFPKRPE PRNHPHFVLWYLPQTRLEPKPLP PQLPSVG*KGPGPSFGLSLTAGPLP LQERLVPTQLLPVGKPGPGFPACA TSSGKPKLRPLCAKSTMP*THPPT VPKPPGQEA VENQAPMASEFPSPSP SVSGDLKPWGFRSFLCQGGAWS
1656	7153	A	1782	1016	1560	KDPELQASHFPCFSYCTPPAHFASLL DFAFSDPHLLGFLSSFLERSSI/CGKT DLSKTFSLD*SFGLNFSRLRESSYRP FGVQDAID*HPPAMFFSASQTLQGP SCGVPICAFIPAVPSTFQLPMFLWVR FLSLPSFSFPNPPVSSGSLFPHTPFL TTP/LPHG*LFPSAPPALHHATHFRT
1657	7154	C	1783	68	223	MSPSSVFFVXXXXXXXXXXXXXXXXX XRASFIPPLDLXXXXFSLFQMKSI DF*
1658	7155	A	1784	1373	1651	LSVLCHCVCVCVCV/CCD*KGLHSY LFPWTWKKIFFYLFK*NLLISSNHI*I NVKAYIVLYVN*ILKITKYMILLSTT
1659	7156	A	1785	6	140	
1660	7157	A	1786	223	397	QTPP*KSKQPFRTSS*DQVPSQP*PPI PPINNPPIPPPFGEVYYFEPILRKWV KGR
1661	7158	A	1787	2287	2854	
1662	7159	A	1788	1	610	SGRPFFFLSGGARATAQLAESWRG GQHLQSSPPPPASPGGPSSDQRS PCSNARW/NTSIYSLVADGTC*D TALVGNKDP\PSIWAAIPGKTFLNIT PAEVGVL/VGKDWVKLLSLNGLDT GGPRNYNLLVPGDFHWLAGWGN* TVDL\QLKSIGGSP\TFNVIVTMTAK TLGLLMGKEGIHGNFIDK*CYEMAS HLQRSQY
1663	7160	A	1789	157	610	GYRKKQLRGDRRWAIHRIRITLTSR NVKSLEK\VCA*L**RRRKEKENLK S*KGPVVRMPTKT\LRITTKKTPCG*/ EGSKDRWDRFPD*GFHKRLHLTLH SSFLRFV*GRFTSFSYLRPGFEVGSS PFADALSQISIHTIDDQLKKKKKKK KI
1664	7161	A	1790	1367	1582	METRWESPDPDNFNIAPVTP*FCSNS D/CVLSVPDSSRLPRHFPPSHCTRKR PHLPTQQQPFRKCALQEKWFF
1665	7162	A	1791	122	344	ALGPLPLFFPPSPLPVQKG*YSNQKL EGAGPGQGGFQPVFP*LGGTSNFP

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						FRKSPSQVQAH*PGSDEDPRL*EDP RPL
1666	7163	A	1792	656	1068	NQINFCLNGKYTYVCIDTLPLYMFN IHTLKHINTSVIISLEFAI*HKGQVEL HIKITYRSN*MWLGHNQRRN/LCPQ EGEEIPNEA*IFSIIKRQSWPGTVAH ACNLITLGG*DGRIS*DQVFKTSLINI VETPSLLKK
1667	7164	A	1793	138	396	
1668	7165	A	1794	143	327	CGVQLLPDRRRESRDIIVEL*AAVA AAGGNPDGKKGGGGWEAGQRKER KESEDPDAEPDCV
1669	7166	A	1795	23	483	KAIVLLHICTEVISIILFNDFIQDKRP CRLFTCCSLLRSASPVSSAANMPEL FSSTSSSTVSWLSLSLSSSLSSCFLSFR FGNSSCMSFSSIIIPVRPEDWKRMLL AK*GPLMALMLCALFFSSSSRLKPL FMSTTILSLKYGGGVQDVGWQ
1670	7167	A	1796	429	1394	TISFEADIIHMYKT*ETD*TIFLEPYD YLLQLPAGKQVRTQT/LSQAFNHWA LKVPEAKLTDYLFVDRKLFGLMPS LLIADDIEDNSKLPTWAFVVAHSIYGI PSVINSANYVYFLGLEKVLTDHPD AAKLFTROLLELHHGQGLDIYWRD NYTCPT*EYKAMELQKTGGLFGLS KCLKHIVSDYQEYLKPLLNTLGLFF QIRDDYANLHSKEYSENKSFCEDLT EGKFSFPTIHAIWSRPESTQVQNILR QR TENIDIKKYCVHYLED\EGSFYET RNTLKELEAKAYKQIDARGGEPLS LVA\LVKHLK*RCSKEGKWNNV
1671	7168	A	1797	145	172	GGCLLESVDTSHGQSLISASLNTK HPTGMHSTCWFHVELCGKGLGSRH TLKQHQSFA*SMPPA/PPAPCHIVPQE PTS*VHPCWVFCVETG
1672	7169	A	1798	197	378	VLMSVLPALGYPPRSMWLYVRGLN ADTP*PPSTTFPLALPPSSTWNQ/PS* VHPLLGVCVET
1673	7170	A	1799	32	377	SSMPPTPGPSILSSLVPIPVSPFHPCPP VLYLWPAPI/Y*KLLPVPDLAHSPPS TPTLHVSHYPMVGITLTPVPLFFIPS NSLPNGGDPEPSSDQVEPVQPGLLS LPSSKGSFCF
1674	7171	A	1800	168	224	
1675	7172	A	1801	224	527	CHQLRQELAIFTSFVILQLFSGHLDV YMQAWAQRDPKYEYDNK*FIEKKI IQFTLISKRMK/YVGINLTR*VKDLH NENYKTLMEIEEDTSEWKDISCSW
1676	7173	A	1802	22	430	SPGCRRAESEKSQGSERGVGPSYRI WVGSGKLQSKGVVLWQAGAGVIR CSAGELLSQEKGFHKVMSSVKAGT SHLHFFCDSSVTSGHVDVYVQAWA QRPDRYSVHCSGDGCTKVSEITTKN LFM*PKTTCTPKTE
1677	7174	A	1803	386	511	
1678	7175	A	1804	362	439	
1679	7176	A	1805	776	1376	GAPWAFGGLPWVHGLAKEGVTAIV

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						AEHGLWNIGVHEGHGTLQLQHMH HYAVALRRHPFIQAQAQRGV LALG GGMGTRE*VRARGQPRVHSNNCH TGQNRYSVPSEGLWT*YLL*GPK MTQDAEQAGRDGGDDGGLALVGE ALLEAHRDAIEQALPWGLRQLSLTV SQIGGHTVGPVHFPGLSHIGEEHGL RGQLSTV
1680	7177	A	1806	420	508	
1681	7178	A	1807	735	841	
1682	7179	A	1808	796	1123	IQWICHNTISAPKNYLEISPHINNKQ F*KKI*KHFPFA*RT*SKKYLGINVQ SLRSLYLEIYK/SLIKMIKN/DT*RYN PY**FGKINIVK*LYNPM*FRFNTVPI KMPIS
1683	7180	A	1809	137	303	
1684	7181	A	1810	122	385	YPALEHILKAQAIQSRCGDCSCLPPS APWDHPGPTTP\SPGRRAAADPWHL SPIDGREHLR*VPVLPVTPPSPTLGH WVTDPSPGVGG
1685	7182	A	1811	77	1181	PLEKCYDLFSQNWSGFLPCFQEFQF QFKRILINRLKPDLEKSRKMGRK/R AEEYRQTFLTADV*RSPKKSRSRPRE SPKKAKKLEVIIGKPQSSSF*QRIR KRERTPATRA*SQ\KREKARRRSRSI DRGFERMR\SDVRNRLTSPSRSDR KGDRRDREREKENERGRRDRD YDKERGNEREKERERSRSRSKEQRS RGEVEEKKHREDKDDRRHRDDKR DSKKEKKHSRSRSRERKHSRSRSR NAGKRSRSRSKEKSSKHKNESKEKS NKRSRSGSQGRDTSVEKSKKREHSP SKEKSRKRS*/ASKERSHKRDHSDS KDQSDKHDRRRSPKYRTREPRKTSI KNKDETV*KYFVKCGSH*ILLND
1686	7183	A	1812	1	585	PLKRS DGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPVEKSAVTAL WGQA*TWMKVGGKALGK/RCWVV LPWDPKRSFEVLWGNLSQLP\DAVN GANP*R*KASMAKEKVLGCPLVNG PWLT/HWTTLKGHPLPHTEVSLHCD K\LRHGS LKNFRAPGATVGLCCLA HSLLAKEFNPNKLQGLPIQEKLVGW VVG
1687	7184	A	1813	505	671	QKNKVYFFFETYEIYWPGTVAHAC NPSTLGS*G/GWIT*AQEFETSLANM LKPCLC
1688	7185	B	1814	277	480	GTGHFYGRTPSDTNCQEYTHRKL CQIKSKADLVLMKNSKSLTRVIRNI LAPQDQNHQQNPLNSQFLQ*
1689	7186	A	1815	32	1386	VLLGPKAERTNSRRNYQRRDYFSA PRSITSNQSAKSSSSRGVYSAYQAP DIHECCHFRSASFLLDKMATPVPV SAPPATPTVPAAVPASAPASVPAPT PAPAAAPVPAAAPASSSDPAAASAT TAAPGQTP\ASAQAPAQTPAPALPG PALPGPFPGGRVVRLHPVILASIVD

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						\SYERRNEGACPS*SGTLFGKLVDK\ HSVE\VTN\CFSVPHNESEDEVAVD MEFAK\NMYETGIKKVSPNKLILG\ WYATGHDITEHSVL\IHEYYSREAP NPIHLTV\DTSLPGTGRMSIKA\YVST \LMGIPLGRT/LWGVMTPLTVKY\ AYYDTERIRRLTLIMK\TCF*PPTRVI WTSQVDLQQEGGGIQLRNPMPPLS TSVANMPEGCTCLGKVSADNTIRK VGHFLMSL\VNQVPENRKPMTFET MLNSNINDLFMVITYLANLTQSRVIA LNEELVNL
1690	7187	A	1816	273	748	VIQNLFNKMDVGTGQVRVVHACNP RHFRRLRQEPKSGVQDQPDQHGET PSLKIQKLARR/GGVVHL*SQLLRR LKQENRLNPGGGGCSEPRSHHCTPV *VTQ*DSVPPAPRKKKMYVVLTCK FHIWHISFTLPNIKRSDSLRNKVT NFSCYCSKVS
1691	7188	A	1817	1	406	LCQLETYPPISQCTASDFPGPVTAS WAIQEAARSGQAKAGA/GSATLS/M AYAGARFVFSLV DAMNGKEGVVE CSFVKSQETECTYFSTPLLLGKKGIE KNLGIGKVSSFEEKMISDAIPELKAS IKKGEDFVKTLK
1692	7189	A	1818	1	1222	FRQRAGAGQCGGRWSHFRTSSCA CYVDAPPAPAMLSALARA VPSACS/ LARSFSTSA\QNNAKVAVLGASGGI GQPLSLLLKNSPLVSRLTYDIAHTP \GSGPQDLS\HIETKSRK*KAYLGTW NSLPDCL\KGL*WW*VIPAGVPTKP GMDRD\DLFTTNATIVGTLTAACAQ HCPEAMICVIANPVNST/ISPITSKK VFKKAWGQHPQKKSSGVTTLNIVR AKTFVAELKGLDPAGVNVPIITGGH AGKTIPLISQVHAYDPVRGFECTPK VDFP\QDQLAALTG\RIQEVAGTEVV KAKAGA\GSATLSQCRNAGARFVF SLVDANELEKERCLWECSLPLSPQE TECTYFS\TPLL\LGKKGIEKKKAKT\ LGIGKSLPFEEK\MISDAIPELKA\SI KKGEDFVKTLK
1693	7190	C	1819	876	1124	MALGLRQRGIVSLAASITGPCPMSP APSPGTQVLLPTKRHPQVCLSHTC VEMRQVTKRLSAFKVRNKPDRFY SALLCSTE*
1694	7191	A	1821	103	483	
1695	7192	B	1822	1	798	MAFLDNPTILAHIRQSHVTSDDTG MCEMVLIDHDVDLEKIHPSPMPGDS GSEIQGSNGETQGYVYAQSVDITSS WDFGIRRRSNTESPKEPEQLRNLFIG GLSFETTNEKRSHCEQWGTLPCDV VMKDSNTRSGGFGFVITYATVEEV DAAMNARPHKRRKKYPLLGNNTN DKQLDLGPEKGRKHALNCHRMKP ALFSVLCEIKEKTGGATQAFKENN QKAYKETYGVSHITRHDMLQIPKL AQNEKSQVPSIRSIQRLKII*

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1696	7193	A	1823	3	545	
1697	7194	A	1824	1	440	VYLHLHSSQDRLLPMTVVVTMASAR VQDLIGLICWQYTSEGRKPKLNDN VSAYCLHIAEDDGEWTHDFTTLD NEPIHKFGFSTLALVEKYSSPGLTSK ESLFVR\INAAHGFSLIQVD\TQKVT MKEILLKAVKRRKGSQKVSGACD
1698	7195	A	1825	293	2142	GNWPTERMAFLDNPTILAHIRQSH VTSDDTGMCCEMVLIDHDVDLEKIH PPSMPGDSGSEIQSGNGETQGYVYA QSVDITSSWDFGIRRSNTAQRLE LRKERQNIQCKNIQWK\VERNSKQS AQELKSLF*KKNLSKEKPPISGKQSI LSVRLEQCPLQLNNPFNEYSKFDGK GHVGTATATKK\TDVYLP\nHSSQDRLL PMTVATMASARVQDLIGLIC*QYT SEGREPKLKDNVSDYCLHIAEDDGE VDTDFPPLDSNEPIHKFGFSTLALVE KNSSPGLTSKESLFVRINAAHGFSLI QVDNTKVTMKDILLKAVKRRKKGQ NVSGPQYRLEKHSEPNVPADLDSTL ESHSAREFCLVRENSSRADGVFEED SQIDIATVQDMLSTLHYKSFPVSMI HRLRFTTDVQLGISGDKVEIDPVTN QKASTKFWIKQKPISIDSDLLCACDL AEEKSPS\HALF*LTYL\SNHDYKHS TFESDAATANEIVLKVN\YIL\ESRAS TAR\ADYFAQKQRKLEQTVRAFSQ KEKEIPGSIEQLAFQPQILVPVASEP ACPGPSALRSPPGVLSFGGEAHPL GPLGTGAGGLFGEGVGGPLRREAA GDIAMGRKFALAMGF
1699	7196	A	1826	436	917	RLSSKLLHGAYQCFKAKIENYLLSW LNRKFRISFKKEKFSKAVCLKNDIW LGTVARDCNPNTVRLKWEDHLSPG I*DQPGKQ*DL/PSLQKNKKLPRHGG VHTLWSQLLGRRLRWENHLSLGDQG CIEVSSRHCTRAWVTEQDPI*KQLG PQGVYHHA\WVIFCFFVEMQVSLFS RLVSNSWAQVILPLQPHSVGIAVTS HCTQPYVIL
1700	7197	A	1827	46	573	SQTPMGHFTTED\KATIT\SLWGK\W NVE\ DAGGE\TPGKGS\LVVY\W\TQ RFFD\SFGNLSSASAIHGQTPK\KAH G\KKVLTFLGTMP\TKHL\DDLKGHL LPKPEVNCTFDKLACGILEELSSFLG KMLLG*PVFGNP\IFGKRISPLEGARF FLGRKMGDLELASALVPSRLPLKPL GP
1701	7198	A	1828	1	388	
1702	7199	A	1829	75	520	TPERGSAYPRLLCGAPPGEATVIM SDQEAKPSTEDLGDKKEGEYIKLV IGSGF\SEIHFKVKMTTHLKKL*ES YCQRQGVPMNSLRFL\FEGQRIAD\ NHTSNKNWGMEEEDVD*SFFREQT GGSFQQFRIFLFFFLSKSFFIF
1703	7200	B	1830	78	236	MSYIPGQPVTA\VVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFSEDKT

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						DK*
1704	7201	A	1831	67	587	IRVEMSYIPGQPGTAVVQRGEIHKLRQGENLILGFSIGGGIDQDPSQNPFSEDKTDKGIYVTRVSEGGPAEIALQIG\DKIMQVNGW\DMTMVTHDQ\ARKRL\TKR\SEEVVRLLG*RGSRMQK\AVQQSMLFLRQPPSPCDSCLPPLCTVTPLP HSGPHLASADR WAPASEGL
1705	7202	A	1832	3	420	HLSGTSEVINKLLVQTPMGHFTEEDKAT\TSLWGK\VNVEADAGGETLGRLLVVYPWTQRF\DFSFGNLSSASAI\MGNP\KVKAHGKKVLTFLGEMPLKHL\DDLQGAFFAQA*SELALVDKPA MWD P*GTSKLLGEMLLG
1706	7203	A	1833	3092	3227	ERQ/WPGTVAHACNPSTLGG*GGGAGIT*GQEFKTS LANTVNPSLL
1707	7204	A	1836	3	1088	SMAA VAAESACICR WRRSCSTGQFEELLRLKAKSLLVVHF WAPWAPQ\CAQMNEV\MAELAKELP\QVSFVKLEAEGVPEVSEKYEISSVPTFLAFFKNSQK\NDRLGWVHMPQELTKKVQADMHL SGLLPTQALMEHL*RKILQPFGL EGNLTSWLAPLAWLFYWK GELPSKEPR\CGFSK\QMVEILHKHNIQASSFDIFS\DEEV RQGLKAYSSWPTYQLA YGSGELIGGLDIKELEA SEELDTICPKAPKLEERLKVL\TNKASVMLFMKGN\KQEA K\CGFSKPN SGKYLNSTWC*NLETFRILEDERKFGQGLKSLTPNW\PNIPLSLYVKGELVGGLDIVKE\ LKRKLGEFAAL*LRGEN
1708	7205	A	1837	3	703	VEFFSSQRAELYATPLTPAPGPNGGIPGWTLWLALPRPGNLRKGPGLSLQEVDEQPQHPLHV TYAGAAV/DDELGKVL TPTQVKNRPT\SISWDGLD/SKGKLYTLVLTDPDAPKQGD PKYRE\WHHFLGWSTLKGQMTSATGTVLS\DYVGLGGLPKGTGLHR\YVWL V\YEQ\DRPLK\CD EPHPSATRS\GDHRGKIQRWASLPVKK**SSRAPGGWAPCYPQPEVGMNQCAPKL
1709	7206	A	1838	717	1390	ASTTTSSVHCARTYMGSVYNTPARVRLRVGWRAADQLLLAASSTSAIVSTRALECAKMQNAEAADATLVFI GYVVPALATLYAAGATLPRSAGKDTPPGTGDHGPAGALGTQAAGGHRVHAVWALDATLSDPAGAHGHLAREARGCTLPGGYCTL*RISPN SWSPAAL*HHFSTAT*TRASPASSNG**KSCPAG/APALLPGPHGGAAGAGVGGPALLGET
1710	7207	A	1839	1	310	RTSPHSPRNILLLS/EPENADSLMLVD FEYSSYNYRGFDIGNHFCEWVYDYTHEEWPFYKARPTDYPTQEQLHFIRHYLA EAKKGETLSQEEQRKLEEDLLCM
1711	7208	A	1840	3	375	HYLA EAKKGETLSQEEQRKLEEDLLEMYS LKDEMGNLRKLL ESTPSPV

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						VFCHNDIHSSS*LHPPTPWISPGASR AGPWREEQRAEGPGDWAEPSET VQETGLFLSLSRSPWLAGQSPVLCM
1712	7209	A	1841	94	429	
1713	7210	B	1842	96	979	XVGEEPREVLLRLYGAILQGVDSL LESVMFILAERSLGPQLYGVFPEG RLEQYIPVRAQSYPLPKAPPPNPT PVPNVCLHIPHPNPITTLIASWVQSR PLKTQELREPVLSSAAIATKMAQFHG MEMPFTKEPHWLFGTMER*
1714	7211	A	1843	5	1463	PEKPRPAGRGAERGRKEPSSESG AHPGLGPRARAMAAEATAVAGS GAVGRCLAKNGLQQSKCPDTPKR RRASSLSRDAERRAYQWCREYLG AWRRVQTEELKVYPVSGGLSNLLF RCSLPDHLPSVGEEPREVLLRLYGAI LQGLDSLVLLESVMFILAERSLGPQ LYGVFPEGRLEQY/IPTSWVQSRPLK TQELREPVL/SQAIATKMAQFHGM EMPFTKEPHWLFGVTMSRTLKQIQD RPPTGLPEMKLRGNVRLKDEMG NRKLLLESTPSPVVFCHNDIQEGNILL LSEPENADSLMLVDFEYSSNYRG FDIGNHFCEWVVDLYSSEE/WPFH KKAGPPSPSPHQRRQVHFIRQLPLA RGK*KVESLPRRSQKKNWKE\DLL VRKSSRVMFWQSHFLWGLWS\ILQ\ ASMSTIEFGYLDLCPSLRFQ\FLLPS KKGQA*PSVHSCILDSTLPLLGFLL PPGQGPWRGGTTSRRPWRLG
1715	7212	A	1844	143	762	CRQERAVAPARRAMERIPSAQPPTV CLPKAPGLEHGDLPGMYPALMYQ MYKSRRGLKRSEDSKETYELPHRLI EKKRRDRINECIAQLKDLLPEHLKL TTLGHLEKAVVLELTLKHVKALTN LIDQQQLFKMHYA*LLIVF*L/SSFPV FILVLSRCLYL*SCYKYILYKIKKE NVSDVYLYNYLIHTVRKNECIPVFE EKNNFFFL
1716	7213	A	1845	203	1507	CRQERAVAPARRAMERIPSAQPPPA CLPKAPGLEHGDLPGMYPAHMYQ VYKSRRGIKRSEDSKETYKLPHRLIE KKRRDRRTNECIAQLKDLLPEHLKL TTLGHLEKAVVLELTFEH/V*KALT NLNLSSSRQKIIAL/QSGLQAGELSG RNVETGOEMFCSGFQTCAREVLQY LA\KHENTRDLKVFASLSTHL\HRV VSELL/QGGTSRKPSDPASKVMDFR EKPSSPAKGSE\GPRKNCVPVIQRTF AHSSGEQSGSDTDTDSGYGGESEK GDLRSEQPCFKSDHGRRFTMGERIG AIKQESEEPPTKKNRMQLWDD\EGP FQLASDLNQLPPFGPTPQHQPFFCL PFYLIPPSS/ATAYLPMLEKC\WYPTS VPVLYPGLNASAAALSSFMNPDKIS APLLMPQRLPSPLPAHPSVDSSVLL QALKPIPLNLETKD
1717	7214	A	1846	628	1061	AHRKSLYLCEACFPRSRASQETSGL

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						KEENWRLGRKTSKCRPGLSKKLGC ERKDRDCSG/CRKDEQQGPWEAPQ AARHSQKSRNARGRPFLEGGPGTE NR*QSFPPKNSREQGFNDPVGQSV EPLEQPLFPWEWQWPALAQDREL
1718	7215	A	1848	88	953	FQAPQLCYDSAFMISSVPSHILRV CFPCFHAHLRVCEFPFHAHLVCCE FPCFHAHLVCCEFPFHAHLVCCE PCFHAHLRVASVNFVFHAHLVCCE FPCFHAHLRVCEFPFHAHLVSVN FCFHIHLVCCEFSFHAHLRVCEFP FHAHLVCVSNFRVFTPTCASVNFV FTPTCVCEFPFHAHLRVASVCEFP CFHAHLQVYEFPCFHAHLRVCEFP FHAHLRVCEFPFHAHLVCCEFP HAHLVCCEFPFHAHLVCCEFP AHLRVASVNFVFHAHLVCCEFP HAHLRVCEFPFHAHLVSVNFCFH IHLVCCEFSFHAHLRVCEFP HLCVSN/CPCFHTHLCVCEFP HLCL*ISVFSRPPASVCECL/CN/CPC FHAHLQ/CL*ISVFSPPAGL*ISVFS CPPACL*ISVFSPPVCL*ISVFSPP ACVCEFLCFHAHLVCDFPCFHAH QSATVLV
1719	7216	A	1849	1	254	
1720	7217	A	1850	3	308	
1721	7218	A	1851	1	380	IPTPLIGNFGPRGPRIRHERPQKRDD RREPSSFGKRRQ*DGTLCLRRCGS\ KA\YHLQKSTCGKCGYPAKRKRKY NWSAKAKRRNTTGTGRMRHLKIV\ YRRFRAWDFREGTTPKPK*GSLLQH SSSS
1722	7219	A	1852	41	544	APSPRRPWGHFTEED\KAT\TSLWG K\VNVEDAGGE\TPGKGSLLVYPW TQRFDSFGNLSSAF\AHHGQTPKV KAHGK\KVLT\SLGDAIK\HLLDLKG TFAQA*VNLHL*QSCNVD\ENFQA PGEMLLVTR\VLAIHF\GK\EFTPGGC KASWAEDG*LAVGQWPCSSRYH
1723	7220	A	1853	145	705	SWRNRTVSNGSASVSSVHLCFAE CKALCGERILTDGSDVSRPTIAAGG CNGTVKYL*QEVLTAPL\HDGP SHVGIPRSCPKPLDKRQAHLCVLAS \NCDEPTMYVKLVEAL\CAEHQNP *LRVD\DNKKLG\EWG*GLLLKFDR GGGKPRKSWLG\CSCFS*FKDY\GK ESQAKDVIV\EFKCKK
1724	7221	A	1854	110	776	SLASGPYL\THQQKVLGLYKRALRH LE\SWCVQRDKYRYFACLMRAF\ EEHKK*KRIWAKATQL\LKEARGKN FWYPVKHPKSQYILPLTSPGGHPP Y*EDHD/CAYKVPRIGCL\DDWHPS E\KAMYP\DYFCQRREQWKENLRR GKAWGTEGLSSLQE\ETP\PG\GPL TESFAPWPEKEGD\LPPLW\WYIVT R\RRPMLERERPHLSCLQVKYVT EHGTC

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1725	7222	A	1855	1	858	
1726	7223	A	1856	165	856	PVSYHPRMCTGGCARCLGG\TLISL AFFGFL\ANILLFFPG\GKVIDDNDHL \SQEIWFFGGILGKRCL**SFPALVF LGA*RNNDCCG\CCGNEGCGRFA\ MFTSTIFAVGWILGELGYSFIISAISI NKGP*NPSMAKK\TWGLPPSNDGD/ YILNDEGLNGTKCAREPLQCGFPGN LDPLSSILLGRREGIQMV\LCANQV\ VNGPPWGTLCGGTCQCCGCCGG\D GPVLNLRA
1727	7224	A	1857	163	1322	PGPYCGPVATMSLHGRRKEIYKYE APWTVYAMNWSVRPDKRFRWALG SFME\EHNNEGYLDGLDEERS*V\N KNILDRPYPTNKVMWIPDTKGVYP DLLATSGDYLRVWRVGETETRLC LLNNKN\SDFCAPLTSFDWNEVDP YLLGTSSIDTTCTIWGLETGQVLGR LNL\VSGHVKTQLIAHDK\EVYDIAF SRAGGRDMF\ASVGADGSVRMFD LRHLEHSTIYEDPQHHPLLRLCWT KQDPNYLATMAM\DGMEVVILDV RVPCTPVARLNNHRACVNGHLLW APHSS\CHI\CTAAG*PPGFSSWDI\Q QMPRA\IEDPILAYTAE\GEINN\Q\ WA\SNSAPNWESPIC\YNNCPWRY ECSVGGAVPHEAGAFVFPASAPPPK
1728	7225	A	1858	1	420	REDRIQLWKPPYTDENKKVGLALK DRKNLLETRLHITGRELRSKIAETFG LQENYIKIVINKKQLQLGKTL EEQG VAHNVKAMVLELKQSEEDARKNF QLEEEEQNEAKLKEKQIQRTYRGL* ILAKRAAETVVDPEMTP
1729	7226	C	1859	28	156	MMYRLMSILTRHVSSLKSYILIHQK WTICCSWGLLPRKPGLV*
1730	7227	A	1860	1	315	
1731	7228	A	1861	1	119	
1732	7229	A	1862	1	1477	
1733	7230	A	1863	3	1866	PLQSGHSAGRGGSGVAQGWHKKK YLQAKMTKFLREERIQLWKPPYTD ENKKVGLALKDLAKQYSDRLECCE NEVEKVIEEIRCKAIERGTGNDNYR TTGIATIEVFLPPRLKK\DRKNLLET RLHITGRELRSKIAETFGLOENYIKI VINKKQLQLGKTL EEQGV AHNVKA MVLELKQSEEDARKNFQLEEEEQN EAKLKEKQIQRTKRGLEILAKRAAE TVVDPEMTPYLDIANQTGRSIRIPPS ERKALMLAMGYHEKGRAFLKRKE YGIALPCLLDADKYFCECCRELLDT VDNYAVLQLDIVWCYFRLEQLECL DDAEKKLNLAQKCFKNCYGENHQ RLVHIKGNCGKEKVLFLRLYLLQGI RNYHSGNDVEAYEYLN\RHVSSLKS YILIHQKWTICCSWGLLPRKHRLGL RACDGNVDHAATHITNRREELAQR KEEKEKKRRRLENIRFLKGMGYST HAGQ\QILLSNPQMWWLNDSPET

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						DNRQESS\SQENIDRLVYMGFDALV VAEPALRVFRGNVQLAAQTLAHNG GSLPPELPLSPEDSLSPATSPSDSAG TSSASTDEDMETEAVNEILEDIPEHE EDYLDSTLEDEEIIIAEYLSYVENRK SATKKN
1734	7231	A	1864	1	727	MVVWDADTQQVIPNGIQLAGLDKS HSGFALAPPTTLFSGGGGGGAKAT AAAGAGLASPGMKTNGGRCRIRAL CWSRREWRGAGEDTAAECPRPQPQ QHCLAPRFPVRLGTSPGQGWSGRG AGDLAKQYSDRLECCENEVEKVIEE IRCKAIERGTGNDNYRTTGATIEVF LPPRLKKDRKNLLETRLHITGRELR SKIAETFGLOENYIKIVINKKQLQLG KTLLEEQGVAHNVKA\MVLELKQSE EDARKNFQL\QEEQNEAKLIEERL QRTKRGLAEILAKRAA\EPVVVPEMT PYLDIANQTGRSIRIPPSEKALMLA MGYHEKGRAFLKRKEYGIALPCLL DADKYFCECCRELLDVTVDNYAVLQ LDIVWCYFRLEQLECLDDAEKKLN LAQKCFKNCYGENHQRLVHIKGNC GKEKVLFLRLYLLQGIRNYHSGND VEAYEYLNRRHVSSLKSYLIHQKW TICCSWGLLPRKHRLGLRACDGNV DHAATHITNRREELAQRKEEKEKK RRLENIRFLKMGYSTHAAQQVL HAASGNLDEALKILLSNPQMWWLN DSNPETDNRQESPSQENIDRLVYMG FDALVAEAAALRVFRGKVPVAAQT PAYNGGSL/FPPELPLS\AEDSLSPAT \SPSDSAGT\SSA\STDEDMETEAVNE ILEDIPEHEEDYLDSTLEDEEIIIAEY LSYVENRKSSN*RCRIRALCWSRRE WRGAGEDTAAECPRPQPQHQHCLAP RFPVRLGTSPGQGWSGRGAGDLAK QYSDRLECCENEVEKVIEEIRCKAIE RGTGNDNYRTTGATIEVFLLPRLK KDRKNLLETRLHITGRELRSKIAETF GLQENYIKIVINKKQLQLGKTLLEE QVAHNVKADGCLN
1735	7232	A	1865	1	513	PRVRNLSREWLCDRHLREKMFSSV AHLARANPFDTPHLQLVHDGLGD LRSSSPGPTGQPRRPRNLAAAVEE QYSCDYGSGRFFILCGLGGIISCGT HTALVPLDLVKCRMKVDPQKYK GIFNGFSVTLKEDGVRGLAKGWAP TFL\GYSMQGLLQVLAFYEVFKVLY
1736	7233	A	1866	2	1296	ALCEPQPFQSGGCVAILGRKMFSS VAHLARANPFNTPHLQLVHDGLGD LRSSSPGPTGKPRRPSQ/HMAAAPV EEQYSCDYGSGRFFILCGLGGIISCG THTALVPLDLVKCRMQVDPQKY KGIFNGFSVTLKEDGV\RLAKGW APTFLGYSMQGLCKFGFYEVFKSL YSNMLGE\ENTYL*RTSLYLAASAS\ AEFFADIALAPMEAAKVRIQTQPIG

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						YANT*EGISFPKCIKEEGLTSILQGG LLPLWMRQIPYTMN*SSPCLERTV A\LYKFV\VPK\PRRE*FKRQSRLVVT IW*QVTIARVFCANCFSPLEFLG*P VLD*GKKVSQCFLWVLQRD LGFK\ GV\WKGLFA\RIIMIGTLT\ALQWFI YYSVKGYFR\LRPPPP\EMQES\LK KKLGVNSVVRIKANCGNLNLLVDPV FEESAKGTFIYLTV
1737	7234	A	1867	127	433	RPLESWIGLVRCNICRSPIAEAVFRK LVTQDNISKNNWRVDSAATSGYEIG NPPDYRGQSCMKRHGIPMSHVARQ DLNRKSNRVKTCKAKIELLSGYDP QKQL
1738	7235	A	1868	2	535	
1739	7236	A	1869	551	1299	PADPPRPSYYRHRTPPQAHWSRLRR SRLRRRGSHTRCPVGVGAGLRRRA GARLAVRLRASACGTPRCLGASAR GKMAEQATKSVLFVCLGNICRSPIA EAVFRKLVTQDNISKNNWEGRQRG NFRWVIDSGAVSDWNVGRSPDPRA VSCLRNHGIHTAHKARQITKEVFP TFDYILCMDESNLARDLNRKSNRVK TCKS*KFELPWEL*SPQKQLIED\PY YGE*LWTLETVYQQ\CVR\CCRAFL\ EKAH
1740	7237	A	1870	85	563	SSFLDIVHVCNTPNVKKMVSGSSHK VIEQDLSIGDHPVTPVQSVYCKRS PKIPKIFVKVSKTNSETQIYLGWQV KIGFPNF*NPVAGILDRTKYRIFP*AP GIHKLKGYPREI*ASYV*KSPSTSMS TAALFPIAKPRAGP*MPTKGSWVK\ KIWYGQK
1741	7238	C	1871	604	804	MKRLRHLRXINNLAKITQPLSKTAL NLSPTQGGSKSRAILEFQLSRGPVN PTLNWPSLNPFREPE*
1742	7239	A	1872	64	73	AFL*RWGSPCCPRAGLK/PP*P/PSI CPRPPKPAGITRREPPGQAYFLII*F PSI*L
1743	7240	A	1873	47	225	NSHHVRGRPRCADSSSPSGDRGQPE AQPAPDSSAPEHAQEPGRAAVKRP DL*SHMTRRP
1744	7241	C	1874	101	232	MTMITPSSKLTLTGKNKSWSTAVA AALELVDPGCRNSARGF*
1745	7242	A	1875	66	723	AIIILLSSSEGLWSSDQHRLVGVDSD PPQGLCCHFSAMATSEQSICQARA SVMVYDDTSKKWVPIKPG\QQGFSR INIYHNTASNTFRVVGKFDQDQV VINYSIVKGMKYNQATPPFPQWRD ARQVYGLNFASKEEATTFSNAMLF ALNIMNSQEGGPSSQRQVQNGPSPD EMDIQRRQVMEQHQQQRQEFLERR TSATGPILPPGHPSSAASAPVSCSGP SPPPPPPVPPPTGA\TPPPPPPL\PAG GAQGSSHDES/SPCSGLAACH*LGPS LRRVPNGPEDASGGSSPSGTSKSDA NRASSGGGGGGLMEEMNKLLAKR

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						RKAASQSDKPAEKKEDSQMEDPS TSPSPGTRAASQPPNSSK\AGRKPW DRNNPLRNPLSSNLVRNPLLAKGPR KLRAPFSQQPHSRMKPAGS\VSDMA \LDAFDLD\RMKQEI*KEVVRELHK GERKEIID\AIRQEA*SGISRKKNLGH RAHPPTRTSFICSQRPRLM
1746	7243	A	1876	1	668	GERGVARHDRPRGTLREYKVVGR LPTPK\CHTPPL\YR\MRIFAP*SMSSL SPRF\WYFVSQKKDEESLQWRFSY CAQVFEKSP\LRVK\NFGIWLRYDS RSG\THNMYREYRDLDHPQAPVHP SCLTRDNGVAPAPAA/HEAHFHFRI ERLEEIAGQQDCRRPGCSKQFPRIS RFKFPAAAPGSLRRQDKPRF\TTKRP KTFKLVQGPSSGVCQNKQTQETPR
1747	7244	A	1877	1	1059	
1748	7245	A	1878	87	260	
1749	7246	A	1879	1	1254	
1750	7247	A	1880	160	615	PSLNTYVTSPLENFSARYRNHSND LTCVHTELQNKTKLTVLEGDILDEP FLKRACQ\DVSVNHTACHIDVFGVT HRESIMNVNVKGRVAWGGDKARW GNEDQKEGQEGKRSLSIEHLLCSGP SDFADHYQLGELKAAIFS FIDEKTRT EQ
1751	7248	A	1881	53	1338	CPLQGHPRVTLES DLLPSIFCFLVSD SCYFGLATMGWSCLVTGAGLLGQ RIVRLLVEEKELKEIRALDKAFRPEL REEFSKLQ\NK\TKLTVLEGDILDEPF LKESLARDRLRSIIHTACFHLMSFGV \THREFF\MNVQC*KVPSSC*EACVQ ASVPVFIYTSSIEVAGPNSYKEIIQNG HEEEPLEN\TWPAPYPRSKKLA\KKA VLAANGWNLKNGGALYTALRPM YIYGEGRFLSVSINEALNNGILSS VGKFST\NPNVYVGNVAWGHILAL RALQDPKKAPSIRGQFYISDDTPH QSYDNLNYTLASKEFGPPPLDSRWAS FPLSLMYWIGFLLGNR*GFLLRPIY TYRPPFNRISSHCNS*ALFHLLFIKE GFSEILGVLRLPLTAGGGKAKAGKR VGSWVWVPFVDPAQGRNLEVPRIQ
1752	7249	A	1882	3	575	HSLFGTSEVINKLLVPDAMGHFTEE D\KATITSLWGK\NVNVEDAGGE\TP GKGSLVVYP\WTQRF\DSFGNLSS ASA\MGKPPKSKAHGKKVLTFLGT MPTKHLE*FSRGTFCPSLK*TCTC*Q ACMWDPGGTFKLPGENVAGLTVFG QSHFRQKNFTPEGARFFLGRKMGD LELASALVPSRLPLKPLGP
1753	7250	A	1883	1	960	GRPAPEDGGPLSLPNAAMARGPKK HLKRVAAPKHWM LDKLTGVFAPR PSTGPHKLARECLPFIIFLRNRLKYA LTS\DEVKKICMQRFIK\DGQVR\TD ITYPAGFMDV\SIDKDGREFSVL/Y LIDTQGVRFCL*HRJTP*GRAKVQSC AKMRKILLWAPKGIPSSWVTHDAR

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						NHPATPDPPSSKVN*YHFRLDLETG KDYLISSKFDTW*PCVMVTGGAN LGRNWVLITN\RRHPGIF*PLVHVK DANGNKLLATSDFSNIFWLLGKGN KPWISL\PRGKGIPPHHLLLEERDKRL AAKQSSWVKWGPWVTWSDLLVP
1754	7251	A	1884	1	1218	FFQNSARGAGAGWQLPWTRFVWT SGLLEINE\TLVIQQRGVRIYDGEEKI KFDAGTLLLSTHRLIWRDQKNHEC CMAILLSQ\VFIEEQ\AAGIGKSAKI VVHL\HPAPPNKEPGPFQSSKNSYI KLSFKEHGQIEFYRRLSEEMTQRRW ENMPVVSQSLQTNRGPPQGRIRAVGI VGTERKLEEKRKETDKNISEAFEDL SKLMIKAKEMVELSKSIANKIKDKQ GDITEDETIRFKSYL\LSMGIANPVT RETYGSGTQYHMQ\LAQQL\AWNIA RVPLEERGGIMSLTEVYCLVNRARG MELLSPEDLVNACKMLEALKPLR LRVFDSGVMVIELQSHKEEMVAS ALETVSEMGSLTS*EFAKLVGMSVL LAKERLLLAEKMGHLCRDDSV EGL RFYPNLFMTQS
1755	7252	C	1885	179	361	MPKVCVFNFLKTSSERDLFALMN TVGKKHSIMSEKGRSKKFLHLIDSK KNEDPHLDGTL*
1756	7253	A	1886	2	913	RRLLLFGWARSGAVSLGSAGVSSS GFLTAPHSRRLTAAAAAAGGAWRF EAERHRGWGAEEEQPEGGA\CPG TERPCAMAYAYLFKYIIGDTGGGR\ SCLLLQFTDKRFQPSAMTLTNGVEF GARMITIDGKQIKLQIWD\TAGQES\ FRSITR\SY\YRGAAGALLVYDITR\ DTSTHLTTWLEDARQHSFHQGS LCLLGNKSDLAESRKE/VSKKRKEGE SFLQPRNHGLHLPWKTSCNCFPM* KEAFINTSKRNFIEKIQ\EGVFDINNE A\NGIKIGP\QHAATNATHAG\NQQG QQAGGGCC
1757	7254	A	1893	138	426	FIHSHCCIVFRLFIHFSLHPKVIHSPIN SLLRIFQF*AIMNSTV*NILIHVFW*V YTFPF\GINPKKGIARL*GVYIFSISIY CQTVFQSDCKKAPF
1758	7255	A	1894	45	1057	FLVFLVETGFHHVAQAVLELLASSD PPALAPPKCWDYRCELLRLAEFCFL RTEFWYLLFFFFWRRSLALSPRLEC SGANL\THCNLR/LPGFKQFCSLSLS SWDYRCMPPHLATFFVF/SVETGFH RVAQASLELLSSGSLPALA/FPKCW DYRAKATV/WSPGVSSFILGL*TS* FHSLEPYLHAWKTTS\HPTKEALT W/VSHTAKTKHLWILVSILMEF*VA LIS/SFFLPGGK*T*VTAPQCPSLGQ DTLS*FLHAACTRSVPYPGLA/CGPS LWLTRVLLLPTPP*QQHNP/DTLEKT SFPGPHWIL*/TPQPSLSETPAPKVPP FPAFGSIPTHEEPGLP
1759	7256	A	1895	2	289	

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1760	7257	A	1896	1	397	
1761	7258	A	1897	1	410	STMISPVLLIFSSFLCHVAIAGRTCPK PDDLPFSTVVPLKTFYEPGEEITYSC KPGYVSRGGM\RKFCPLTGLWPIN TLKCTPRVCPFAGNLRKMGAVRLIT DFLNYSPTRFSSLLTWGFILEWAL DS\AKCIEGG
1762	7259	A	1898	19	1215	CQCDSSSTMIFSRCSLLFSSFLCHVAI AGRTCPKPDDLPFSTVVPLKTFYEP G\EEITYSCKPGYVSRGGIEESLSCPL VTGTVGPFNTSGNVTPRVCPF\AGIFR KMGGRTLITTF*NYPNTDPVFSLLTL GF*FWNGALDFWPSCTGGKGKWS P\ELPGLVAPIN\CPPPSIP/TGFATLH VLLRPFRLGNNSPPIGDTAVFECLA HNMAMFG\NDTIT\CTTHGKLDLNY PECRGSKMPPFPHQDPDNGIW*TYP CQNPNTLFTRVKAPHLGLPHDGIFS GMGPRKEIEC*PQTWKGKPSWPLA PSW*KPSLVKGTVPVKRPTVV\YPQ GERVKDSREKFKEWECLHG**KFLS FCKNKEKKCSYTEDAQCIDGTIEVP KCFK\EHSSLAFWKT\DASDVKPC
1763	7260	A	1899	58	446	
1764	7261	A	1900	1	954	MGEVSGTSDCTDDQCRQVKKALEG GKAARGHRSKIKIRFFRPGGLGPGP AITAVAGMPRVYIGRLSYQAREHA V\ERLLNGHAKILEVDLKNYGFVE FDDLRLDADDAVYELNGKDLGGERV IVEHARGPRRDGSYSGRSGYGYR RSGRDKYGPPTRTEDRLIVEN\LTR CSWQDLKDYMRQAGEVTYADAHK GRQKMKGVIEFVSYSMDMKRALEKL DGTEVNGRKIRLVEDKPGSRRRRSY SRSR\SHSRSRSRSRHSRKSRSRSGSS KSSHSKSRSRSRSGSRSRSKSRSRSQ SRSRSKKEKSRSPSKDKSRSRSHSA\ GKSRSKSKDQAE\EFQNDNV\GK PKSRSPSRHKS\SKSRSRSQERRVEE GRKRGSF*QGQ/EAQEKSLRQSRSR\ SRSKAGSR*PVDRSRSKSKDKRKS KRSREESR\SRSRSRSKSERSRKRGS KRDSKAS\SCKKKKKEDTDRSQSR PSRSV\SKEREHA/RSLESSQREGRG ESENAGTNQEDPGPGPRSM\SKSKP NLPIRMHRSKIKSQASKTPISGPMR SR\ASRSP\SRSRSKSRSRSQSRSR KKEKSRSPSKDKSLQPQP
1765	7262	A	1901	3	180	
1766	7263	A	1902	227	440	GMHNVCYVAVNE*FCGFIIR*SLAE RRQIS*EFQLFKFTLCLELILARRAC RESMA\$PVAGSWSHFPEREF
1767	7264	A	1903	2	438	HEELDTSERKIEFDSASGTY\TYLNI GDAHFEEPQSLWNVADLVHQSPPE EKAPLDLSCPQNLFTPK\QEIQWIRI GA\NVSNFTFAP\STIIFHLGHA\AM LGLMYVYWTQLNMF\QTLKYLAIL GSVTFLAGNRMLAQQAVKRTAH

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1768	7265	A	1904	1	1660	
1769	7266	A	1905	156	2369	PVLKTHPGPQSLPRVPGVPCGGLLE PLSRAEVSPRFLRRDLLGGMAPP SSTVFLALTIISTWALTPTHTLTK HDVERLKASLDRPFTNLESAFYISV GLSSLGAQVPDAKKACTYIRSNLDP SNVDSLIFYAQAISQGLSGCEISISN ETKDLLLA/VSE/DSSVYPRSYHAS WQL*SGLLGLSLWAVPKESTQVAL NWL VFKQ GKETVLA/TVQALQTAS HLSQQADLR SIVEEIEDLVARLDEL GGLYLQ\FEEGLETTALFVAATYKA /LMDH/VGTE\PSIKE/DQVIQLMNAI FSKKNFESLSEAFSVAASGAAVLS HNRYHVPVVVVPEGSASDTHEQAI LRLQVTNVLSQLTQATVKLEHAK SVASRATVLQKTSFTP\VGIVFELNF MNVKFSGG*CDFLVEVEGDNRYIS\ NTVELRVQDPPTVEGITNVDLSTV\ DKDQSIAP\QTTRVTYPAKAKGTFH SAGQATRNFGVLSSW*DVNTGVAE LTPHQTFVRLHNQKTGPGSGCLFAE PGQQGTCYKFELDTSERKGLNLTSR SGTYTLYLIIG*CQL*RTQILWKCGL MWVIKFP*GKEASFDCLCSQEPFSL PKQGNFRHLFPGRP*GRRAPPWCP NTFTAPESFFGPLL/LCFLRLLWIRD WVPKCLPTFTFCFLSTIIFHPWDM LAYAGTSMYVY*TQAQPCSQTLEVP WPILGQCDRFLAGQSGMLAPARQV KRIAAEQSSRLAKYRTLRTAH
1770	7267	A	1906	37	404	PQLSRCRSECMYVNPTVMTSMGQ ATWSDPHKAKTMLNRIPLGKFAGE SGGSPASVVPAPVPCALGRGGRER WAAASFLYAPDPRPAHEVEHVVN AILFLLSDRSGMTTGSTLPVEGGFW AC
1771	7268	A	1907	271	1086	YTQCPGIEPVCVDLGDWEATERAL GSVGPVDLLVNNAVALLOPFLEV TKEAFDR*ACEGGTSGRGCPGGRS SPNL*PGSVPRPLDPLRVNLRAVIQV SQIVARGLIARGVPTGPS*NVSSQC FPAGQ*TNHSVLLLPKGVPLDMLD QG*WAL\ELGPHKLSRCRSGVNAIV NPHSGG*RSMGPGPPWSDPHKIAKI MLNRIPLGKFAGESEVEHVVNAIL FLLSDRSGMTTGSTLPVEGGFWAW LSSLHTPQAPWACFILTPNPSNKT
1772	7269	A	1908	2	305	ARESGSLVAPRSRPPWEHGLPGEHS *DAPRPHKSPTLPWLPHLHLSKEAL DTHQRSQHEECMPLYKFTPTSEKR PQLMLPLPEQQCEQLCRFGSTPVTW A
1773	7270	A	1909	2	529	GTVAACGACYWLLGLMAVRASFE NNCEIGCFAKLTNTYCLVAIGGSEN FYSVFEGELSDTIPVVHASIAGCRIIG RMCVG\TEEILADV LKVEVFRQTVA DQVLVGSYCVFSNQGLVHPKTSIE

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						DQDELSSLLQVPLVAGTVNVRGSEVI AAGMVVNDWCAFCGLDTTSTELSV VE
1774	7271	A	1910	18	889	GVQGTVAACGACYWLLGLMAVRA SFENN\CEIGCFAKLTNTYCLVAIGG SENFYSVFEGELSDTIPVVHASIAG CRNIGRMCVGN\NRHGLL\VPNNTTD Q\ELAQHISATGLPRHSGRFRAGWKE RFLSLWGNFFNHLAIDYVGLGSNQ D\LDKGRQEEISGQMLFKGWVFRQ TV\ADQVLVES\YCVFSNPGRWVP SPRPFQ*RPRLNELSSISFKVPL\VAGT C*TKGSEVICLLGMGGEMNWCA\FC GPGTPNPAQSCQVVEECLQS*NEAP ALAPIANRACGNSL\IDSLT
1775	7272	A	1911	132	440	
1776	7273	A	1912	149	389	FSWV*REIFSFLISLIFIYETFSKLIKIF QDHPLQKTYN\YNVLMV\PKPQGGLP NTALLSLVLMAGTFFFAMMLRKFK NSS
1777	7274	A	1913	3	153	
1778	7275	A	1914	94	593	LVVFSSPSQSWERTECLGFLQIFQD HPLQKTYN\YNVLMV\PKPQGGLPNT ALLSLVLMAGTFFFAMMLRKFKNS SYFPGKLRRVIGDFGV\PICILIMVLV DFFIQDTYTQKLSVPDGF\KVSNSA RGWV\HPLGLRSEFPIWMMFASAL PALLVFILIFLESQITT
1779	7276	A	1915	115	3015	TTGHSGPRHGGGAAGGCSLASAVLP PGGSGDLVDSYLRWGWS\PSQPS LSGHFPQDDYEDMMEENLEQEEYE DPDIPESQMEEPA\AHDTEATATDYH TTSHPGTHKVYVELQELVID\ERIPD LQWMEAAPLR\QLDENLGENGAW GRPHLSHLTFWSLLELRRVFTKGT LLDLQETSLAGVANQLLDRFIFEDQI RPQDREELLRALLLK\HSHAGELEAL GGVKPAVLTRSGDPSQPLLPQHSSL ETQLFCEQGDGGTEGHSPSGILEKSP PDSEATLVLVGRADFLEQPV\LGFR LQEA\AELEAVELPVPIRFLVLLGPE APHIDYTQLGRAAA\TLMSEVFRID AYMAQSRGELLHSLEGFLDCSLVLP PTDAPSEQALLSLVPVQRELLRRRY QSSPAKPDSSFYKGLDLNGGPDPL QQTGQLFGGLVRDIRRRYPY\LSDI TDAFSPQVLA\AVIFIYFAALSPAITF GGLLGEKTRNQMGVSELLISTAVQ GILFALLGAQPLL\VGFGSGLLVFEE AFFSFCETNGL\EYIVGRVWIGFWLI LLVVLVVALRGVASLVRFIS\RYTQ EIFSFLISLIFIYETFSKLIKIFQDHPL QKTYN\YNVLMV\PKPQGGLPNTALL SLVLMAGTFFFAMMLRKFKNSSYF PGKLRRVIGDFGV\PISILIMVLV\DF IQDTYTQKTSQVPDGF\KVSNSARG WV\HPLGLRSEFPIWMMFASAL\PC LLVFILIFLESQITTLIVSKPERKMKV

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						GSGFHLDLLLVVGMGGVAALFGMP WLSATTVRSVTHANALTMGKAST PGAA\AQIQEVK\EQRISGLLVAVLV GLSILMEPILSRIPALVFGIFYMGV TSLSGIQLFDRILLFKPPKYHPDVP YVKRVKTWRMHLFTGIQIICLAVL WVVKSTPASLALPFVLILTVPLRRV LLPLIFRNVELQCLDADDAKATFDE EEGRDEYDEVAMPV
1780	7277	C	1916	20	202	MAAIKYLGISAILYYKYKCPRGQGN QPEELGTGSILCGNFSLGMLFPVQM YTVKKAYRAV*
1781	7278	A	1917	1	493	
1782	7279	A	1918	214	612	
1783	7280	A	1919	287	847	SDRPTMAPGVARGPTPYWRLRLG GAALLLLLIPVAAAQEPGGAACSQN TNKTCEECLKNVSLWCNTNKA CLDYPDTSVLPPASLCKLSSARWGVC WVNFDAIITMSVVGGLLLGIA\NC CCCCRRKRSRKPDRSEEKAMR\ER EDR\WILQEERRAEMNTRHDEIRKK\ YGLFKEENPYARFENN
1784	7281	A	1920	61	515	
1785	7282	A	1921	1	2175	
1786	7283	A	1922	3159	3441	
1787	7284	A	1923	36	387	
1788	7285	A	1924	64	408	
1789	7286	A	1925	1	10514	
1790	7287	A	1926	64	601	VNNILGLGHTFWALLASPKMEHKE VVLLLLLLFLKSGQGEPLDDYVNTQ GPSLFSVTKKQLGAGSREECAAKCE EDKEFPAGAF\QYHSKEQQCVIMA ENRKSS\INRVRDAVLFGKGKCLF RVQDLGMERTTEGRCPKQKMASPC QKWEFHFPADLGQTFPFIFVFIYCK VVPLCL
1791	7288	A	1927	173	491	AGEARWESQSAHLKPEFGGPTGPN NAQSPPREADAQVWREPPGPASK APHSPVGYSSPGHESHLPGDDPA KDGSCPP\PFPLGIEAPVPGPRKRIR TCCCMN
1792	7289	A	1928	1	735	
1793	7290	B	1929	1	1026	MRARRLPWALTVAELGWDQTGGG DQTSPGGNDRMSMEAECSTTVSP LSCSIPTGCGQTREEVSARATPPPSL GASLLQTLTPDTHCTGVSATIMSML VVFLLLWPFSSSTLAKHKRIHTGE KPYKCEECKAFSRSTLAKHKRIH TGEKPYKCECKAFRQSSTLTKH KJIHTEKPYKCECDKAFKRLSTL AKHKIHHAGEKLYKCEECKAFNRS SNLTIHKFIHTGEKPYKCEECKAF NWSSSLTKHKRIHTREKPFKCECK KAFIWSSTLTRHKRIHTGEKPYKCE ECKKAFSRSTLTKHKTIHTGEKPY KCECKGKLLSTPQPLLNIK*
1794	7291	A	1930	1	2832	

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1795	7292	A	1931	98	3867	PAGIGRATAKMPGTPGSLEMGLLTF RDVAIEFSPEEWQCLDTAQQNL YRNVMLENYRNLAFLGIALSKPDLITY LEQGKEPWNMKQHEMVDEPTGICP HFPQDFWPEQSMEDSFQKVLLRKY EKCGHENLQLRKGCKSVDECKVHK EGYNKLNQCLTTAQSKVFQCGKYL KVIFYKFLNSNRHTIRHTGKKCFKCK KCVKSFCIRLHK\TOHKCVYITEKSC KCKECEKTLW\SSSTLTNHKEIHTE DPYKCEEKGKAFKQLSTLTTHKIIC AKEKIYKCEEKGKAF\WSSSTLTRHK RIHTGEKPYKCEEKGKAFSHSSSTLA KHKRIHTGEKPYKCEEKGKAFSHSS ALAKHKRIHTGEKPYKCKEKGKAF SNSSTLANHKITHTEKPYKCKECD KTFKRLSTLT\KHKIIHAGEKLYKCE ECGKAFNRSSNLTIHKFIHTGEKPY KCEEKGKAFNWSSSLTKHKRFHTR EKPFKCKEKGKGF\WSSSTLTRHKRI HTGEKPYKCEEKGKAFRQSSTLT\KH KIIHTGEKPYKFEEKGKAFRQSLTLN KHKIIHSREKPYKCKEKGKAFKQFS TLTTHKIIHAGKKLYKCEEKGKAFN HSSSLSTHKIIHTGEKSYKCEEKGKAF FLWSSSTLRRHKRIHTGEKPYKCE\EC GKAFSHSS\ALAKHKRIHTGEKPY KCKEKGKAFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLT\KHKIIH AGEKLYKCEEKGKAFNRSSNLTIHK FIHTGEKPYKCEEKGKAFNWSSSLT KHKRIHTREKPFKCKEKGKAFIWSS TLTRHKRIHTGEKPYKCEEKGKAFS RSSTLT\KHKTIHTGEKPYKCKEKGK AFKHSSALAKHKIIHAGEKLYKCEE CGKAFNQSSNLTTHKIIHTKEKPSKS EEDKAFIWSSSTLTEHKRIHTREK PYKCEEKGKAFSQPSHLTTHKRMHT GEKPYKCEEKGKAFSQSSTLTTHKII HTGEKPYKCEEKGKAFRSSTLTTEH KIIHTGEKPYKCEEKGKAFSQSSTLT RHTRMHTGEKPYKCEEKGKAFNR SKLTTHKIIHTGEKPYKCEEKGKAFI SSSTLNGHKRIHTREKPYKCEGCG\K AFSQSFN/TLTGHKRLHTGEKPYK CGEKGKAFKESALT\KHKIIHTGEK PYKCEKCKAFNQSSILT\NHKKIHT ITPKIHTREKPYKYKECGKSFNRSS FTKHKVIHTGVKLYKCEEKGKSF WSSALTRHKKIHTGQQPYKQEKFG KAFNQFSHLTTR
1796	7293	A	1932	590	891	
1797	7294	A	1933	1	1527	
1798	7295	A	1934	13	1668	PESKMAGSRHRGLRARVRPLFCAL LLSLGRFVRGDGVGGDPAVALPHR RFEYKYSFL\GPHLVQSDGTVPFWA HAG\IAISSDQIRVAPSLKSQRGSV WTKTK\AAFENWEVEVTFRTVTRG

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						RIGADGLAIWYAENQGLEGPVFGS ADLWNGVGIFDSDNDGKKNNPA IVIIIGNNGQIHVDHQNDSQALAS CQRDFRNKPYPVRAKITYVQNTLA TVMINNGVFTPDKNDYEFCAKVEN MIIPAQGYFGISAATGGLADDHDVL SFLTFQLTEPGKEPPTPDKEISEKEK EKYQEEFEHFQQLDCKKEEFQKG HPDLAQWQPAEEIFESVRDRELRO VFEGQNRHLEIKQLNRQLDMILDE QRRYVSSLTEEISKRGAGMPGQHG QITQQLDTPVKTQHEILRQVNEM KNSMSVEPVLVSGMQHPGSIAGGV YGTTQHFIDIKHEHLHVKR\IDIDL VQRNMPASNEKPKCELPFPSCSLST VHFQ\FVQVQTVLFIGYIMYRSQQ EAAAKKILLTTIFLCTSSICVQNDVV LREFKYLNCFIV
1799	7296	C	1935	238	360	MGGLGLSLRSLSSASPAXFRPAHAP VGAAGLGPASPQGPL*
1800	7297	A	1936	1	1656	
1801	7298	A	1937	83	260	
1802	7299	A	1938	1	678	
1803	7300	A	1939	1	1097	
1804	7301	A	1940	1	1706	MQLLLAECMGQSGPPGAVCHCQR VWQARAVRRSKRPVPSTTQGLKSV GAWRGSGRQLHLQPQYRIHWVKP AGLLSLVGTMENICVWPSDCKYTN RHSVSSRLLDSLKRDIYAGKPQPI KSERRNPPSYAMAAAQLRDSEETG GSEFVFAEKTLRKCVKCPQVELENV AFAKDAEESRDAQRLGHWWPCIME TLNASGTFAIRLLKILCQDNPSHNV FCSPVSISSALAMVLLGAKGNTATQ MAQALSLNTEEDIHRAFQSLTEVN KAGTQYLLRTANRLFGEKTCQFLST FKESCLQFYHAELKELSFIRAAEESR KHINTWV\SKKTEGKIEELLPGSSID AETRLVLVNAIYFKGKWNEPFDDET YTREMPFKINQEEQRPVQMMYQE ATFKLAHVGGGLRAQLE\LPYARK ELSLVLLPDDGVELSTVEKSLTFE KLTAWTKPDCMKSTEVEVLLPKFK LQEDYDMESVLRHLGIVDAFQQGK ADLSAMSAERDLCLSKFVHKSFVE VNEEGTEAAAASSLWVVAECCME SGPRFCADHPFLFFIRHTRANSILFC GRFSSP
1805	7302	A	1941	3	428	ETLERIKNNDPKLEEVNLLNNIRKIPI TLKAYAEALKENSIVKFKSIVGTRS NDPVAYALAEMLKENKELKTLNVE SNFISGAGILRPGEALPYNTYLVEM RSDNQSQPPGKNVEMEIVSMLAEKN ATLLRVR*HFSQQDAR
1806	7303	A	1942	1	1258	ALARPLPAGAPRPPASICPPAPVP QPASAPAPQLCVRVLLSTEIQETQTS SSTMSYRRELEKYRDLDEDEILGAL TEEELRTLENELDELDPDALLPAG

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						LRQKDQTTKAPTGPFFKREELLDHLE KQAKEFKDREDLVPYTGEKRGKV WVPKQKPLDPVLESVTLEPELEEAL ANASDAELCDIAAILGMHTLMSNQ QYYQALSSSSIMNKEGLNSVIKPTQ YKVPDPDEPNSTDVEETLERIKNND PKLEEVNLLNIRNIPIPTLKAYAEAL KENSIVKKFSIVGTRSGDGVAYAL AEMKENKVLKTLNVESNFISGAWI LRLVEALPYNTSLVEMKIDNQSQPL GNKVEMEIVSMVEKDPHHFLKFGL PPYPSKEPRLR\ASTAMMNTIALVR EIRRLAAPDLGPSFPKCRSGV
1807	7304	A	1943	2	382	EIAHQIIEQQMG/EG*NFVAIESVV*K IVTEQQTGQKIQIVTALDHNTQGKQ FILTNHDGSTPSKVILARQDSTPGK\ VFLTTPDAAGVNQLFFTTPLDSAQ HLQDVIMGAVTCEGCKGFFKRSIRK N
1808	7305	A	1944	240	454	
1809	7306	A	1945	1	1851	
1810	7307	A	1946	128	512	TAPLAAGRPPGDALGPRPLAVGVK GTPWPPPPTRSLVSPPSVSYYRFCAL LTPASGADATVPRLPLVDWGALRE ERLKKADGMWDRDSRRRELSVFG ACALATGRSGERRS*RSQGGVEGSE GRAAAL
1811	7308	A	1947	1	705	
1812	7309	A	1948	124	1583	IMATIEEIAHQIIEQQMGIEIVTEQQT GQKIQIVTALDHNTQGKQFILTNHD GSTPSKVILARQDSTPGKVFLTTPD AAGVNQLFFTTPLDSAQHLQLLTD NSPDQGPKNVFDLCVVCGDKASGR HYGAVTCEGCKGFFKRSIRKNLVYS CRGSKD\CIINKHHRNRCQYCRLQR CIAFGMKQDSVQCERKPIEVSREKS SNCAASTEKIYIRKDLRSPLTATPTF VTDSESTRSTGLLDSGMFMNIHPSG VKTESAVLMTSDKAESCQGDSTL ANVVTSLANLGKTKDLSQNSNEMS MIESLSNDDTSLCEFQEMQTNGDVS RAFDTLAKALNPGESTACQSSVAG MEGSVHLITGDSSINYTEKEGPLLSD SHVAFRLTMPSPMPEYLVNHYIGES ASRLFLSMHWALSIPSFQALG\QEK QP*SLVKAYWNEFLTGLAQCWQV MNVATILATFVNCLHNSLQQDAKV IAALIHFTTRAITDL
1813	7310	A	1949	6	2028	KILRTLTPQKYPRTESSLRRESRSHM PTAFLNLSCRSAPQSTRGSRGTVAS APDAGGSRAQKRREIMATIEEIAHPI IEQQMGIEIVTEQQTGQKIQIVTALD HKTQGKQVILTNHDGSTPSKVILAR QDSTPGKVFLTTPDAAGVNQLFFTT PDLSAQHLQLLTDNSPDQGPKNVF DLCVVCGDKASGRHYGAVTCEGC KGFFKRSIRKNLVYSCRGSKDCIIN KHHRNRCKYCRLQRCIAFGMRQDS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VQCERNPLEVSREKSSNCAASTEKI YIRKDLRSPLTATPTFVTDSESTRST GLLDSGMFMNIHPSGVKTESAVLM TSDKAESCQGDSTLANVVTSLANL GKTKDLSQNSNEMSMIESLSNDDTS LCEFQEMQTNQDVSRFDLAKAL NPGESTACQSSVAGMEGSVHLITGD SSINYTD\KEGPLLSDSHVAFRLTMP SPMPEYLVNHYIGESASRLLFLSMH WALSIPSFQSGRGKEN\SISLVESLLG IELFTLGLAQCWQVMNVATILA\TF VNCLHNSLQQDKMSTDRRKLLME HIFKLQEFCSNMVKLCIDGYDYAYL KAIVLFSPDHPSLENMEQIEKFQEK AYVEFQDYITKTYPDD\TYRLSRLLL RLPALRLDGCTITEELFFKGLIGNIR IDSVIP\HILKMEPADYNSPIIGHSI
1814	7311	C	1950	65	286	MDYCNTFLPSNPETVFGDIMPRVNK PDLGTALSRGFTHEINKTYLSHLKL GSQKTHFWFIISFYAHLTLIIYP*
1815	7312	A	1951	15	82	
1816	7313	A	1952	2	1934	CVQAATSLSVGICPLPGPGSPPPWY PGVSVNVWIFKQIDDEGLRLLINK EVLSGVVVISKDSVQHQGVSLTME GTVNLQLSAKSVGVFEAFYNSVKA QLRRSVQATGLEERPALPERLQQEG SEEAGGLSGAEAALPRRARGSPIQII NSTIEMVKPGKFPSPGKTEIPFEFPLH LKGKVLVYETYHGVFVNIQYTLRC DMKRSLLAKDLTKTCEFIVHSAPQK GKFTSPVDFTITPETLQNVKEHS HQ TEAGQQRAFQRFRSALRGGRLTAR ADNSSSSNVAQGSQKSGHPCSRPSS VLPQQRQVCRVKRALLPKFLL/RRT SQLNKLCHHAATNGRAGGGELGSR HQKRGAAAGARGDPGQQSRP*P*L* KTRGRRGSKSKSVAVP*Q*PRV*GK VCR\SYARDATEIQNIQIADGDVCR GLSVPIYMVFRLFTCPTLETTNFKV GKWHSPSPHGMGRAAQRQGLL WVTELRTCPSVPQCQGLPQAIQLR ACCPAAQQNLVKELLCRTGDTPT GSPGACGTSTVTWNTQTHISVDM GRPQPQVGTDSKAPSTAELPQCGA QHRVPSAHTMPFPPLLTLGKEMVL VCRQDQQGSPISAEESVEKESCLLK EFEVNIVVLLHPDHLITENFPLKLCR I
1817	7314	A	1953	262	1274	ATAGREGKGRGPQPSGEAPLVSLGS RAATSGGCCGELEMTGLDIKSKR ANKVYHAGEVLSGVVVISKDSVQ HQGVSLTMEGTVNLQLSAKSVGVF EAFYNSVKPIQIINSTIEMVKPGKFPS GKTEIPFEFPLHLKGKVLVYETYHG VFVNIQYTLRC\DMKRSLLAKDLT KTCEFIVHSAPQKGKFTSPVDFTIT PETLQNVKERALLPKFLLRRTS\QLN KLCHHAATNGRAGGGELGSR\HQK

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						RGAAAGARGDVRVCR\SYARDAPE IQNI\QIADGDVCRGLSVPIYMFPR LFTCPTLETTNFKVEFEVNIVLLHP DHLITENFPLKLCRI
1818	7315	A	1954	2	236	DRCLMLKQGSEAWLTSISIEPPAPPV YQAPCQSCPEPPGAHEPSDSPHHTP VHPPPE\TRTPVLPQRAVPPPRSSM S
1819	7316	A	1955	760	925	HLEYLPTYANSSYS\WPSSVAHTCN PSTLGGRGGRITGGQEFKTSVANIT KPCLY
1820	7317	A	1956	32	487	SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG
1821	7318	A	1957	41	638	APSPRRPWGHFTEEDQGLLSTSLWG KVNVEK CWKEKTPGKGS LVVYP\ WT\QRFFD\SFGNLLSSAF\AHHGQTP KVKAHGK\KVL TFLGRCQQSTLDD LKGTFAQL\SELHCDKLHVDPENFK LLGNVLVTVL\AIHF\GKDFTPGGC RASW\QKMGD*SGQCPVLQIPLSS L\PMMQSFSRIRLLFLQAITNNKSISA KRSP
1822	7319	A	1958	3	227	
1823	7320	C	1959	171	366	MHTPSVEKPSCGSQLFVYIRKFWKK RNLVKVLNMTTSSVTEDVPLYPEW CMLWRYPASRPNVRKP*
1824	7321	C	1960	332	421	MEEKIFSQPGMVAPT CNPSTLGGQG RWIT*
1825	7322	A	1961	322	1145	RFSKSPDSDGAQLVSPSGSRTRQQV ELAATPTQCSTLLSPWASDGTGCHG AAGRSSGRLRPTGALRWVPLHFPS PARGDSQARSLPTRAAASADSSLPG CGRREVCGSRAPAGG/PPLAPAPPA APVPASAAAQPPAPAWAYEQVWA GRGALRSPSASSGEAADD SYGVVA GRWGRPVQDSRLGTAGEGIAGRES WGSVTSWVLGSHMVKFGLVAELGI CETQDWRRGSEGGAGEFGAVAIHC IGTWVADNAVTCPLLNTTQLEIPFG VQFWML
1826	7323	A	1962	30	2814	LPRAKVEGAPRAPSPQDPGVPPRAP SPRSPSPALRALPAPLSRSP\LDPEM ARPRRAREPLL VALLPLAWLAQAG LARAAGSVRLAGGLTLGGLFPVHA RGAAGRACGPLKKEQGVHRLEAM LYALDRVNADPELLPGVRLGARLL DTCSRDTYALEQALS FVQALIRGRG DGDEVGVRCPPGVPPLRPAPPERV VAVVGASASSVSIMVANVLR\FAIP QISYASTAPELSDS\TRYDFFSRVVP DSYQAQA\MVDIVRALGWN\YVSTL ASEGNYGESGVEAFVQISREAGGVC

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						IAQSIKIPREPKPGEFSKIVIRRLMETP NARGIIIFANEDDIRRVLEAARQANL TGHFLWVGSDSWGAKTSPILSLEDV AVGAITILPKRASIDGFDQYFMTRSL ENNRRNIWFAEFWEENFNCKLTSSG TQSDDSTRKCTGEERIGRDSTYEQE GKVQFVIDAVYAIAHALHSMHQAL CPGHTGLCPAMEPTDGRMLLQYIR AVRFNGSAGTPVMFNENGDAPEGRY DIFQYQATNGSASSGGYQAVGWQA ETLRLDVEALQWSGDPHEVPSSLCS LPCGPGERKKMVKGVPCCWCEA CDGYRFQVDEFTCEACPGDMRPTP NHTGCRPTPVVRLSWSSPWAAPPL LAVLGIVATTTVVATFVRYNNTPIV RASGRELSYVLLTGIFLIYAITFLMV AEPGAAVCAARLFLGLGTTLSYSA LLTKTNRIYRIFEQGKRSTVPPFISP TSQLVITFSLTSLQVVGMIAWLGAR PPHSVIDYEEQRTVDPEQARGVLKC DMSDLSLIGCLGYSLLLMTCTVY AIKARGVPETFNEAKPIGFTMYTTCI IWLAFVPIFFGTAQSAEKIYIQTTLT VSLSLASVSLGMLYVPKTYVILFH PEQNVQKRKRSLKATSTVAAPPKG EDAEAHK
1827	7324	C	1963	334	387	MKCYIYIMTLVLLIV*
1828	7325	A	1964	1	489	
1829	7326	A	1965	152	717	VESIEDVGNHRTDHGADMISIHYYE ENAFILDTLAKKQWKGPDDILLGMV YDTDDASFkWVDNSNMTFDKWD VQDDEEDLVDTCAFLHIKTGEWKK GNCEVSSVEGTLCKTAIPYKRKYL DNHILISALVIASVTVILTVLGAIIWFL YKKHSDSRFTTVFLTGPQLPYMEN CVLVVGEENEYPVQFD
1830	7327	A	1966	3	614	LLFFPSAKMALETGPKDLRHLRACL LCSLV/KGTIDQFEYDGCDCYAYL QMKGNR\EMVYDCTSSSFDGIIAM MSPED\SWVSK\WQAKSSNFKP\GV YA\SVVTGRLAPKIR/VRELKSR\G VALQIPGDTANKDLAKMQGCQHLC SPPPCLCIISCSWNLNEQNFQILPTLQ FRLSSTVERAAHHFIILSSLDYRWG GRDLGWVD
1831	7328	A	1967	66	407	
1832	7329	A	1968	2	1272	CPWPESTGQSGVTSSKARPSLAERW AGPAKKKRKGVEHGPAIREAGLM KRLSS/LGDLLTSPEIEVLFTDIKVR THCPKSLPGTETVQIELSSFFLNILG GKKKKQSWEQEGCHLKDFGDLST PVPKDDLNNLIVNPRSVGLANQEL AEVVSRAVSDGYSCVTLGGDHSLAI GTISGHARHCPDLCVVWVDAHADI NTPLTTSSGNLHGQPVSFLLRELQD KVPQLPGFSWIKPCISSASIVYIGLR DVDPPEHFILKNYDIQYFSMRDIDR LGIQKVMERTFDLLIGKRQRPIHLSF

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						DIDAFDPTLAPATGTPVVGGLTYRE GMYIAEEIHNTGQRNTTENFDTSSQ TLTEGLLSALDLVEVNPQLATSEEE AKTTANLAVDVIASSFGQTREGGHI VYDQLPTPSSPDESENQARVRI
1833	7330	A	1969	212	460	
1834	7331	A	1970	1	1223	TVVECLSPAWEHSSGGRWRSIPA SNRAEPLPWRFSVLRLMSLRGSLSR LL\QTRVRSILKKS\HSHVIGAPFS QGQKRKGVEHGPAAREAGLMKRL SSLGCHLKDF/GQDLSFTPVPKDDL YNNLIVNPRSVG\LANQELAEVVS AV/SQDGYSCVTLGGDHSLAIGTISG HARHCPDLCVVWVDAHADINTPLT TSSGNLHGQPVSFLLRELQ\DKVPQ LPGFSWD/IKPCISSARIVYIGLRDVY PPEHFILKGTMDIQYF\SMEEILDR GIQEGHGNGTDFL\LIGKRQRIHLS YDIDAFDPTHAPAHRT\PPVGDITYR EAMYIAEKIHNTGLLSALDLVEVN PQLATSEEEAKTTANLAVDVIGLPS LWVQTREGGAYWSYDPTFPTPSSP DESENQARVRI
1835	7332	C	1971	162	425	MVGPSLHAGXXXVYIPRFLYIRSWL PCIFFSGGVTVGNIQRQLAMGVPEK PIVIESSKPXILESXGRFLEENLXLVD YXKGLSFFLK*
1836	7333	A	1972	89	308	
1837	7334	A	1973	2	454	
1838	7335	A	1974	570	1418	PMPRLHDHFWSCSCAHSARRRGPP RAIAAGLAAGVEMHIVFVSGPSLM AVLSASDADPAPRGRSAVKS GPYP GSPYPNTWHHSLMQKSLVLFVGE VLALVLNLLQIQRNVTLPFEEVIAT FSSAWWVPP\CCGTAPADVGLLYPC IDSHLGEPHKFKERMGOVSMRCIAV FVGINHASAKLDFANNVQLSLTLAA LSLGLWWTFDRSRSGLG\ITIAFL ATL\ITQFLVYNGVYQYTSPDFLYIR SWLPC\IFFSGSVTVGNIGRQLGYG VFLEKPHSD
1839	7336	A	1975	1	287	KFQERGIIQIKYPP/RAFTLSHTHTRH AHIQAPTVTNQTP/DFP/RPRR*ESSS SSEGANSFLKIMT*RQSSSPKEKDV RPATSTTSCSMILLSILFIG
1840	7337	A	1976	1	166	
1841	7338	A	1977	37	448	GGCTCPCSRWQGSPPQAPAGLPPL ASGPAPSASASPQSGGPIPLH/VR*E SSSSSEGANSVCSSRSCSLAETFS*S AHCLE*NLTPSPSFYETPLSVVSLA LVVSSGGRPVLGPCAESPGHRGWV ASPWSSGWSP
1842	7339	A	1978	45	249	
1843	7340	A	1979	77	3801	KGGVFAHDLVPLPFQGTDSPPRAP PGRGVPLPPGALTMNTRD\TPRVAE TSHHLKIFLPKLLLECLPRCPLLPE RLRWNTNEEIASYLITFEKHDEWLS

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						CAPKTRPQNGSILYNRKKVKYRKD GYLWKKRKDGKTTREDHMKLVQ GMECLYGCYVHSSIVPTFHRRCYW LLQNPDIVLVHYLNVPALEDCGKG CSPIFCSISSDRREW LKWSREELLGQ LKPMFHGIKWSCGNGTEEFVVEHL VQQILDTHPTKPA PRTHACLCSGGL GSGSLTHKCSSTKHRIISPKVEPRAL TLTSIPHPHPPEPPPLIAPLPPELPKA HTSPSSSSSSSSSGFAEPLEIRPSPTS RGGSSRGGTAILLLTGLEQRAGGLT PTRHLAPQADPRPSMSLAVVVGTEP SAPPAPPSPAFDPDRFLNSPQRGQTY GGGQGVSPDFPEAAEAHTPCSALEP AAALPQAAARGPPQSVAGGRRG NCFFIQDDDSGEELKGHGAAPPISP PPSPPSPAPLEPSSRVGRGEALFGG PVGASELEPFLSSFPDLMGELISDE APSIPATPQLSPALSTITDFSEWSY PEGGVKVLITGPWTEAAEHYSCVF DHIAVPASLVQPGVLR CYCPAHEV GLVSLQVAGREGPLSASVLF EYRAR RFLSLPSTQLDWLSLDDNQFRMSIL ERLEQMEKRMAEIAAAGQVPCQGP DAPPVQDEGQGPGEARVVVLVES MIPRSTWKGPERLAHGSPFRGMSLL HLAAAQGYARLIETLSQWRSVETG SLDLEQEVDP LNVDHFCTPLMWA CALGHLEAAVLLFRWNRQALSIPDS LGRLPLSVAHSRGHVRLARCLEELQ RQEPSVEPPFALSPPSSSPDTGLSSVS SPSELSDGTF SVTSA YSSAPDGSPPP APLPASEMTMEDMAPGQLSSGVPE APLLLMDYEATNPKGPLSSLPALPP ASDDGAAPEDADSPQAVDVIPVDM ISLAKQIIEATPERIKREDFVGLPEAG ASMRERTGAVGLSETMSWLASYLE NVDHFPSTTPSELPPFERGRLAVPSA PSWAEFLSASTSGKMESDFALLTLS DHEQRELYEAARVIQTAFRKYKGR RLKEQQEVA AAVIQRCYRKYKQLT WIALKFALYKKMTQAAILIQSKFRS YYEQKR FQQSRRAAVLIQQHYRSY RRRPGPPHRTSATLPARNKGSFLTK KQDQAARKIMRFLRRCRHRMRELK QNQELEGLPQPLAT
1844	7341	A	1980	1	4333	MQVQDDGVNLIPIFAKCSRVSRSPP PRLPSQSLRPM PQRYGDVFWKNLN QRPTPTWLEE QHIPMLRATGCSQL GLYPPEQLPPPEMLWRRKKRRPCLE GMQQQGLGGVPARVRAV TYHLED LRRRQSIINDTDSPPRPLRPGVTLP GALTMTNKTDTTEVAENTRPLKIFLP KKLLECLPRCPLPPERLRWNTNEEI ASYLITFEKHDEWLSCAPKTRPQNG SIILYNRKKVKYRKDGYLWKKRKD GKTTREDHMKLVQGM ECLYGCY VHSSIVPTFHRRCYWLLQNPDI VLV

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HYLNVPALDCGKGCSPIFCSISSDR REWLKWSREELLGQLKPMFHGIKW SCGNGTEEFSVEHLVQQILDTHPTK PAPRTHACLCSGGLGSGSLTHKCSS TKHRIISPKVEPRALTLTSIPHAHPPE PPPLIAPLPPELKAHTSPSSSSSSSSSS GFAEPLEIRPSPPTSRGGSSRGGTAIL LLTGLEQRAGGLTPTRHLAPQADPR PSMSLAVVVGTEPSAPPAPPSPAFDP DRFLNSPQRGQTYGGGQGVSPDFPE AEAAHTPCSALEPAAALEPQAAAR GPPQSVAGGRRGNCFFIQDDDSGE ELKGHGAAPPISPPPSPPSPAPLEP SSRVGRGEALFGGPVGASELEPFSL SSFPDLMGELISDEAPSIPAPTPQLSP ALSTITDFSPESWYPEGGVKVLITGP WTEAAEHYSCVFDHIAVPASLVQP GVLRCYCPALPLPYTQKSALLGDLK DHQSDRLAALLSTSVFSPSLYSSIQH VSHEVGLVSLQVAGREGPLSASVLF EYRARRFLSLPSTQLDWLSLDDNQF RMSILERLEQMEKRMAEIAAAGQV PCQGPDAPPVQDEGQGPGEARVV VLVESMIPRSTWKGPRLAHGSPFR GMSLLHLAAQGYARLIETLSQWR SVETGSLDLEQVDPLNVDHFSCTP LMWACALGHLEAAVLLFRWNRQ ALSNPDSLGRPLSVAHSRGHVRLA RCLEELQRQEPSVEPPFALSPPSSSP DTGLSSVSSPSEL\TDGTFSVTAAYS SAPDGSPPPAPLPASEMTMEDMAPG QLSSGGPEAPLLMDYEATNSKGPL SSLPALPPASDDGGGPEDADSPQAV DVIPADMISLAKQIHEATPERIKREDF VGLPEAGASMRERTGAVGLSETMS WLASYLAENVDFPSSTPPSEL\PFER \GRLGLSLTAPSWAEFLSCIPPVGKI GKLIFALLTLASD\QEQRELYEAARVI QTAFRKYKGRRLKEQQEVAAAVIQ RCYRKYKQFALYKKMTQAAILIQS KFRSYEQKRFQQSRRRAAVLIQQH YRSYRRRPGPPHRTSATLPARNKGS FLTKKQDQAARKIMRFLRRCRHRH SALPFKTHRPLSVTPKMADLLGSILS SMEKPPSLGDQETRRKAREQAARL KETTRARETTESGVS
1845	7342	A	1982	1	145	
1846	7343	A	1983	1	419	
1847	7344	A	1984	3	532	PRASRSRPTGLREAAGSGPREAPRR SGCKSPGLGTVAMLRPKALTQVLS QANTGGVQSTALLNNEGSLLA\YS GLRGTTDAPGSPAAIAISNIWA\AYG PETGTQAFNEDNLQ\IILHGTCMGG AVLGHSPELANLSCLLYCIAKEDRG AFGNCFKAKGPGLLGGSYLEEPLTQ VAAS
1848	7345	A	1985	2	555	
1849	7346	A	1986	90	323	

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1850	7347	A	1987	1	4695	
1851	7348	A	1988	81	523	SCLCRDRACLTSLPVSFQVQGVGSK GWRDVTTFSGKAEGPLDSPSEGH YQNSGLDHFQNSNIDQSFWETFGSA EPTKTRKSPSSDS\WTCADTSTER\R SSDSWEVWGLASTNR\NSNSDGV GGEGTKKAVPPAVPTDDGWDNQ W
1852	7349	A	1989	1187	1720	QNQSRDKMRDLREGQMEPPKSELI GWGGGETSRWVRGGASPPPVALSP LFLITWSGHKDLKDLKVRGLRGLE APRVNVWETEANQAGLQPLGPAT IGLRPRERPGPRVGREGGPAWPLG EFGIPGVGLRARHQHELRRWRPGR ASPRPERKAAWKGGQPGQPAGPADG RAARSRG
1853	7350	A	1990	738	1086	GTASENLGCKILKHRQQMLRKVYP VVLHILSYRGSHSSRKKNWGRLKNI LKTFFFLGGGGDGSCWQRPGWELQ WALFSGSLQSPPGFKQFSCSLLS SWEYRCTPPCLANFCIFQ
1854	7351	A	1991	1	340	LGEGRATAVEALPGPSLDHWYRSA GEEKDGP/VYCAAQHLRGRSLPKA WPPPPSSLPVLTDQKSR/YPGHEAH DQGG\WDARQSIIRKVVDPETGRTR WGAFLTYTTGSGSVG
1855	7352	A	1992	1	142	
1856	7353	A	1993	58	328	LKKKGKEKAEAAQVVEALPGPSLDQ WHRSAEEEEGPVLTDEQKSR/YPG HEAHDQGG\WDARQSIIRKCGGPLR RGAPGLLKGDGEGPKRKS
1857	7354	A	1994	120	416	LFFGESSRLTVLEDLKNVFPQVAV FEPSKAEIFHTQKAPLVFLATGFYPD HVELSWVNGKEVHSGVSTDPQP LMEQAALNDSRYCLSSRLRVSATF
1858	7355	A	1995	1	977	VKLPSCPDAMGTSLLCWMALCLL GADHADTGVSQNPРНITKRGQNV TFRCDPISEHNRLYWYRQTLGQGPE FLTYFQNEAQLEKSRLSDRFS PKGSFSTLEIQRTQGGDSAMYL CAS SIGAGLPSSNQPHFGDTRL SILED LNKVFPPEVAVFEPSEAEISHTQKAT LVCLATGIFPDHVELSWVNGKEV HSGVSTDPQLKEQPALNDSRYCLS SRLRVSAFWQNPРНHFRQVQFY GLSENDEWTQDRAKPVTVQIVSAEA WGRADCFTSVSYQQGVLS\ATIL YEILLGKATLYAVLVSAVLMMAMV KRKDF
1859	7356	A	1996	2	883	FVSQLSPEKVVCGHHLKMLSLLLLL LGLGSVFSAVISQKPSRDICRGTSV KIECRSLDFQATTMFYRQFPKKS MLMATSNEGSKATYEQGVKDKFL INHASLTLSTLTVTSAHPEDSSFYICS ARESTDPKNEQYFGP\GTRLTVLE DLKNVFPPEVAVFEPSEAEISHTQK ATLVCLATG\FFPDHVELSWVNG

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						KEAHSGVSTDPOPLKEQPALNDSRY CLSSRLRVSATFWQNP RNHFRCQV QFYGLSENDEWTQDRAKPTQIVS AEA WGRAGEWGLGRCLLEIR
1860	7357	A	1997	195	1133	PQHGGHFPRKIKSCSWQARPLEDEA TLGQCGVEALTTLEVTRPACLEVKS MVPWPVLEKVRGQTPKVAKHGEK KKKKTGRAKRRMQYNRRFVNVVP TFGKKKGTTFTKIFVGGLPYHTTDA SLRKYFEGFGDIEEAVVITDRQTGK SRGYGFVTMADRAAAERACKDPNP IIDGRKANVNLA YLGAKPWCLQTG FAIGVQQLHPTLIQRTYGLTPNYMY PPAIVQATVVIPAAPVPSLSSPYIEYT PASPAYAQYPPATYDQYPY\AASPA TVRSFVGYSYPAAVPQALSAAAPA GTTFLQYQAPHVQPD RMH
1861	7358	B	1998	60	378	NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIH FISPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX*
1862	7359	A	1999	1	437	DPRATEGMVVADKTCQKSTGR LPE LVTAIRMLKQMLFRYQGYIGAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISKNLDFLRP YTVPNKKGTRLGRYRCEKGT TAVL TEKITPLEIEVLEETVQTMDS
1863	7360	A	2000	2290	2481	
1864	7361	A	2001	3	860	FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKL\PRPRKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIH FISPNIYCCGAG\TAA DTAMTTQLISS\NLKLHSL\STGR L P RV\VTANRMLKQMLFRYQGYIGAA LV LGGVDVTGPHLYSIYPHGSTD K VP\YVTHGFLAPLA\AMAVFEDKFR P\D\MEEEEA\KNLVSEDSPPQFP PPS WRIFND\LGSGSNIDLCVISK\NKLDF LRP\YTVPNKKGTRLGWRYRCEKG VTAVLTEKIPLLWST
1865	7362	A	2002	1	340	RQGTIVAISSIQGKMSIPFRSAYAAS KHATQAFFDCLRAEMEYIEVTVI SPGRSC/VEVAQDVLAAGKKKKD VILADLLPSLAVYLRTLAPGLFFSL MASRAR*ERKSKNS
1866	7363	A	2003	56	385	RPWTSSPPQSPCCSAAWASSASS GCCSGCAGRPTCGMLWW*SQAPA QGRSPVEVAQDVLAAGVKKKKDVI LADLLPSLAVYLRTLAPGLFFSLMA SRARKERKSKNS
1867	7364	A	2004	2	409	
1868	7365	A	2005	1	1092	
1869	7366	A	2006	50	1101	LTMVSPATMKSLPKVKAMDFIT\ST AIL\PLLFGCLGV\FGL\FRLQWVR GKAYLRNAV VVITGATSGLGKECA KV FYAAGAKLVLCGRNGGALEELI\

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						RELTAS\HATKVQTHKPLLGGPSDL TDSGAIVAAAAEESFSCF\GYGRHY FVNNAGISYRGTVTMDTVTVDVDR VMETNYFGPVALTALLPSMIKRR QGHIVAIISSIQGKMSIPFRSGICQPS KHATQ\AFFDCLAVPEMEQYIEIV TVISPG\YIHTNLS\VNATADGSRYG V\MDTVTSPGPESPVEGGPRMFLAC LWGKKK\KDV\TLADLPALPLAVY\ LRTLAP\GLLPSSLPLPRAQKRAGN PKNSLVL
1870	7367	A	2007	75	461	
1871	7368	A	2008	3	426	DAWVCLSPAFILLELCAARV*EGLP NRVHRTEEVNHVDFYAFSYYYDLA GGAGPIDAEKGGSLVVGDFEIAATKY VCRTLETQSQSSPFSCMDLTYVSL LQEVGFPRSKVLKLTRKIDNVYTT WAPGAIFHYIDSLNRQKS
1872	7369	A	2009	3	421	QALGNRGVVSRRGWRPGRWRPGRG SPKDRLPAPRKRALVSVGVAERA VHETPTLTHETFKALKPGLSAYADD VEKSAQGIRELLDVAKQDIPDF*K ATPLILK/ATAGLRLLPKKAQR*LA K\GKEVFKAWLFFEGNDW
1873	7370	A	2010	337	769	PLALCLAPAASLHELCAAKVSEVLH NRVHRTEEVKHVDFHAFSYYYDLA AGVGLIDAEKGGSLVVGDFEIAAK YVGVTVSVKGRVSSPVCRTLETQP QSSPFSCMDLTYVSLLLQEFGFPRS KVLKLTRKIDNVETSWALGAIF
1874	7371	A	2011	2	486	
1875	7372	A	2012	176	1643	MKKGIRYETSRKNTNYIFQQPQHGP WQTRMRKISNHGSLRVAKVAYPLG LCVGVFIYVAYIKWHRANATQAFF SITRAAPGARWGQQAHSPLGTAAD GHEVFYGIMFDAGSTGTRVHVQF TRPPRETPTL/TAHETFKALKPGLSA YADDVEKSAQGIRELLDVAKQDIPF DFWKATPLVLKATAGLRLLPGEKA QKLLQKVKEVFKASPFLVGDDCVSI MNGTNE\GVSAWITINFLTGLSKTPR RSNVGMLDLGGGSTQIVFLTHVEG TLQASPPRYLTALRMFNRTYKLYC YSYLGLGLMSARLAILGGVEGQPA KDGKELVSPCLSPSFKGEWEHAEVT YRVSGQKAAASLHELCAARVSEVL QNRVHRTEEVKHVDFYAFSYYYD LAAGVGLIDA\EKGGSLVVGDFE AAKYV/CVRTLGETQP\QSSPFSCMD LTYVSLLLQEFGFPRSKVLKLTRKID NVETSWALGAIFHYIDSLNRQKSPA S
1876	7373	A	2013	21	119	PGWPQTPDFKRS/PPLWPPKVLGLQ V*ATAPGPK
1877	7374	A	2014	1420	1627	IGLNPSSVPSTFFSYSPQFTEGVPP/P GMERP/PFPWEQRPTGWSFFSPCPQ TP\SPPTSEHGTPPNWPKC

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1878	7375	A	2015	447	775	QIPKEHLHHP/PQTSHSNRPLR/P/GN RPNPESPTGSPPECCSCLAPRGS WGDPNPLQRTPGAGKVAGGPFPPP TQQSPGKALCINLKGFAAIKLLD NVLQPSSALGFL
1879	7376	C	2016	49	519	MYGKGKSNSSAVPSDXQAREKLAL YVYEYLLHVGAQKSAQTFLSEIRW EKNITLGEPPGFLHSWWCVFWDLY CAAPERRETCEHSSEAKAFHDYPFM SPRYPGGPRPLRIPNQALGGVPGS QPLLPSGMDPTRQQGHPNMGGPMQ RMTPPRGMVP*
1880	7377	A	2017	1	1155	
1881	7378	A	2018	56	1416	WVDRCVTVGAALGTSMYGKGKS NSSAVPSDSQAREKLALYVYEYLL HVGAQKSAQTFLSEIRWEK\NITLG EPPG\FLHSWWCVFWDLYCAAPER RETCEH\SSEAKAFHDYSA\AAA\PS VLG\NIPPGRWACQLGPVTTRGSFQ PFMFTFGYPG\GPRSPLRV\PNQALG G\VPGGQPLLPSGMDSTRQQ\GHPN MGGAMQR\MTPPRGMVPLGPQFLT PWLSLQNYGGA\MRPPLNALGGPG MPGMEQGSRCGRPW\PNPTNA\NSL PFSSAFSWNLLGPPGGGGPPG\TP MPSSSRFQPTSGDNMYTLMNAVPP GP\NRPNF\PMGP\GSDGPMGGGLG MESHMMNGSLGS\GDMASISKNSPN N\MSLSIQ\GIPK\DDGAMGANFLN PFQSESYSPSKPYKCVFPFGLFMKP TVSQPFPELRTENYSSTSVPVKQR NLSHTKPTFLFPALSPLL
1882	7379	B	2019	162	349	LEELEEEEEEELDLVLLRAFCLLLSW DVEAEQFLEV\SFLLFFFLFSDPRPRD RLRLLERLREPT*
1883	7380	A	2020	2	353	SSSDGRKKRGKYKDKRRKKKKKKR KKLKKKGKEKAEAAQQVEALPGPSL DQWHR\SAGEEEDGPVLTDEQKSR/ YPGHEAHDQGG\WDARQSIIRKV DPETGRTRWGAFGLTYTTGSGSVG
1884	7381	A	2021	1	142	
1885	7382	A	2022	404	946	PVCACPRPEQGTKVYLFPSWLSLT FSLHHREKQAEGRGEEEDASSASS SSSSSSSSSSSSSSSSSDGRKKRGK YKDKRRKKKKKKRKLKKKGKEKA EAQQVEALPGPSLDQWHR\SAGEE DGPVLTDEQKSR/YPGHE\THDQGG WDARQSIIRKCGGPLRRGAPGLLKG DGE\GPKRKS
1886	7383	A	2023	3	634	
1887	7384	A	2024	131	546	VAGTPGRHPHTRLIFPVFCRGGVFL CFPGWSFFFFKPSDLD\SFHLEMIHPR CESWKMPGALPM/YCSF/CCLLVLL KDQGGQASTGVRRRKESWLPAPHS STVQVTQEGWREQSRELPKTECQL GWFLFLLQPYSR\SRFY
1888	7385	A	2025	363	578	RPYPCLSPR\SSSTNPLSS**LNKIPS

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						LPSSWEKW*IPPKNNCLSLNPSPPS LAPSLDDIKEGLSWKKKKK
1889	7386	A	2026	166	191	KNVIHQSKNCVFKLLDQIHNFPLS TLLHVIVDLFLGLFGVPE/CSDP*RLP GTPPYQPAPARQPAPADHRQWPVPQ RGPEASG
1890	7387	C	2027	358	405	MSSREGARDGGEGRLS*
1891	7388	C	2028	306	347	MSPGRGPGMEGRG*
1892	7389	A	2029	2	358	QCGGIRFWRAPVFLVLSWSPQDGIT GEEPDTSHDPRHLHQASSCPAHPPLP PTQSCSSCQGWLCPPQGCPPGGPRT A/CIVPWPSFVASAATQERGQCPL DPLSPNQTRALHLSGTSGK
1893	7390	B	2030	1043	1146	MPSSVSWGILLLAGLCLVPVSLAE DPQGDAQAQKTDTSHTDQDHPTFNK ITPNLAFAFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNLTEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEASPVISGASKRA KKQINGKMGETLLKSKDPRKEDFT LDQVTTVKGAYDEAFRACTSSHX *
1894	7391	A	2031	2	402	SQTQREPTMVLSPADKTNVKAA/W GMFLSFPTTKTYFPHFDLSHGSQAQV KGHGKKVADALTNAAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR
1895	7392	A	2032	9	509	NSARATDSERTHHGARLLPDKTNV KAAWGVKGAHAGEYGAELERM FLSFPTTKTYFPHFDLSHGFAQVK GATAKKVA\DALTKAAVAHVVDGHA QTALSALSGPATAHKL\RVGPGSTF KLLASHLPCWLTGRPPSPAEFQPLA VARLPWNKVPGLLVEAPLLEPSK
1896	7393	A	2035	413	674	CRSDRWAKEHRGKRGQDSSKDVM ARLMEAPKQTAQYFFIFYFFETKSY SVTQAGVQWLDLGSQRPPPGP\SD SPASASRAWPQTAH
1897	7394	A	2036	2525	2734	LTNGTESTPPRPPTPSRCSRQCPES VGPPFCSPFCVPAHFKLLPWTFQG TVISSPQIISSSSVCAFF
1898	7395	A	2037	168	392	NKSFFPPSSSFDLSILNTFSFPLTLSSL RSGPTHHTHTAN/THHTHTHTHT HTPSSPDPAHPHTLTDNWVSTL
1899	7396	A	2038	216	528	AGEKLGAGDTSWRVWVPAACT PGRVERVGWCRV\GPADPSGGLTPG \ACGASWQGPFSWAKDLQGPWSW WPVWPTRPFLDLGSSGLLIWVHK WPWGVCVYV
1900	7397	A	2039	37	424	RWNFLATTPSAVFRVWEAQMLTCE RWPTLSGRRQTYLLLPFAP*PQTGC WSPDGSRLFTVLGEPLIYLSFPER CGEGKGALEVQSQQRLWQICLRQ QYRHQMVRRLGERLTPWSGTPVG NVWLCL

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1901	7398	A	2040	1	442	PEFRVDDFVLRYPAYESSPGTELRECGL/WPFRPGVCRLQTSCEPWNLPLQLTKDPLKTPGRLDHGTRTAFIH HREQVWKRCINIWRDVGLFGVLNE IANSEKEVFEWVKTAGSWALALCR WASSLHGSLFPHLSLRNEDLIAEF
1902	7399	A	2041	722	1395	CLCLGLWACQS\CILIWTL\DPSTLFT TRPSSG\CAQVLSHPGHTPVTS LAWAPSGGRLLSASPVDAAIRVWDVSTE TCVPLPWFRGGGVTNLLWSPDGSKI LATTPSAVFRVWEAQMWDLWRRW PTLSGRCQTGCWSPDGSRLFTVLG EPLIYSLSPERCGEKG\ALEVQSQ QRLWQICLRQQ/YTRHQMVRRLG LERLTPWSGTPVGNVWLCFMKGKA QGLPGW
1903	7400	A	2042	1	418	MPEQEPTAEQLS*IAAENEDEHSV NYKPRAQKSIQEIQLDKDDESLRK YKRALLGRVAVSADPNVPNVVAP GRVRLLPQALSATTPGRPSLTQPGT NKGPSAHIAESRLLCLPRPIGLRVV SARLRQRRLSLLLF
1904	7401	A	2043	1	525	LSQQASLESF*KHFFCLKEVVEYRIK ISFRVNREIVSGMKYIQHTYRKGVK ID\KTDYIVGSYWPRAEYEFLLPKS PRWTASPTPSVLQSGAPLGHQYLLP PSVPSSGHWPVCSPRLLVPPLLGR PSLTLPGTNKGPSAHIAESRLLCLPR PIPLRVVSARLRQRRLSLLLF
1905	7402	A	2044	354	487	
1906	7403	B	2045	61	516	KSIQEIQLDKDDESLRKYKEALLG RVAVSADPNVPNVVVTGLTLVCSS APGPLEDLTGDLESFKKQSFVLKE GVEYRIKISFRVNREIVSGMKYIQHT YRKGVKIDKTDYMGVSYGPRAEY EFLPRPIGLRVVSARLRQRRLSLL F*
1907	7404	A	2046	11	328	
1908	7405	A	2047	1	507	LTFVCSFRPVPLYDLRSNLDCKNQ SFLFKEAVDYRIKISFRFHPKYISLI*\ YIQHTYSK/GVKIDKTDYMLGSY/GP RAEYEFLLTPVEEAPKGMLARGSYS IKSRFTDDDKTDHLSWEWNLTISIY CLRPCRPWATGLAPVPPGSQCHPR QAFDPARNKQGTKCTHC
1909	7406	A	2048	1	327	TAEQLAQIAAENEDEHSVNYK/PP AQKSIQEIQLDKDDESLRKYKEAL LAPLAVSADPNVPNVVVTGLTLVC SS/APGPLEDLTGDLESFKKQSFVL KEGVECTVGP
1910	7407	A	2049	1	452	
1911	7408	A	2050	3	868	SHFVLDVIPGVGHLTLPQRMPLSRN RGGGEERRCPPWSPFGAPLQPTLLL RSAPPLGIQVQGLSPSRPQVSRPRLS LSMAEQEPTAEQLAQIAAENEDEH SVNYKPPAQKSIQEIQLDKDDESL RKYKEALLGRWPFSADPNVPNVV

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						VTGLTLVCS\SAPGPLELDLTGDLAE SFKKQFVLCLEGEVEYRIKISFRFNP RDNCPGMKYIQHTYRKGVKIDKTD YMGVSYG\PRAEGSFELTPVEEAP\ KGMLA\RGYSIKSRFTDDDKTDHL SWEWNLTIKKDWKD
1912	7409	A	2051	1	618	TLLVPQDSERTHPWLLSPADK\ITNV KGPPGGKVGAAHVRSMCAEALER MFLSFPTTKTYFPHFDLSHG\SAQV\ KGHG\KKVADALTNVAHV\DDMP N\ALSAL\SDLHAHKLRVDPV\NF\KL LKPLACLVDPPGAHLPAEFQPLAV ATSSLGQSFLGFLWANLKFEQIPV KLGSLGWAMLSLPLWAFPPAPPPLS CTRTPVVFEIKS
1913	7410	A	2052	3	398	
1914	7411	A	2053	1773	3913	FEQNTKLDQAQQAPEDHYPISLLLP SHMAIGLLMAQEGHCKDSSAMGEE AHHPLTPATPPFPPLSPDWGHMQPD FFVPVAVPAVFRGPPQLQCHGRRLF LNSPCAQKSSSGLVVEPGLSRTLLE MVKLTSMRGQFLEAQIPTGISLTLO YQLYQKQTNKNMSYSFVFLKWW ALGQRRAGYPSLEDADSRFRNGS RSFLITVIGITLTVEIVTSGMMKGTR VRWSGAGNEGMMGLEEGRNERSV KEAPPRRAVEAQPKDRTWDVGKG QGTEGEGRGLEVEGQQHQGSEPGTI PFSVSWGVLLLAGLCCLVPSLVED PQEDAAQKTDTSHHQGDWEDLA CQKISYNVTDLAFDLYK\SWLIYHN QHVLVTPTSVAMAFAMLSLGTKA DTRTEILEGLNVNLTETPEAKIHECF QQVLQALSRPDTRLQLTTGSSLFVN KSMKLVDTFLEDTKKLYHSEASSIN FRDTEEAKEQINNYVEKRTGRKVV DLVKHLKKDTSALVDYISFHGKW KDKFKAERIMVEGFHVDDKTIIRVP MINHLGRFDIHRDRELSSWVLAQH YVGNATAFFILPDPKMWQLEEK TYSHLENIQRAFDIRSINLHFPKLSIS GTYKLRVPRNLGITKIFSNEADLS GVSQEAPLKLSKAVHVAVLTIDEK GTEATGAPHLEEKASKYQTVMFN RPFLVIIKEYITNFPLFIGKVVNPTQK
1915	7412	A	2054	3	409	PGPVVVSNNSSAHGSQRTSGPESSM K\YCCPEMVEYQKKGKSLDSEPSVP SAKPPSPEKTAPVASTPSSTPIPAL PPTKVPEPNENVGDAVQTKLIMLV DDFYGRDGGKVAQLTNFPKVATS FRCPHCTKRLY
1916	7413	C	2055	235	366	MRIPETKPLTRNGSEVKELAHSSPQ DNQNDQMSFFIVLLPRNG*
1917	7414	A	2056	3	484	STTPTATQPTSLWQLAVQSPGQSNQ TTNPKLGKASEEEMAEPGLGWWE NR*LSLGHRA\PSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIP SLGQSPGPVVVSNNSSAHGSQRTSG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PESSMKGTIT*KTLSSQSFKNINKVF VVSELYTQK
1918	7415	A	2057	2	4256	FVHGSMADTDLFMECEEELEPWQ KISDVIEDSVVEDYNSVDKTTTVSV SQQPVSAPVPIAAHASVAGHLSTST TVSSSGAQNSDSTKKTLVTLIANN AGNPLVQQGGQPLILTQNPAPGLGT MVTQPVLRPVQVMQNaNHVTSPPV ASQPIFITTQGFVRNVRPVQNAMN QVGIVLNVQQGQTVRPITLVAPGT QFVKPTVGVPQVFSQMTVPVRPGST MPVRPTTNTFTTVIPATLTIRSTVPQ SQSQQTKSTPSTSTTPTATQPTSLGQ LAVQSPGQSNQTTNPKLAPSFPSPP AVSIASFVTVKRPVGTGENSNEVAK LVNTLNTIPSLGQSPGPVVSNSS AHGSGRTSGPESSMKVTSSIPVFDL QDGGKICPRCNAQFVRVTEALRGH MCYCCPEMVEYQKKGKSLDSEPSV PSAAKPPSPEKTAPVASTPSTPIPAL SPPTKVPEPNENVGDAVQTKLIMLV DDFYGRDGGKVAQLTNFPKVATS FRCPHCTKRLKNNIRFMNHMKHHV ELDQQNGEVDGHTICQHCYRQFSTP FQLQCHLENVHSPYESTTKCKICEW AFESEPLFLQHMKDTHKPGEMPYV CQVCQYRSSLYSEVDVHFRMIHED TRHLLCPYCLKVFKNGNAFQQHYM RHQKRNVYHCNKCRLQFLFAKDKI EHLQHHKTFRKPKQLEGLKPGTK VTIRASRGQPRTPVSSNDTPPSALQ EAAPLTSSMDPLPVFLYPPVQRSIQK RAVRKMSVMGRQTCLECSFEIPDFP NHFTYVHCSLCRYSTCCSRAYAN HMINNHVPRKSPKYLALFKNSVSGI KLACTSCTFVTSVGDMAMAKHLVFN PSHRSSILPRGLTWIAHSRHGQTRD RVHDRNVKNMYPSPSFTNKAATV KSAGATPAEPEELLTPLALPSPAS TATPPPTPTHPQALALPLATEGAEC LNVDDQDEGSPVTQEPELASGGGG SGGVGKKEQLSVKLRVVLALCC NTEQAAEHFRNPQRRIRRWLRRFQ ASQGENLEGKYLSEAEKLAEWV LTVQREQQLPVNEETLFQKATKIGRS LEGGFKISYEWAVRFMLRHHLTPH ARRAVAHTLAPKDVAENAGLFIDFV QRQIHNQDLPLSMIVAIDEISLFLDT EVLSSDDRKENALQTVGTGEPWCD VVLAILADGTVLPTLVFYRGQMDQ PANMPDSILLEAKESGYSDDEIME LWSTRVWQHTACQRSKGMVMD CHRTHLSEEVLAMLSASSTLPAVVP AGCSSKIQLDVCIKRTVKNFLHKK WKEQAREMADTACDSVDLLQLVL VWLGEVLGVIGDCPKLVQRSFLVA SVLPDPDGNINSPTRNADMOKELIA SLEEQLKLSGEHFESSTPRPRSSPEE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TIEPESLHQLFEGESENE\SFYGFEEA DLDLMEI
1919	7416	A	2058	3	824	
1920	7417	A	2059	1	1077	MLSGVGGFVLGLLFLGAGLFIYFRN QKAEESFVSALSIDLSGGGNMALLS MVCLKFPGG\SCMAALTVTLMVLS SPLALAG\DTR\PPVRLRKTEDEPLG CVLSGLRVGPDSVFPGGRFCNRIVL VPPARFLEQVKHECHFFNGTERVRF LDRYFYHQEEYVRFDSDVGEYRAV TELGRPDAEYWNSQKDLLEQKRAA VDTYCRHNYGVGESFTVQRRVYPE VTVYPAKTQPLQHHNLLVCSVNGF YPGSIEVRWFRNGQEEKTGTVSTGL IQNGDWTFTQTLVMLETVPRSGEVY TCQVEHPSLTSPLTVEWRARSESAQ SKMLSGVGGFVLGLLFLGAGLFIYF RNQKGHSGLQPTGFLS
1921	7418	A	2060	2	867	GRVGLPAALAPGPVLFSSMVCLRLP GGSCMAVLVTLMVLSSPLALAGD TRPRFLEYSTSECHFFNGTERVRYL DRYFHNQEENVRFDSVGEFRAVT ELGRPDAEYWNSQKDLLEQKRAA VDNYCRHNYGVVESFTVQRRVHPK VTVYPSRTQPLQHHNLLVCSVSGF YPGSIEVRWFRNGQEEKTGTVSTG LIHNGDWTFTHTLVMLETVPRSGEV YTCQVEAPRA*QAPLTVEWRARS ESAQSKMLSGVGGFVLGLLFLGAG LFIYFRNQKGHSGLQPRGFLS
1922	7419	A	2061	3	940	RNFRVDPRVRREEGFIVLPERDLPA SLAPGPVLVSSMVSLKLPGGSCMTA RTVSLMVLSSPLALAGDTRPRFLW QPKRECHFFNGTERVRFLDRYFYN QEEVRFDSVGEYRAVTELGRPDA EY\WNSQKDLLE\QRRAA\VDTYC RHNYGVGESFPVQRR\VEPKVTVY PSKTQPLQHHNLL/VFCVSVGFYPGS IEVRWFLNGQEEKAGV\VPQALIQN GDWTFQTW\VMLETVPRSGEGLHC QSE\HPGVTSLLTVEWRARSESAQS KMLSGVGGFVLG\LLLPLGPGLFIY FRNQKGHSGLQPTGFPELKCR
1923	7420	A	2062	25	384	EFHRLRENPPMVAVSCPTKTNVKG PPGGKVGAAHVRSMCAEALERMFL SFPT\TKTYFPFHD\SHG\SAQVKGP RQRRWPNALTKRRGAPLDDMP\NT ALSALSDLHAHKLRVDPVQLSSS
1924	7421	A	2065	47	353	AGRVRLWDCVEVDLTGAGQSV EASRHAEVVRNRCHWAPQLFSL FAPGWGG\GEGRVGDGGAVGWFP PQPPSSPPGVMPCPHDRRGTEPGRD LVPAQ
1925	7422	A	2066	3	692	KRLPKMAEVQVLVL\DGRAHSSLG\ RLAGHRGLNQVLLGRK\VVVVVRCE G\NISGNFYRNEVKVPWLFPSKRM NTNPSRRPLTTSGAPSRI\FWRTVRG MLPHKTQAEAKA\LDRL\KVFDGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PPPYGQEKSGMVVPAALKVVRLK PTRKFCLIFFFSGGGAL\AHQVVGWK YQAVTAPLEE\KRKREKPRFHYRK KENSIMRL\RKQAREETWRKKIDKY TEVLKTHGLLV
1926	7423	A	2067	1	2091	
1927	7424	A	2068	384	4189	ERTSPAMITSELPVLQDSTNEATAH SDAGSELEETEVEKGRIRGRPRPP STNKKPRKSPCEKSKIEAGIRGAGR GRANGHPQQNGEGEPVTLFEVVKL GKSAMQSVVDDWIESYKQDRDIAL LDLINFIIQCSGCRGTVRIEMFRNM QNAEIIRKMTEEFDEDSGDYPLTMP GPQWKFRSNFCEFIGVLIRQCQYSI IYDEYMMDTVISLLTGLSDSQVRAF RHTSTLAAMKLM TALVNVALNLSI HQDNTQRQYEAERNKMIGKRANER LELLQKRKELQENQDEIENMMNSI FKGIFVHRYRDAIAEIRAICIEIGV WMKMYSDAFLNDSYLKYVGWTLH DRQGEVRLKCLKALQSLYTNRELF KLELFTNRFKDRIVSMTLDKEYDVA VEAIRLVTLILHGSEALSNEDECENV YHLVYSAHRPVAVAAGEFLHKKLF SRHDPQAEALAKRRGRNSPNGNLI RMLVLFFLESELHEHAAYLVDSLW ESSQELLKDWECMTELLLEEPVQGE EAMSDRQESALIELMVCTIRQAEEA HPPVGRGTGKRVLTAKERKTQIDD RNKLTEHFIITLPMLLSKYSADA EK VANLLQIPQYFDLEIYSTGRMEKHL DALLKQIKFVVEKHVESDVLEACS KTYSLCSEETYIQNRVDIARSQID EFVDRFNHSDVLLQEGEEADDDDI YNVLSTLKRLTSFQNAHDLTKWDL FGNCYRLLKTGIEHGAMPEQIVVQA LQCSHYSILWQLVKITDGSPSKEDL LVLRKTVKSFLAVCQQCLSNVNT VKEQAFMLLCDLLMIFSHQLMTGG REGLOPLVFNPDTGLQSELLSFVMD HVFIDQDEENQSMEGDEEDEANKIE ALHKRRNLLAAFSKLIYDIVDMHA AADIFKHMYKYNDYGDIIKETLSK TRQIDKIQCAKTLILSLQQLFNLVQ EQGNLDR TSAHVSIGIKELARRFAL TFGLDQIKTREAVATLHKDGI EFAF KYQNQKGQEYPPPNLAFLEVLSEFS SKLLRQDKKTVHSYLEKFLTEQMM ERREDVWLPLISYRNSLVTTGGEDDR MSVNSGSSSSKTSSVRNKKGRPPLH KKRVEDESLDNTWLNRTDTMIQTP GPLPAPQLTYTVLRENSRPMGDQI QEPESHEGSEPYFLHNPQM QISWLG HPKLEHLNPKDITGMNMYMKVITGA RHAALCLMEEDAEPFEDVMMSSR SQLEDMNEEFEDTMVIDLPPASRN RRERAELRP\DFVDSAAIIEDDSGFG MPMF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
1928	7425	A	2069	1	2661	
1929	7426	A	2070	1	1454	
1930	7427	A	2071	1	2364	
1931	7428	A	2072	1	1368	
1932	7429	A	2073	114	1473	VKGDRFGALRFNDPCAGIKLPMTFF TELEKTTLKFIWNQKRARIAKSILSQ KNKAGGSTLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTGPSEITPHT YNYLIFDKPEKNKQWGNDSLFNKW CWENWLAICRKLKLDPFLTPYTRIN SRWIKDLNVRPKTIKTLEENLGITIQ DIGMGKDFMSKTPKAMATKDKIDK WDLIKLKSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIY KKKTNNPIKKWAKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIHKKSGNNRCWRG CGEIGTLLHCWWDWKL VQPLWKS VWRFLRDLELEIPFDPAPILLGIYPN DYKSCCYKDTCTRMFIVALFTIAKT WNQPKCPTMIDWIKKMWHIYTME YYAAIKNDEFM/SFVGTWMKLEIIL SKLLQEQTCK
1933	7430	B	2074	1	1890	MDKFLDITYTLPRLNQEEVESLNRPI TGSEIVAINSLPTKKSPGPDGFTAEF YQRYKEELVPFLLKLFQSIEKEGILP NSFYEASIIIPKPGRDTTKIENFRPIS LMNIDAKILNKILANRIQQHIKKLIH HDQVGFTPGMQGWFNICKSINIIQHI NRTKDKNHMISIDA EKA FDKIQQH FMLKTLNKL GIDGTYLKMIRTIYDK PTANIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVMELLARAIRQEKEIKGI QLGKEEVKLSLFADDMIRIKYLGIO LIRDMKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTLNFI WNQKRARTAKSILSQKNKARGIML PDFKLYYKATVTKTAWCWYQNRD IDQWNRTEPSEITPHIYNYLIFDKPD KNKQWGKDSLFNKWCWENWLAIC RKLKLPFLTPYTTINSRWIKDLNV RPKTIKTLEENLGNTIQDIGMGKDF MSKTPKAMATKAKIDKWDLIKLS FCTAKETTISVNRQPTKWEKIFATY SSDTGLISRIYNELKQIYKKKTNNPI NKWAKDMNRHFSKEDIYAAQKHM KNAHHHWPSEKCKSKHNEIPSHTS*
1934	7431	A	2075	1	2676	MKAIEIKMFFEINENKDTTYQNLWD AFKAVCRGKFIALNAHNRKQERPKI DTLTSQLEKEKQEQTSHKASRRQE MTKIRAELEIEIQKTLQKINESRSW FFERINKIDRPLARLIKKKREKNQID AIKNDKGDITTDPTIEIQTIREYYKH LYANKLENLEEMDKFLDITYTLPRL NQEEVESLNRPI TGPEIVAINSLPTK RSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYEASIIIPKPG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RDTTKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPGMQG WFNIRKSINVVQHINRTKHKNHMII SIDA EKAFDKIQPFMLKTLNKL SID GTYLKIIRATYDKPTANIILNGQNLE AFPLKTGTRQGHPLSPLLFNIVLEVL ARAIRQEKEIKAQNLLKLISNFRKVS VYKINVQKSQAFLYTNNRQTESQIM RELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNIPCS WIGRINIVKMAILPKVIYRFNAIPIKL PTTFFTELEKTILKFIWNQKRAHIAK TILSQKNKAGGIMLPDFKLYYKATV TKTA WY WYQKR DIDQWNRIELSEII PHIYNHLIFDKPDKNKKWGKDSVF NKRCWENWLAICRKLKLDFTLTPY TKINSRWIKDLHVRPKAIKTLEENL GITIQDIGMGKDFTSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRVNR QPTKWEKIFAIYSSDKGLISRIYKEL KQIYKKKTNNPIKKWAKDMNRHFS KEDIYAANRHMKKCSSSLAIREMQI KTTMRYHLTPVRKAIKKSGNNRC WRGCGEIGTLLHCWWDCCLVQPL WKT VWQFLRDLELEIPFYPAIPLLGI YPKDY
1935	7432	A	2076	1	3045	MDKFLNTYTLPRLKQEEVESLNRPI TGS DIEAIINSLPTKKISPGPDGFTAE FCQRYKEE/LEKEGILPNSFYEASIILI PKPASDTTKKENFRPISLMNINAKIL NKILAKQIRQHIKKLIHHDQVGFIPG MHGLFNICKSVNIIQHINRTNDKNH MIISIDA EKPFDKIQHFMLKTLNKL AQNLLKLIGNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMNEFPFTIASKR IKYLG IQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCSWEKTTLKFI W/NQKRAHIAKSII SQKNKAGGITLP DFKLYCKATVTKTA WY WYQNRDI DQWNRTESSEIMPHIYNHLIFDKPD KKKKWGKDSL FNKWCWENWLAIC RKLKLDPFLTPDTKINSRIKMDLNR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYA AKKHMKK CSSSLVIREIQIKTTMRYHLTPVRMA IIKKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKS VWRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVIIIHVFWDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLP CSSAC RRPVIGLQLVMINSGNFQVIAMEGT VASECCHGNGKLTWHRPVLSVCSF SRCTVQAAGGSAILEDGDPLLTA PL GSTPQAAVCRGPRGRELRAAPADS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HLFQRDLWPFNKVIVHGEKGSNQTSQGLLNTGSEMTIVLENPKYHSGPPVRVSPDGGQVIEVLADPSYTGPTALLNVFFAFQCNFYFDHIPENC GFSDPSDPQNLQKGEGCPSLVRASTAPPQEKATEQPLLCKTTESPFGMTVGPCTDETLDHGAPSKHVPGTAHNELALLDLRVKSAGSAAVHHKLKVLHWRSLSNNKGTGRLYEQVA
1936	7433	A	2077	1	2142	
1937	7434	A	2078	1	1551	MRFKEKIHLHNIKEPSEAAASADGGA VASYPDLAKIVDEGRYKAEVMQLRCGWRAPASDCVHSVA VVGVD SVLEVLARAIRQEKEIKGIQLGKEEVKLSLFADDMIVYLENPTVSAQNLLKLISNFSRVSGYKINVQKSQAFLYTNNKQTESQIMSELPFTIASKTIKYLGIQLTRDVKDLFKENYKPLLNIKEDTNKWKNIPCSWIGRINIVKMAILPKVIYRFNAIHIKLPMTFFTELEKTTLKFIWNQKGVHIAKSILSKKNKAGGIMLPHF KLYYKATVTKTAWYQYQNR YTDQCNRTEPSEIHPHIYNHLMFDKPDKNK KWGKDSL FNKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNVRPKPIKTLEENLGITIQDIGMGKDFMSKT PKAIATKAKIDKWDLIKLSFCTAKETTIGVNRQPTTELEKIFAIYSSDKGLISRIYKELKQIYKKKNPIKKWVKDMNRHFSKEDIYAVNRHMKKCSSSLVIREMQIKTTMRYYLTPV
1938	7435	A	2079	1	1458	GLSGDLLGAHQLPDVLGCVQPLPD LLLPPQNLLALQSLQDDLLWALDPAAAAPWAMDRGAATQWAVGPVVS DPWVMEAVASLPSAMDLDSAAQP TWLLGAASLLVTDQPMQPSADQLAEFPDLLSKVSQSLRIKYLGIKLTRNVKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMTFFTELENTTLKFIWNQKRACIAKSILSQKNKAGSIMLPDFKL YHKATVTKTAWYQYQNRDIDQWNGTEPSEIMSHIYNYLIFDKPEKNKQRGKDSLFSKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKIKTLEENLVNTIQDIGMGKDFMSKTPKAMATKAKIDKWDLIKQSFCTAKET TIRVNRQPTTEWEKIFAIYSSDKGLISRIYKELQQIYRKKTNNPIKKWAKDMNRHFSKEDIYAANRHMKKCSSSLAIREMQIKTTMRYHLTPV
1939	7436	A	2080	1	2028	
1940	7437	A	2081	2	1547	
1941	7438	A	2082	3	1945	
1942	7439	A	2083	1	2124	
1943	7440	A	2084	1	2250	
1944	7441	A	2085	2	2483	GKYYKLSSGTAPTCVSLGWGLARG

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						DSAAPALGSRTSACAPCSHGWTWKL SLEPSDRLSPCDRSSEEATHAPHRL LALVASLPWSRLPLLAPQSHSEAEA TSQPTGVENHHQKTRYVKAGGPVI CRSLPESRGFLWASEGRKCMLIGSW AAMGRLRKSTISSRFGPQTLAGTGR PQAIPVLKKHSDAVLLGVCFLKLLH QHHQELGENADSQTLPTQTHWEFELS EDYNKMTVPVKNYQVLEVLARAMR QEQIKSIQLGKEEVKLSVFADDMI VYLENPIVSAQNLLKLISNFSKVS KINVQKSQAFLYTNNRQTESQISEL PFTIPSKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNI PCSWV GRINIMKMAILPRVIYIFNAISIKLPM TFFTELEKTTLKFIWNQKRARIAKTI LSQKNKAGGITLPDFKLYYKATVT KTAWYWYQNRGVDQWNRIEPISEII PHIHNLIFDKPDKNKKWGKDSLFT KWCWENWLAICRKLKLDPFLTPYT KINSTWIKDLNVRPKTIKTLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKETTIRVNRQ PTEWEKIFTIYPSDKGLIPRIYKELK QIYKKKSNNPIKKWAKDINRHFSK EDIYAANRHMKKCSSSLVIREMQN KITIR/YHLTPVRMAIIKKSGNNRDM DEAGNHHSQTIARTENQAPYLLTH RWELNNENTWTQVEEHHTLGPIVG VICRKVFPNGSGPSKPSGLHFSQPLP QVTSVVAKITIVPWEMKLIAMGVQ DELNIAFHKNHLLMNDTTIHMTPIYI QPAPKS
1945	7442	A	2086	1	2622	
1946	7443	A	2087	853	2831	YPESTMNSNKFTRKKQTPPSKSG*R I*TDTSQKKTFMQPKDT*KNAQHH WSLEKCKSKPQ*DTISHQLEWRSLK SQDRKD*QSTLLAILIKKGQKNQI DT/IKNDKEGITTDPREIQTIREYYK HLYTNKVENLEEMDKFLDTYTLPT LKQKKEVKTLNRPITGSEIEAIINSLP T/KKSPGPDRTAEFYR/DIRSSGQG NQARERNKGYSIRKRGSIQVPVCR* HHCIFRKP HHLSPKSS*ADKQLQQS LRIQNQSAKITSIPHQ*QTNREPNE *TPIHNCFKENKMPRNPTYKGCEGS LQGELQTTAQ*NKRGHKRMEEHSM LMDRKNQYRENGHTAQGNL*IQCH PHQATNDFFHRIGKNYFKVHMEPK KSPHRQVNPKEQSWRHHTT*LQ TILQGYSNQNSMVLVPKQRHRPME QNRAPGNNTIHLQLSDL*QI*QKQE MGKGFPI**MVLGKLANHM*KAET GSLPHILYKN*FKMD*RLKC*T*NH KNPRRKPRQYHSGHRHGQGLHD*N TKSNGNKSQN*QMGSN*TKELLHST RNYHQSEQATYRMGENFCNLLI*Q RANIQNLQRT*TNLQDKNKQPHQK

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						VGKGYEQTLKRRHLCSQKTHEKM LIITGHQRNANQNHNEIPSHTS*NGD H/SNQVRKQQVLERMWRN
1947	7444	A	2088	1	4954	MVFSIDAQKAFDKIQHRFMLKTLN KLGIDGTYLKIIRAIYNKPTGNIILNG QKLEAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVK LSLFADDIIVYLENPIVSAQNLLKLI GNFSKVSGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYLGIQL TRDVKNLFKENYKPLLNEIKEDTDK WKNIPCSWIGRIHIVKMATLPKVIY RLHAIHIKLPMTFFTELEKTTLKFIW NKKRARIAKSILSQKNKGGGITPPDF KLYYKATVTKTARYWYQNRDIDQ WKTREPSEIIPHIYNHLIFDKPDKNK KWGKDSL FNKWCWENWLAICRKL KLNPF LTPYTKINSRWIKDLNIRPKT IKTLEENLGNTIQDKGVGKDFMSQT PKAMATKAKIDKWDLIKLSFCTA KETTIRVNRQPTWEKIFAIYSSDKG LISRIYKELKQIDKKKANNPINKWA KDMNRHFSKEDIYAANRHMKKSSS SLAIREMQIKTTMRYHLTPVRMVII KKSGNNSEGLNPGYKGFPTIHWAPL PVAQSKDSGLASLNSDPDIPSMLEC SLKAPQLYRSKNVGQVFISSASQAF TKKARIYARLRVSQALKTLCKSSCH DGWSFERLARIQEVSLPISPDILCSE AYHYGTPQWLVAATGTAQTFLLEL NQKSQQYQKQEQTHSKASRMQEIT KIRAE LKEIETRKT LQKIDESRSWFF ERINKTDRPLARLTQKREKNQIDA IKNGKGDITDPTGIQITIREYYKHL YAKKLENLEEMDKFLDTYTLPRLN QEEVD SLNRPITGAEIVAIINSLPTKK SPGPDGFTAIFYQRHKEELVPFLK LFQSIEKEGILPNSFYEASIIIPKGR DTTKKENLRPISLMNIDAKILSKILA NRIQQHIKLIHHDQVCFIPGMQGW FNIRKSINVIQHINRAKDKNHMISID AEKAFDKIQQTFMLKTLNKLIGDGT YFKIIRAIYEKPTANIILNGQKLEAFP LKTGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFSKVS GYKIYKIDVQKSQAFLYTNNTDKQ ESQIMSELPFTTASRIKYLGIQLTR DVKDLFK\ENHKPLLNEIKEDTNKW KNIFIPCLWVGRINIVKMAILPKGIY RFNAIPIKLPMTFFTELEKTTLKFIW NQKRARITKSILSQKNKAGGITLPDF KLYYKATLTKTAWYWYQHRDINQ WNRTEPSEIIPHIYNHLIFDKPDKNK KWGKHS LFNKWCWESWLDICRKL KLDPYTKFTPYTKINSRWIKGLNVR PKTIKTLEDKPIQVFNTIQDIGMGKD FMSKTPKAMATKAKIDKWDLIKLK

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						SFCTGKETTIRVNRQPTWEKIFAIY SSDKELISRIYKELKQIYKKK\TNMPI KKWAKDMNRHFSKEDIYAANKHM KK\CSSSLAIREMQIQTMMRYHLTPV RMANIKKSGNNRCWRGCGEVGTLL HCWWD CNLVQPLWKS VWRFLRDL ELEIPFDPAIPLLGIYPKDYKSCCYK DTCTRMFIVALFTIAKTWNQPKCPT MMDWIKKMWHIYTMEYYAAIKND EFMSFVGTWMKLEIILSKLSQEQT KHRIFSLIGGN
1948	7445	A	2089	93	225	
1949	7446	A	2090	133	849	PVWPKWSGWPLLMRSFAPARIATV VIGGVVAMAAVPMVLSAMGFTSV GIAASSIAAKMMSTAAIANGGGVA AGSLVAILQSVAWLYSSSHQEPLRK STPDPKATELTRAGMEASALTSSAV TSVAKVVRVAS/GSCVVLP/LARIAT VVIGGVVAMAAVPMVLSAMGFTS VGIAASSIAAKMMSTAAIANGGGV AAGSLVAILQSVAWLYSSSHQEPLR KSTPDPKATELTRAGMEASALTSSA VTSVAKVVRVASGSVVLPPLAALS PNISLLRPLLGALEASSFMLGSLTGT LFCNLEMGNRLRKWRGSQCGSTHR MFFWFPARIATSCDWRSCGPMAGC ANGCSSAMGLQLRAGIALVLP
1950	7447	A	2091	161	1344	TCPVLRHYSTMSSHKGSAVAQNG APASNREADTVELAEGLPLEEKGK \RVIANPPK\AEEEQTCPVPQEEEE VRVL\TLPLQAHAMEKMEEFVYK VWEGRWRVIPYDVLDP\WLKGND\ YLLHGRPPMPSPFRACFKSIFRIHTE TGNI\WTHLA/LGFVLF\FLGILTML RPNMYFMAPLQ/EKKVVF\GMFFLG AVLCLSFSWLFHTAYCHFGGVFSTF PQRELFKGLLLLNMGELWSPGLYY SFYCSP\QPARLIYLSIVCVLG\ISANV AQWDRFATPKH\RQTRAGVFLG\LG LSG\VVPTMHFTNRWRALSKATTV GQ\MGWFFLMAV\MYITGKLAFNAA \RIPERFFPGK\FDIWFQSHQ\FHVL\ VVAAAFVHFYGS/VSNLQEFPLTGL EGGL
1951	7448	A	2092	2	1419	RLRDPYRSSRLCRRGASRTSSAARS RSRSPAVEGCNRSPGAPQAPARRR RPSRGAPGRAMVKVA\FNSALAQK EAKKDEPKSGEEALIIPDAVAVDC KDPDDVVLVGQRRACGWRMCFGL AFMLAGVILGGAYLYKYFALQPDD VYYCGIKYIKADDVILN/ESPSADAP AA\LYQTIE\ENIK\IFEERRSLNFISVP VPEF\ADSDPAKIVQDFNRKLTAYL DFNL\DKCYVIP\LNTSMCYATPKTL LELLIN\IKAGNLFALSPYLD\SMRHM GYLLDR\ENIDHLGF\FIYRLCHDK\ ETYKLATRRKLFKGIQKREGQQLF SAISGIFENKFAVETLICSW

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1952	7449	A	2093	1	669	
1953	7450	A	2094	267	550	GRTMMFGAKRRQEEWEKVRKPED PEECPEEVYDPRSLYERLQEQKDRK QQELRGTVSNCKNM\VRG\LDEDET TFLDEVSRQQELIEKQPKRRRT
1954	7451	A	2095	1	418	
1955	7452	A	2096	272	383	
1956	7453	A	2097	118	379	RSGGGRGRRGPEVLHLKHPMLKRP DFLYRKPFSSRGWEHGPPSRKSHLL/ GAPPPFPKFFCHLC*APSPFRVLSPY QKRIHLVPPTQLH
1957	7454	A	2098	1	276	
1958	7455	A	2099	1	341	
1959	7456	A	2100	1	450	ACPYLALNSSMFCPDLILPTCLISST GFVGEGKFLQGFKSLSPGSLWLSEG LDYFLSVPGDQYDVCAICLDEYED GDKLRVLPCHAHYHSRCVDPWLTQ TRKTCPIK\QPVHRGPGDEDQEE\ ETQGQEEGYEGE\PRDQP\ASERTPF LG
1960	7457	A	2101	238	525	
1961	7458	B	2102	178	373	XLPOPLRGPLAHS DPERPAPFASSLF IGVLGTTKTKRKKLKGKEGDERGS KGTNPALRKDPTFGF*
1962	7459	A	2103	634	1940	SGVDISFFELVFLPRRPHVAGKWDL GGGWDPGIPKGGAGRAQNSASAPC YQDARPPQPLSSRCHAPLQPFPLPV VVA AVLWGSGDPGASFRATS\DH NCQHGFADLPALFGATLSLEGPGQ LALGEPHPDNACSPIAPPPAPVNGS VFIALLRFD CNFDLKV LNAQKAG YGAAVIHNVNSNELLKMVWNSEEI QQQIWIPSVFIGNRSSEYLALFVYE KGARVLLVPDNTFPLGYLIPFTGIV GLLVLAMGAVMIARCIQHR\KRLQ RNRLTK\EQLNQIPTQTNQKRDQ\Y DVCAICLIEYEDGDKLR\VFPGAHA YH\NRCVDPWLTQTRK\TCPIK\Q PVHR\GPGDEDQEEETQGQK\EGDE GE\PR\DH PASERTPLL\SSPTLPTS\ FGFLRPKFPLVFSLGP\STD PPLSPPS SPCYPGLITPHTYTFG
1963	7460	A	2104	25	527	EFHRLRENPPMVA VSCPTKTNVKA\ AWGKVGAHAVRSMCAEALERMF LSFPT\TKTYFPHFDL\SHG\SAQVKG ATGKKVADALTNAVAN\DDMPN VAVRPEATLHAHKLRVDPVNFKL LKPLACLVDPGPAHLPRPSFTPGGA TSSLGQSFLGFLKHKRCLNLPNYR
1964	7461	A	2105	262	364	
1965	7462	A	2106	3	1265	PRPGLRAPDAPGSAPRERAQPRDPR AGQVRRLDGDKARPAQLRRESG GAESVTRPLRAASPAPPRAARAA MSEKPKLGRRAPASLSARCRAPR CCSCRARRPRIPPOQCPRSVFACSSP ESLLVGVALSPGIALGAGSCVECTE SAREQASGVTPKGRALRGLAPVSST

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						AVLPGRPSRPRYSPTSPHRVPAIASP SVRPPLSFVSPQSCPQCAPTPTHRAP CAPTASIASPGVRPPLPIAPPGVRPR LPITPPMEGVKTENDHINLKVAGQD GSVVQFKIKRHTPLSKLMKAYCER QGLSMRQIRFARFDGQPNQWKLDDL STAGDWKDEDTNIDVFPSSKTGRCA GEQPWQGTVSRGPVPKPGPSILALL LNGEHGDHADHKGVCGNSRTFTT MIFLSLMYFKLQLKTISAGMNL
1966	7463	A	2107	4	408	
1967	7464	A	2108	1	465	PACGYVPALSSASKSRSALGFPLPR CPRGRVDPELAALWPLLQCCCQLL QMGCFLGLGPAI*SPHPHQSHSLGI DRS*FQNAQSPPGFCVSCGPLREVS VCLP*PG*ARCCLGCSFGSGHSRLG NTAQ TANQCILPQASSTLCC*LHPQ NLVCP
1968	7465	A	2109	126	488	
1969	7466	A	2110	1	5586	
1970	7467	A	2111	68	310	TDLPTQNMVFTFSSNWG/TVRQVLS /YSCTRETLQHRELDKTRARGPE*GS VVLTSPLWSPCRKCATGTYHGSPI CQSSGGGR
1971	7468	A	2112	2	630	FFFFSDLLNFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*KPVNSSPSSVFVFCVASP AYRRSSSFSRISFSVSGICPWWSR DGEVGTTFPSQFAKGRKGLIRRGGP QHPLRLSPGPIEEQK*GLVSPKARLG ISPCQLCPGFWSYLADSVSPPPGGSC SGCTVPGSSHNVSPVSHPSGPACGV RTALSSA
1972	7469	A	2113	331	754	NFLKTNNVWSKWTHVLSQFWYQG FILFCLGSIVKCTEIDSSICTE\PSHTK QHMLGGKNQTLNS/DPQGVKCSG* EAM*PRGGISQKDNMGEMNGTT TTKTFCFIFMPGEDQGCSSCVSTRTT RKSQVQKSRGTISRYFHK
1973	7470	B	2114	110	225	XLGRPQLAGSLRSRFPISGMRGEFFT QDCQRNAGREELQGRLSIQSFSPILA LGPDDSCETKTGMDKLS*
1974	7471	A	2115	83	287	SLLKCSGVIVLRRPLGYGQVMK* PGAAY*GRTG*SHPFFSTDWSTDGTG VRKSIWCHRNCRWESPS
1975	7472	A	2116	167	397	EPLLALLKSGEVAPARQEATGLGEA KCSCAMGLSGPKTQPQEGCEERRL QSKR*SSGDPGWGDEGHWP TPNRS CLL
1976	7473	A	2117	1	540	FCHLQIYYFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*NTSNSSPSSVFVICVTSP AIRKLLNLSLGLSLKFLGSPVGGT AGMGKSVPLSPSQVCCGFRS FNHQ AGHAPGCTVPGSSP*CVSRVQHPSG PCMWWVTYPALSLSFNKSCPWVFP LPTMPPG

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1977	7474	A	2118	1	3121	RQEAELARMGFDLQNVWIVSHINS NYKLCPSYPQKLLVPVWITDKELN VASFRSWKRIPVVVYRHLRNGAAI ARCSQPEISWWGWRNADDEYLVTS IAKACALDPGTRATGGSLSTGNNDT SEACDADFSSLTACSGVESTAAPQ KLLILDARSYTAAVANRAKGGGCE CEEYYPNCEVVFVGMANIHAINSF QYLRAVCSQMPDPSNWLSALESTK WLQHLSVMLKAAVLVANTVDREG RPVLVHCSDGWDRTPOIVALAKILL DPYYRTLEGFQVLVESDWLDFGHK FGDRCGHQENVEDQNEQCPVFLQW LDSVHQLLKQFPCLFEFNEAFLVKL VQHTYSCLYGTFLANNPCEREKRNI YKRTCSVWALLRAGNKNFHNFLYT PSSDMVLHPVCHVRALHLWTAVYL PASSPCTLGEENMDLYLSPVAQSQE FSGRSLDRLPKTRSMDDLSSACDTS SPLTRTSSDPNLNNHCQEVVRVGLEP WHSNPEGSETSFVDSGVGGPQQTV GEVGLPPPLPSSQKDYLSENKPKSH KSCSPSYKLLNTAVPREMKSNTSDP EIKVLEETKGPAPDPSAQDELGRTL DGIGEPPEHCPETEAVSALSKVISNK CDGVCNFPESQNSPTGTPQQAQPD SMLGVPSKCVLDHSLSTVCNPPSAA CQTPLDPSTDFLNQDSSGSVASISH QEQLSSVPDLTHGEEDIGKRGNNRN GQLENPRFGKMPLELVRKPISQSQI SEFSFLGSNWDSFQGMVTSFPSGEA TPRRLLSYGCCSKRPNSKQMRATGP CFGGQWAQREGVKSPVCSHSHNGH CTGPGGKNQMWLSSHQKQVSSTKP VPLNCPSPVPPLYLDDDGLPFPTDVI QHRLRQIEAGYKQVEQLRRQVRE FQ\MLRDIRHWCAPPAEPPMDYEDD FTCLKESDGSDEDFGSDHSEDCLS EASWEPVDKKETEVTWVPDHMA SH\CYNCDCEFWLAKRRHHCRNCG NVFCAGCCHLKLPIPDQQLYDPVLV CNSCYEHIQVSRARELMSQQLKKPI ATASS
1978	7475	A	2123	3	259	FPHRAGPILSSFQVPQRWLVGGFGR NCIAGGESVWDRTNKYTRN*AQE WGMFWSLDGHLGESIIRGRSNTG ALSCPWPLGHL
1979	7476	A	2124	1171	1784	KLYLSVLVKGEAKVVLLKPA\YDV SSFSFF\QRPTVQEFMTFTSQLIVER S/SRKGTRASVKEQDYLCHVYVRN DSLAGE/VVVIADNEYPSRGGPFLL\ EKVLDEFSQAKSHRIDWPVGIPWL TIHYPALDGHLSTRYQNPREADPMT KVQAELDETKIILHNTWPWESLLERG EKLDDLVSKEVLGTQSKAFYKTA RKQNSCCAIM
1980	7477	A	2125	2	262	RGNWVFLHTTEFSLTRSLISFNSCFI TRLECSGAITAHCSLDLLGSS/QSPTS

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						PSRVAGTTGVCHHTQLIYLKQFFLE MRSPFVAQLV
1981	7478	A	2126	36	376	PFDPAVLTAKEAAVRALVASRLAAA SAFTSLSPGGRTSPSQRALHLSVPRP AARVAL\LVHLSRGGAEVQIFAPD VPQMHVIDHTKGQPSGESRCGGGI GTCFLSTSHGAFF
1982	7479	A	2127	3	724	LAAASAFTPLCPVCRTSPSQRALHL CVPRPAGRVSLVLSGCGVYNGTDIH EASAILVHLSRGGAEVQIFAPDVPH MHVNDHTKGQPSGESMNVLTES ERIRRGKITDLANLSAANHDAAIFF GGFGAAKNLSTFAVDGKDCKVNKE VERVLKEFHQAGKPIGHSLKDLPGH CPGRPLKWSLRKRCRLRAPEGGPC CSRVTAGVKVSPMVSTSGSRPCQRS VPWMSAQREEMALSSVTD
1983	7480	A	2128	172	1020	PSDPAVLTAKEAAVRALVASRLAAA SAFTSLSPGGRTSPSQRALHLSVPRP AARVALVLSGCGVYDGTIEHEASA\ ILEHLSRGRAEDHIFAPDVPHMHVI DHTKGQPSGESRNVLTESARIARG KITDLANLSAANHDAIAIFF/GEGFG AAKNLSTFCRWTKICKVNKEVER VLKEFHQAGKPIGLCCIAPVLAAG VLKGVEVTVGHEQEEGKWVYAG TAEAILALGAKHCVK\EVVEAH\VD QKNKVVTTPAF\MCETALHYIHDG\ GAMVRKVLELTGK
1984	7481	A	2129	1	416	IQYRSDLELHSITMKKGGVLFLLGII LLVLIAAHGTPVVRKGRCSCHITNQ GTIHLQSLKDLKPFGPSQCKIDIIA TLKNGIQTCLNPDSDA\VKELIKKW EKQVSQKKKQKNGKKHQKKKVLK VRKSQSRQKKT
1985	7482	A	2130	2	81	
1986	7483	A	2131	2	130	
1987	7484	A	2132	1	524	RPRIRHEPQTQREPTMVLSPA\DKTK AQRPPRLKLGATPGEYGGEPLER\ VLFPPPTPKPYFPH\DLSHG\SAQVK GATAKKVA\DALTKAVAHVDGHA QTALSALSDLHGAQAFGWDPVNF QASLSHLPCLGEPWAGPPSPAEPHP LAVARLPWGQSFLGFLKHKRCLNL PNYR
1988	7485	A	2133	388	654	GLFFVLQFFFLFCFVFLRSHSVSQAG VHWCRRHGSAAST/SPGSSDPPTLAS\ KVLGVTDMSHCTWAESYFFTKMGS SPVVACACSSSYLGG
1989	7486	A	2134	384	622	INAPPRCPQLC\TSEVCAME/CPQRV PAGPCPGCPRGNLLIHAPSNRPGTTS QINDPQPFLRICFWGSPKTPSHRHS FFF
1990	7487	C	2135	44	340	MKCSQPXRCHFQSD\FQKCAPCPRA QTHWLEPPGRVQTISSMRNAQKGF ADSIRLWRLPASGVGVVVSPEGAG DPSHLLDPPGHSAPYSPAPRQLSRV

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						P*
1991	7488	C	2136	2413	2829	MFPRRACATCPNLKRACVCAPLRP RFGTSRVWCACLLPSPEPTGSVNVI FYVPLPSGLLSTSAPGSRASGVGV LEGARGSFSSPWTLPGHFWSLFPSS LGSLSRCPLGKGDQEALVQGALGW GQRAWTPAQCSVDNG*
1992	7489	A	2137	69	332	YQVLKTDKNMSRISFFPFLRKGLAL SPRMECSGAITAHCSLRISQSQ/DDP/ AHVSLSSWGLQGTCHHTQLIFLFF VGDEGLCCPGVRS
1993	7490	B	2144	73	358	XVPGSRGPETKLWDDFSMSQATKR KHVVKEVLGEHIVPSDQQQIVRVLR TPGNNLHEVETAQGQRFVLSMP YRKNIWIKRGDFLIVDPIEEGEK*
1994	7491	A	2145	80	201	
1995	7492	A	2146	498	748	FLPRRGDNDSTYPQ/WTKACRRRRRT CW*T*TWIRSGQRKMWSCGRRSL TTCMPRTRTAARLMACGSGSWRR SGPSCGRLSP
1996	7493	A	2147	1	1764	MTTSQKHRDFVAEPMGEKPVGSLA GIGEVLGKKLEERGFDKAYVVLGQ FLVLKKDEDLFREWLKDTCGANAK QSRDCFGCLRE/WCAKSRPAAEVSE LKADSKEGPQAQGPEQERTGL
1997	7494	A	2148	842	1186	FLPRRGDNDSTYPQ/WTKACRRRRRT CW*T*TWIRSGQRKMWSCGRRSL TTCMPRTRATTTWRSLNLSCP SMTKSLKSGHPSAWSRAARLMA CGSGSWRRSGPSCGRLSP
1998	7495	A	2149	526	1158	SCGLSLIKMTTSQKHRDFVAEPMGE KPVGSLAGIGEVLGKKLEERGFDKG L/YVVLGQFLADIEKMTSFREWLK DTCGANAK\QSRDCFRMPFEKWCE ALLVDALLGKFSIPPAPQSRSLASRS RDSSPCPSYEGKD\CYC\RTHL\RRYF RGSFGEFSPLNHFQLFFGILRSWHAF PRPFFPWVPSWVTVYQLFEWDFP GPIPHPHFQSV
1999	7496	A	2150	150	446	HEGLLLKLRLSDVYFLLFFETRSCF VAHAGVQWHHYNLSL/T/PPGT PPLLASQVAGSTGMNHQAQIKKTF FGENMILLCCSGWLSGIFVLYSLY
2000	7497	C	2151	203	427	MNFVRSIWMAQSTILLTARGXATLI IAISFLAPXLAQSVHAVSSFQSQAD LLNGQCGFQQSSEPQPHVHTTSS*
2001	7498	A	2152	1	1065	
2002	7499	A	2153	597	1292	QTFSNTIFLLTRHKQHSMLVPMNT PGVKIIRPLSVFGYTDNFHGGHFEIH FNQVR\VPATNLILGEGRGFEISQG RLGPGRIHHCMRTVGWAERLLQI MCERATQRIAFKKLYAHEVVAH WIAESRIAIEKIRLLTLKAAHSMDTL GSAGAKKEIAMIKVAAPRAVSKI VDWAIQVCGGAGVSQDYPLANMYAI TRVRLADGPDEVHLSAIAATMELRD QAKRLTAKI

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2003	7500	A	2154	1694	1886	ASDSRVPAAGIS/PSAPFPTQLSPRRS PPSPPPPPQSPGLGIFSPKASPVGILHL FKTLFCILNV
2004	7501	A	2155	1002	1480	MLLLKTTERFEVSVCMACTYV\SNL GKKQRSVSFLASGLMRVSTGPELRL HHSFVLTDVGRRICRLLVGLFTKG DTSSKR\HPFSPGP\CFLLCDLAR\V GSSPKJNRVPHFTRTQTSTQRSCTVF VWQRCSLVGPFQVTFTMYFHHSLS RSISRFS
2005	7502	A	2156	1	1623	RLPFVDVDARVYADAPAKLLLPL AFWELAVRLRGAEAAASERQVYSVA VKLLLHPAFQSCLLLTLLGLWRTT PEAHASSLGAPASAAASFLQDLHRY GEGDSLTLQQLKALLNHLDVGVGR GNVTQHVQGHRNLSTCFSSGDLFT AHNF\SEQLRIGSSELHEFCPTILQQL DSRACTSENQENEENEQTEGRPSA VEVWGYGLLCVTVISLCSLLGASV VPFMKKTLYKRLLLYFRALAIGTLL LKRLFQLIPGAVWFQPLEDYVVS AVVFGGFY\FFTEKILKILLKQKNE HHHGHSHYASESLPSKKDQEEGVM EKLQNGDLDHMIPQHCSSELDGKA PMVDEKVIVGSLSVQDLQASQSAC YWLKGVRYSDIGTLAWMITL\SDGL HNFIDGLAIGASFTVSVFQGISVAV LCEEFPHELGDVFIL\LNAGMSIQQA LFFNFLSACCCYLGLAFGILAGSHFS ANWIFALAGGMFLYISLADMFP NEVCQEDERKGSILIPFIIQNLGLLTG FTIMVVLTMYSQIQIG
2006	7503	A	2157	1	604	MGTRWEPGWAPGLAPAAQARSS GRAAPAAGSERARERERDGGSVGG GGSSAIPSERAAAHGEDSGAYR WERANRPFSNNCCCLAFYLGMEEA RWLYAGLFCVYGASLIAIAITHVPLF GSQIKAE/DPSGDSAPAAHLPPQPAQ /PHLPQAQLMLTGSQLAGHPLGMR WSMATQHAGCVSQRCLFPMTVG CSQGNILWSL
2007	7504	A	2158	22	1358	VHFSMGAPEIRMSKPLEAEKQGLDS PSEHTDTERNGPDTNHQNPQNKTSP FSVSPTGPSTKIKAEPSGDSAPAAP LPPQAQPHLPQAQLMLTGSQLAG DIQQLLQLQLVLVPSHHLQPPAQF LLPQAQSQPGLLPTPNLFQLPQQT QGALLTSQPRAGLPTQPPKCLEPPS HPEEPSDLEELQFARTFKQRRIKLG FTQGDVGLAMGKLYGNDFSQTTIF RFEALNLSFKNMCKLKPILLEKWL DAETMSVDSSLPSIQLSSPSLGF LPGRRRKKRTSIETNVRFALEKSFL ANQKPTSEEILLIAEQLHMEKEVIRV WFCNRRQKEKRINPCSAAPMLPSPG KPASYSPHMTVPQGGAGTLPLSQAS SSLSTTVTTYILSCGDAPPQPD SWR GWGRGRGCAPPQFHPLCHSPTPGH

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						HQQHKPQPLKAATRLSACQA
2008	7505	A	2159	3	452	
2009	7506	A	2160	9	633	NSARATDSERTHHGARLLPDKTNV KAAWGKVGAGAHAGEYGAEALERMF LSFPT\TKTYFPFDL\SQRSAQVKG ATGKKVADALTNAVA\HVD\DMPO TALSGPEATLHGAQSFGVDPVQLSS SLSHWPAWLTGPAHLPRPSFNPW RLQRLPWGQSFLGFLVEEPLLEPSKI PVKAWKPSGWPCFLCPFASPGQGP SLSWNPYPRWSFE
2010	7507	B	2161	55	372	MERFLMDGFQPQQLSTYALTLYKH TATVDGKTILVADINVTQKSFNFAK KFSPLPLYFVSAADGTNVVKLFNDAI RLAVSYKQNSQDFMDEIFQELENFS LEQEEEN*
2011	7508	A	2162	552	1809	QLRGRGASRKWSALRRELGRRAWF ESAQSPDWRQGPGRTPSRVPLSSP HSEPHPEMAEDKTKPSELQDGKYD ADDNVKIIICLGDSAVGKSKLMERFL MDGLYPSRFEVLLVPVGLPTLMYQ CPTAHPFVPAAQEGGLDFWDTAGQ DTLSSPPTPHPSMELVPVCSQPQLS TYALTLYKHTATVDGKTILVDFWD TAGQERFQSMHASYYHKAHACIMV FDIQRKVTYRNLSTWYTELREFRPEI PCIVVANKIDDRPMSYLLSTADINV TQKSFNFAKKFSLPLYFVSAADGTN VVKVWLTAEVASKLFNDAIRLAVS YKQNSQDFMDEIFQELEVGVQVHISG GMEETAPLQG*GLQPSRVTLA*VCP TKCIRAAVEQMGGQASPATLFTNF SLEQEEEDVPDQEQQSSSIETPSEE
2012	7509	A	2163	807	1389	EPMAENKTKPSELQDGKYDADDNV KIIICLGDSAVGQSKLMERFLMDGFQ PQQLSTYALTLYKHTATVDGKTILV DFWDTAGQERFQSMHASYYHKAH ACIM/LDINVTQKSFNFAKKFSLPLY FVSA\ADGTNVVKLFNDAIRLAVSY KQNSQDFMDEIFQELENFSLEQEEE DVPDQEQQSSSIETPSEEVASPHS
2013	7510	A	2164	3	923	RAARTRAEPEVECAAARAGPAGVV RERAESRHGGRRAGADPQRPWSLQ PSLGTARDNTLPSLGPGLSTARS QWAKNKTKPSELQDGKYDADDNV KIIICLGDSAVGKFKLMERFLMDG\ FQPQQLSTYALTLYKHTATVDGRTI LVDF\HTAGQERFQSMHASYYHK AHA\CIMVFDVQRKVTYRNLSTWY TELSGSRPEIACIVVANKIDADINV TQKSFNFAKKFSLPLYFVSAA\DGT NVVKLFNDAIRLAVSYKQNSQDFM DEIFQELENFSLEQEEEDVPDQEQQS SIETPSEEAAASPHS
2014	7511	A	2165	1	2715	
2015	7512	A	2166	1	2256	
2016	7513	A	2167	339	1086	IQMNRFL\LMSLYLLGVSARGTSSQ

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						PNELSGSIDHQTSVQQLPGEFFSLEN PSDAEALYETSSGLNTLSEHGSSEH GSSKHTVAEHTSGEHAESEHASGEP AATEHAEGEHTVGEQPSGEQPSGE HLSGEQPLSELESGEQPSDEQPSGEH GSGEQPSGEQASGEQPSGTILNCYT CAYMNDQQKCLRGEGETCITQNSQQ CMLKKIFEGGKLQFMVQGCENMCP SMNLFSHGTRMQIICCRNQSFCKNI
2017	7514	A	2168	2	425	
2018	7515	A	2169	2	169	GRVGDTLKAGINAVERRSNRCNGN SGFEGQSRYPSSGMSAKELCEND DLSTSLVLDPYLGFQTHKMNTR*FG S
2019	7516	A	2170	2	227	
2020	7517	A	2171	177	1400	LNAPGSQLSVGMKGLGESKNMVV NGRRNGGPLSNDHQQNQSKLQHTG KDTLKAGKNAVIERRSNRCNGNSG FEGQSS/RYPVSYGMTAKELCEND LATSLVLDPYLGFQTHKMNTSAFPS RSSRHF\SQSDSLSHNNPVFRPIKG RQEELKEVIERFKKDEHLEKAFKCL TSGEWARHYFLNKNKMQEKLKE HVFIYLRMFATDSGFELPCNRYSS QNGAKIVATKEWKRNDKIELLVGCI AELSEIEENMLLRHGENDFSVMYST RKNCAQLWLGPAAFINHDCRPNCK FVSTGRDTACVKALRDIEPGEEISC YYGDGFFGENNEFCECYTCERRGT GAFKSRVGLPAPAPVINSKYGLRET DKRLNRLKKLGDSSKNSDSQSV/SA LNTDADTTQEKNIASK
2021	7518	A	2172	3	114	
2022	7519	A	2173	328	471	
2023	7520	A	2174	1	190	
2024	7521	A	2175	2	132	SGLGRLPGPWQEAGSSRGPSGDM AGVKALVALSFSGAIGLTF/LHMLG CALEDYGVYWPLFVLIFHAISPIPHF IAKRVTYDS DATSSACRELAYFFTT GIVVSCLWISPVILARVALIK\WGAC GLCV/VAGNAVIFLTIQGVFFPIFGRG DDFSWEQWGYWTDFS
2025	7522	A	2176	191	479	NTSLPNPSEVSHSSLRLDSGGAEAF VGGGTGVLKKPEGAGPAAPS/LGW RPRG*APHRTGSAQPPTAVPCR/PGA LGEDSSPGPPGALGGLGVIPQPSM
2026	7523	A	2177	1920	2524	TQYPPAEQRSQTLMQDVFALPLNSL CAQSSKTLNCKTQCHPCSILCKNLL KNKCLILHSRFTIQTAFEGGQLRI PLFPKPKVRSSQFQASVLELRRSQK PFVGGGTGVLKKPEGAGPAAPTSG WRPRGEAPHRTGTAQPPTAVPSGG RIWGKIPLPGPPGALEGVGFPSASPR FQLQPRCLKLDAGRRLRSGSKPHVK HL
2027	7524	A	2178	239	380	
2028	7525	A	2179	34	202	EPTTRQTLYMLITFTPHNHLVRETSS

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						VPFEQMKN*GSERFNTLSKALQTISAKTRI
2029	7526	A	2180	1	1566	
2030	7527	A	2181	574	1949	KSKCRFPEGLSEGFGPMRKEALSSG SVQEA EAMLDEPQEQAEGSLTVYVI SEHSSLLPQDMMSYIGPKRTAVVRG IMHREAFNIIGRRIQVAQAMSLTE DVLAAALADHLPEDKWSAEKRRPL KSSLGYEITFSLNPDPSKSHDVYWD IEGAVRRYVQPFLNALGAAGNFSV DSQILYYAMLGVNPRVYSASSSYIF GHAQLPHVINPVESRLGSSAASLYP VLNFLLYVPELAHSPLYIQDKDGAP VATNAFHSPRWGGIMVYNVDSKTY NASVLPVRVEVDMVRVMEVFLAQ LRLFLGIAQPHLPPKCLLSGPTSEGL MTWELDRLLWARSVENLQATT LTSLGAASWARSATLFIKGRRGHLE VLQRL LAPVQKSAEELASGHL DLP LSPAREAVTSSELAFFDPSLLHLLYF PDDQKFAIYIPLFLPMAVPILLSLVKI FLETRKSWEKA
2031	7528	A	2182	76	419	
2032	7529	A	2183	71	350	AFIPAMAELIQKKLQGEVEKYQQQLQ KDLSKSMGRQKLEAQLTENNIVK EKRYESQLRDLERQSEQQRETLAQ LQQEFQRAQA AKA GAPGKA
2033	7530	A	2184	175	1032	GLLPHLGPRVQRLPRLSLSTLPCSLT RCPHPFLLPQIHHLTRIVGIGGTFDV SKLPFLSSPDLSKSMGRQKLEAQL TEYNIAKEVRDWDLWGEEGPVLA MVLITYVPSLHQELALLDGSNVVFK LLGPVLVKQELGEARATVGKRLDY ITAEM*VFIPPPCAAPCDASEPLE*R C*TIAEQLSIVAPSPVPPTLSFPF*PP FFSLPWISRSTYLFLAFSTLHSESY* FLPFCLSPSLLSKRYESQLRDLERQ SEQQRETLAQ LQQEFQRAQA AKA APGKA
2034	7531	A	2185	112	520	AFIPAMAELIQKKLQGEVEKYQQQL QKDLSKSMGRQKLEAQLTENNIV KEELALLDGSNVVFKLLGPVLVK QELGEARATVGKRLDYITAEIKRYE SQLRDLERQSEQQRETLAQ LQQEFQ RAQA AKA GAPGKA
2035	7532	A	2186	635	1015	GGQKHPTGLLKPPANTAATMPKRRK AKGDAKGDKAKVKDEPQRRSARLS AKPAPPKPEPGLKKASIAKKGEKL/P KGRKGGKADA\GKGLGNNPAKNPR LPLHFQFQKAE\GTGGLPSEMFIFES SGTYW
2036	7533	A	2187	302	471	TLSHRVLVEAQSREQLAALKKHHE EEI\VHHK\KEIERLQKRNL SRHK\QK DSKLLKH
2037	7534	A	2188	3	399	LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLGRV/WGVRTMQA RFGSDQSENFTGPRAHP/RKAG

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						GALGKREQAEEERYFRAQSREQLA ALKKHHEEE\VHHKKKE\ERLA FERHKQK\KMLKH
2038	7535	A	2193	2	406	ARAEMSRVALAVLALLSLSGLEAI QRTPKIQVYSRHPAENGKSIFLKCY VSG\FHPSDIE\VDLLKNGKE\RLKK VEPSDLS\FSAKDW SFYLLPYTEFH PQLKKDGVCPARVN\HVTLSAPARL VK\WDRRHVKQHQ
2039	7536	A	2197	319	393	WL/TPVIPTLWEAEVGGSFHRSSR
2040	7537	C	2198	84	290	MLPSKGLSFFSLQHLRDSRSLFPM SMITMLELECCRASSNHEVRWLKX HXVSQICSLICFPXMLTIRA*
2041	7538	A	2199	2	743	PRVRSEVSRYRSLADPEPTGRDTMT YADLFKYIIIGDTGVGKTCFLLOFTD KRFQPVHDL SLGVEFGGSLCSTLME NQFKLHIWD\TAGQESFRSITRSY\Y RGAAG\ALLVYDITRALKPFNHLAS WLGGLPGQHFSFPTWVIHCFIGNKS DLESRRDVKREEGEAFARE\HGRIFR GTSAKTACN\VEEAFINTAKR\YRKI HQGLFDVHNEANGIKIGPQQSISTSV GPSASQRNSRDIGSNSGCC
2042	7539	A	2202	20	222	
2043	7540	A	2203	1	458	RSSLTSLSNSAAAMAPVKKPCGEG GAKKKKQVLKFTLADCTHPVEDGI MDAAQF*ASFCKERIKVRKKLGT LSGGG/V*PIERSKISKITVT\SEVPFS KRV/YLKYLTKKY\LKNNLRDLV CRVVAYQPKREL RNYSYFQINQ\DE GRREED
2044	7541	A	2204	2	321	FIFFSFSFFSFFSETGSCSVAQAG VQCHDHGSPQS/PNLP GSSDLPTSAS \KVLGITGVRHHSPLPLGFQMGIFLL FSMLKFCFWVCSALLCTVLEFLRTN YFLS
2045	7542	C	2205	46	234	MTLRXWITWPFLFLSPSSKCLHLI ASILLDLQLGSTHSSLSTIFFVVLAF RKIGLVCP*
2046	7543	A	2206	1	243	
2047	7544	A	2207	144	479	RPLKPRRTF\CKK\CGKAPNPHKSDH STKKGKDSLYAPGKAAMTRKQS GYGGQ\TKPIFRKKA\TTKKIVLKA LSALSPTCRSKRMLAFKRWQAFNL LGDKKRGPSASS
2048	7545	A	2208	75	540	GGSGSVRVLRSESPREEAVEEEVAA VAVVVAVAEAGTNQLRAETMANI AVQR\IKREFKEVLKSEETSKNQIKV DLVDENFTELRGEIAGPPDTPFERG RFP\LELKIP\ETYPFNPPK/VFRFYAL KLWHPNISSV\TGAICLDIL\KDQWG SWQWT
2049	7546	A	2211	1	2640	MYSGNRSGGHGYWDGGGAAGAE GPAPAGTLPAPLFPSTYERLALLL GSIGLLGVGNLLVLVLYYKFQRLR TPTHLLLVNISLSDLLVSLFGVTFTF VSCLRNGWVWDTVGCVWDGFGSGS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LFARPAPLPARPRAPRPTPPRSPLAS STLPDPSRMAGAFLLRPLPPHAVQ DSIPVVSHLPPTCHQTLLLPKMADN LPTEFDVVIIGTGLPESILAAACSRSG QRVLHIDSRSYGGNWAFFSFGSL SWLKEYQQNDIGEESTVVWQDLI HETEEAITLRKKDETIQHTAFCYAS QDMEDNVEEIGALQKNPSLGVSNT FTEVLDSALPEESQLSYFNSDEMPA KHTQKSDTEISLEVTDEESVEKEK YCGDKTCMHTVSDKDGDKDESKST VEDKADEPIRNRITYSQIVKEGRRFN IDLVSKLLYSQGLLIDLLIKSDVSRY VEFKNVTRILAFREGKVEQVPCSR DVFNSKELTMVEKRMLMKFLTFC EYEQHPDEYQAFRQCSFSEYLKTKK LTPNLQHFVLHSIAMTSESSCTTIDG LNATKNFLQCLGRFGNTPFLFPLYG QGEIPQGFCRMCAVFGGIYCLRHKV QCFVVDKESGRCKAIIDHFGQRINA KYFIVEDSYLSEETCSNVQYKQISR AVLITDQSILKTDLDQOTSILIVPPAE PGACAVRVTELCSSTMTCKMDTYL VHLTCCSSKTAREDES VVKLFT YTETEINEEELTKPRLLWALYFNMR DSSGISRSSYNGLP SNVYVCSGPDC GLGNEHAVKQAETLFQEIPTEEFC PPPNPEDIIFDGDQKPER/PLGTNN VVMAKLESSE\ESKN\ESPEKHPSK LEKSNLEMLFWTSFMASEFSLKDR RFPI
2050	7547	A	2212	328	583	
2051	7548	A	2213	1	416	PSSGDMAGVKALVALSFSGAIGLTF LMLGCALEDYGVYWPLFVLIF\HAI SPIPHFIAKRVTYDS DATSSACRELA YFFTTGIVVSCLWISPILARVALIK\ WGACGLVLAGNAVIFLTIQGFFLIF GRGDDFSWIEQW
2052	7549	A	2214	1	180	AAATGAVGAAIYPCAAPNWK*RND EKTAADYKILGGSVLHLVLALRGG GGLRQ
2053	7550	A	2215	162	557	VASEHSPKIGASQGLDYEPLL VVAK VWYLTRPTGTKAGSVFSQYLPFLEP GILGPASLPWLRQTLTGKEIEIDIEP TDKVERNQRSVWEEKEGNPPPPQQ RLHLQVAKQMNDKDSLIYKILR WVQSFQT
2054	7551	A	2216	684	1496	LETSGLSENPLGQAVGFGQDEFFLE QTKKKGVKRPARLHTKPSQAPAVE EAPSGA\SYNPSFEDHQTL LSAHE VELQRQKEAEKLERQLRPCATEQ ARHPRSSTFQELCEGLLEESDGE PGQGEPEAGDAEVCSTPARLATT EK\KTEQQRREKAVHRLRV TARA ALRAA\RLRATQELVFRVRGIQRPQ V\ALRLA\ELARRRRRRQARREAEA \DKPRRLGT/RFKYQAPDIDVQLASSE LTDSLRTLKPEGQHPSRPVQELPRG

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						GI
2055	7552	A	2217	116	285	KLRNQRIQERHTDGGGEPLKSL*CSP KTRVESRSASRRGPLFLNKGHARAR SSLTLA
2056	7553	A	2218	3421	3698	AGRGPLRLQSHRFGPQSQVDCLSPA APDQPGQHGKTPSPQK\IQKLAGHG GAHLQSQPLGRLRREDPLSPGGGGC SEPRSHHCTPAWAREYGD
2057	7554	A	2219	381	1772	KMAESEN\RQELSES\SQEEAGNQIM VEGLGEHLERGEDAAAGLGDDGKC GEEAAAGLGEEGENGEDTAAGSGE DGKKGDDTDEDSEADRPKGLIGYV LDTDFVESLPVKVKYRVLALKKLQ TRAANLESKFLREFHDIERKFAEMY QPLLEKRRQIINAIYEPTEECEYKS DSEDC\DDEEMCHEEMYGNEEGMV HEYVDEDDGYEDYYYDYAVEEEEE EEEEDDIEATGEENKEEEDPARGIPD FWLTVLKNVDLTPLIKKYDEPIK LLTDIKVKLSDPGEPLSFTLEFHFKP NEYFKNELLTKTYVLKSLAYYDP HPYRGTAIEYSTGCEIDWNEGKNVT LKTIKKKQKHRDL/WGTIRTVTEDF PKDSFFNFFSPHGITSNGRDGNDDFL LGHNLRTYIIPRSVLFFSGDALESQQ EGVVREVNDAIYDKIYDNWMAAI EEVKACCKNLEALVEDIDR
2058	7555	A	2220	17	250	
2059	7556	A	2221	2	899	GFSKKCVSSRSPELRVTRLRYLRIQ AFRGSLATADLLLLVSPLRHPEPA KVLVLFLLSFASCWAGPGRAGPPG RSLTMA SLF\KKKTVD DVIKEQNR ELRGTQRANRDRAALEKQEKQLEL EIKK\MAKIGNKEA\CKVLAKQLVH LR\KQKT RTFAVSSKVTSMSTQTKV MDS\QMKMAGAMSTTAKTMQAVN K\KMDPQKTLQTMQEFFGRENMK M\EMTEEMINDTLDDIFDGSD\EEE SQ\DIVNQVLDEIGIEISGKMAKAPS A\ARSLPSA\T\SKATISDEEIERQLK ALGVD
2060	7557	A	2222	3	586	ARAMGISRDNLHKRRKTGGKRKPY HKKRKYELGRPAANTKIGPRRIHT VRVRGGNKKYRALRLDVGNFSWG SECCTRKTRIIDIVYNASNNELVRTK TLVKNCIVLIDSTPYRQ/WTPEEEEIL NKKRSKKIQKKYDERKKNAKISSLL EEQFQQGKLLACIASRPGQCGRAD GYVLEGKELEFYLRKIKARKGK
2061	7558	A	2223	2	727	LFPASAEQMGISRDNW\HKPARKTG GPRESPTYQAEAKSM SLGRPAA\NTK ILAPRRIQHSPVCRGG*QVNTVPLRF D\VGNFWSWG/SKECCTRKTRIIDVV YNAI**PSWVRYRPLVERICIVLID EQHPYRQWVRSPTYALPLGPQRK GAKLDSL RKEEJFKPKTDLK*IQKK YD*/ERKKNCQNSASLPGRSSFQQG KASLRCIAFK/RPGQCGRADGYMT

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						RGHRVRSYYLRKIKARQSKINT
2062	7559	A	2224	298	408	CGII*ALNKKEHRGCDSPDPDTSYV LTPHTEEKYKKINEEFDNMMRNH KI APGLPPQNFSMSVTVPTSPNALS YTNPSS
2063	7560	A	2225	1	1369	
2064	7561	A	2226	409	1944	LKMGRKKIQITRIMDERNRQVTFTK RKFGMLMKAYELSVLCDCEIALIIFN SSNKLQYASTDMDKVLLKYTEYN EPHESRTNSDIVEALNKKEHRGCD SDPDPDTSYVLTTPHTEEKYKKINEE FDNMMRNH KIAPGLPPQNFSMSVTVPTSPNALS YTNPSSSLVSPSLAASS TLTDSSMLSPQTTLHR\NVSPGAP QRPPSTGNAGGMLSTTDLTVPNGA GSSPVGNGFVNSRASP NLIGATGAN SLAGKVMPTKSPPPGGG NLGMNSR KPDLRVVIPSSKGMMPPLSEEELE LNTQRISSSQATQPLATPVVSVTTPS LPPQGL\VYSAMPTA YNTDY\SLTS ADLSALQGFNSPGMLS LGQVSAWQ QHHLGQAALSSLVAGGQLSQGSNL SINTNQNISIKSEPTSPPRDRMTPSGF QQQQQQQQQQQPPPPPPQPPPPQPP QPPRQEMGRSPVDSLSSF\SSSYDGSD REDPRGDFHSPIVLGRPPNTEDRESP SVKRM RMDA WVT
2065	7562	A	2227	3	168	PCPTHSRMLGSPQPKRQLPVAPVPT AQP\PPSPPKGRCQGQEPKPPRLSP AQGPW
2066	7563	A	2228	272	416	VGRCFLLSSGGFFSLTSALPPPS/PSA HPGVLVTPFGAPTKPDRGRSRG
2067	7564	A	2229	109	866	DTRVGYFSSGAFAFFFLWARAECRP LSKDSL VKPRATLPSIVGLGSVAVP RARRARRQRERSRPTGPGACLPPS LAPYGFARVERRRAMKAGFPVRR SGRKAPYGC GGME LALRCLAEHG HSLGG\SAALGAS\AAAARCKAAEA AADEPALCLQCDMND CYSRLRLV PTIPPNNKVKVEILQHVIDYILDQ LALETHPALLRQPPPPAPPHHPAGT CPAAPRTPLTALNTDPAGAR\NKQ GDSILCR
2068	7565	A	2230	107	1073	
2069	7566	A	2231	23	538	LPEVPHSLRPRVKPHLCCAQPAVRV MARLPKLAVFDLDYTLWPFWVD T HVDPPFHKS/KVR*GQRLGAR*DP ARAERTLALSSDGTVRDRRGQDVR LYPEVPEVLKRLQSLGVPGAAASRT SEIEGANQLLELFDLFRCYLHSHPE WNESSNSKSRVRDICEGPNWAFEV QP
2070	7567	A	2232	685	1161	TFPLLPLADYTLWPFWVDTHVDPPF HNSR*GRDREDW/PAR*DPARAERT LALSSDGTVRDRRGPDVRLYPEVPE VLKRLQSLGVPGAAASRTSEIEGAN QLLELFDLFRYFVHREIYPGSKITHF

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						ERLQQKTGIPFS\QMIL\FDDERRNIV DVSKLGTE
2071	7568	A	2233	79	564	SPTSAARSLRLRVMARLPKLAVFDL DYTLWPFWVDTHVDPPFHKSSDGT VRDRRGQDVRLYPEVPEVLKIDLQS LGVARCGCFQGQVRLGRGQPATGA LLTFFRYFVHRAEIYPGSKITHFERVA AE\TGISF\SQMIFDDERREYCRRSA NWCVTCTSHPEW
2072	7569	B	2234	48	209	XKNQCETRTMQENGYSSHAVDGT GPAGGAGRPAGSTGAQVSVQPNFQ QDKFLGRX*
2073	7570	A	2235	2	353	
2074	7571	A	2236	3	676	SAVEFPPLSHTTGTRPRTPIILQQE NGYFIHTLWMGLALLGVLGDLGSGQ HRRRSPCQPNFQDKFLGRWFKR G\LASNSSWLREKKAALSMCKSVV APATDGG\FNL TSTFLQEKTSVETR TML\LPQPRGVPSASLQLTGVPHWGQ A/HYSVSVVETDYDQYALLYTRAS KGPGEFRMATLYSRTQTPRAELK EKFTAFCKAQGFTEDTIVFLPQTDK CMTEQ
2075	7572	A	2237	1	1165	MGVTEVFLKDV TILLNLEELVQCRQ TWGEARTRGKRVLGSLADEIVVRT QPPSLEHKAWNATCKHWLAEEA ALEKYYLSIFYGIEFVVGVLGNTIVV YGYIFSLKNWNSSNIYLFNLSVSDL AFLCTLPMLIRSYANGNWIYGDVLC ISNRYVLHANLYTSILFTFISIDRYL IIKYPFREHLLQKKEFAILISLAIWVL VTLELLPILPLINPVITDNGTTCNDF ASSGDPNYNLIYSMCLTLLGFS\IPLF VMCLFYKIALFLKQRNRQVATAL PLEKPLNLVIMAVVIFSVLFTPYHV MRNVRIASRLGSWKQYQCTQVVIN SFYIVTRPLAFLNSVINPVFYFLLGD HFRDMLMNQLRHNFKSLTSFSRWA HELLLSFREK
2076	7573	A	2238	1	567	
2077	7574	A	2239	58	544	GKKMGSKAKKRVLLPTRPAPPTVE QILEDVRGAPAEDEVFTILAPEDPP VFRMMEDAEAPGEQLYQQSRAVY AANQRLQQAGNVLRQRCELLQRA GEDLEREVAQMKQAALPGGEGWL LGLTLWGLGALGRAQGSATQAL PGGPSAPDWHSRGPSRGC
2078	7575	B	2240	1	1551	MCELDILHDSLYQFCPELHLKRLNS LTLACHALLDCKTLTLTELGRNLPT KARTKHNIKRIDRLLGNRHLHKERL AVYRWHASFICSGNTMPIVLVDWS DIREQRLMVLRSVALHGRSVTL YEKAFPLSEQCSKKAHDQFLADLAS ILPSNTTPLIVSDAGFKVPWYKSVE KLGWYWLSRVRGKVQYADLGAEN WKPISNLHDMSSSHSKTLGYKRLTK SNPISCQILLYKSRSKGRKNQRSTR HCHHPSPKIYSASAKEPVVLATNLP

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						VEIRTPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDIMLLI ALMLQLTCWLAGVHAQKQAFPCD DSSAVHRLRYCKGRDYNRVRSSCV QRHAPVLNRKIGTGSDQHANEFGLS WILLGARTPTCKADLSRPYSCPH QPQQRFLGDSGITTTSVPRYRGQEH CLHPKLQSTKRFIKCTTAWNENRRK YQVMPIEAQRPKCQLLFPNRSPTWQ ISIDKGRQDTFMLFPPIKI*
2079	7576	A	2241	2	456	GTRSTRTARRRWLSSPPRACPGTEV RSTACTPSCAPPVSMRLAAALLL LLALYTARVDGSKCKC\SRKEPKIR YSDVKKL\EMKPK\YPHCEEKMMVIIT TKSVSRYRGQEHCPHPKLQSTKRFI KWYNA\WNEKAQRRVYEEAQGLR RRIG
2080	7577	A	2242	308	615	ETRVASWGTGAAEV*GMVRLDISE GRAAVAAVVGGVVAVGTVLVALS AMGFTSVGIAASSIAAKMMSTAAIA NGGGVAAGSLVAILQSVGAAGLSV TSKVIG
2081	7578	A	2243	332	484	
2082	7579	A	2244	240	610	LWVEVQSEWRLTEAKGPTMGKES GWDSGRAAVAAVVGGVVAVGTV\ PWRSSAMGFTSVGIAASSIAAKMM STAAIANGGGVAAGSLVAILQSVGA AGLSVTSKVIGGFAGTALGAWLGS PPSS
2083	7580	B	2245	158	2382	MARGKAKEEGSWKKFIWNSEKKEF LGRTGGSWFKILLFYVIFYGCLAGIF IGTIQVMLLTISEFKPTYQDRVAPPG LTQIPQIQKTEISFSSMAIRDAGFEIS AMQMFNMDRVNVEQFYEVYKGV VTEYHDMVTEMYSGPCVAMEIQQ NNATKTFREFCGPADPEIARHLRPG TLRAIFGKTKIQNAVHCTDLPENGL LEVQYFFKILNN*
2084	7581	A	2246	753	1007	LAQGCSPGPSQDTALGPPPPCTEP/ CPVPYVLRSTPEPPQHGTCHSPCLLP IPLCSSPSLGGGGNSEGEKALTFHV CGDHPVKN
2085	7582	A	2254	188	833	ALIMSFIFEWIYNGFSSVLQFLGLYK KSGKLVFL\GLDNAGKTTLLHWLK DDQIGPTLFPPLPPTSEELTIAG\MT\ FTTFD\LGGHGAKHVAVWKN\YLP QLMGFVFLVDCA\DHFSPSWNPKE LNALMT\DETILMCPIL\ILGNK\IDR TDAISEEKLREIFGLYGQTTGKGNV TL\KELNA\RPMEVFHVAVLLKEGK VYGRGFSAGLLPVLF
2086	7583	A	2256	333	621	CRKNSCYQAQNFNLRIPFSTTKLINL FHF*NDSQKST*/SDSHLARSSQFCS LN*NY*I*TAKSHDVVCTRQHFP ESYIWHVKEKKYNPTAAAI
2087	7584	A	2257	29	659	LSVASFSFLSNASAEDTMSRLSRLL WAATCLGVLCVLSADKNTTQHPNV

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						TTLPPIVRETSAPVTPLPLVTTTPAPET CEGRNSCVSCFNVSVVNTT\CFWIE CK\DESYCSHNSTVSD\CQVGNTTD FCSVST\ATPVPTANS\TAKTHSSSP LLQLPRQLLHQGTNTNTVNS\TSQP VRKSTFDAASFIGGIVLVLEIRCHTR NYIPDLKK
2088	7585	C	2258	101	411	MEMKMQSERLSKEYDQLLKEHSEL QKQREILPHRRGESTVTXXXXXX XEPQQRNADXXXXXXXXXXXXXXXX XXSSSRSMALQPIKXXXXXXXXXX XXXXXLF*
2089	7586	A	2259	2	575	
2090	7587	A	2260	1	265	SDALSKAQNDVMEMKMQSERLSK EYDQLLKEHSELQHSSFGFLSKRS HKNGSIGKQTGSRKGSFRKRQKEK TVNFIKDTLQYTVSK
2091	7588	A	2261	47	906	RKKLPLQWPAVPPFLYAEIGLILIFC LPFIPPQRWQKIF\SFNVWGKIATFW NKAFLTIIILLIVLFLDAVREVRKYSS VHTIEKSSTSRPDAYEHTQMKLFRS QKNLYIPGISLFFWLVLRLVTLITQ LAKEPVTQRCALYLQAENTNKA K\VFMEENEKLRILKSHGKDEECVL EAENKKLVEDQEKLTTELKRTSDA L\SKAQNDVMEMKMQSERLSKEYD QLLK\EHSELQVPLGSFYLAFAFAPGL HNPHPSRSGGGFSAIDNPRGALPP CLVCVLFHHL
2092	7589	A	2262	669	995	KVFFCFYRIYVCICVCVCVCVC/TLQ TL/CYSIANMLTSSQCLQSCGSQSW CQMHIKSSKAIMTIPCKFISRKPWEG DCSSLEPHGVSAFDIWVPQLCIKKV LNHFSPRKN
2093	7590	A	2263	3	379	WPFLKLRLGTCGTCCSHEGRAAA WSAESSLQHSVVMTSLPLNPKPFL N\GLTGKPMVKLKWGMEYKGYL\ VSVD\GYMNMQLANTEEYIDGALS GHLGEVLIRCNNVLYIRGVEEEED GEMRE
2094	7591	A	2264	68	268	QYLSLLLTQYSLVFICWLFICL\LYV YLFLCMLLCKYGLQLFLCGILSFRIS CKLLESRIHVIPLFL
2095	7592	A	2266	190	554	HGVRSDLGRWPDHLCVCRHYHH LLHLLLLPLQDVPPTTSLSPPH PLWCM/PPYPQPPSVPPSYGPSLPG LPHHAASARECQHPYPIAVPHTLT HAHAHGPTTRTPPLAGRSSRD
2096	7593	A	2267	2	445	
2097	7594	A	2268	200	894	TSPRARPHCSLCLPNLPPVTYMHY ETDGFSLGVFLKSGTSIPLHDHPG MHGMLKVLYGTVRISCMKDLDAG GGQRPRALPPEQQFEPPLQPRREA VRPGVLRSAEYTEASGPCILTPHR DNLHQIDAVEGPAAFLDILAPPYDP DDGRDCHYYRVLEPVRPKEASSA CDLPREVWLL\ETPQADDFWCEGEP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						YPGPKGLPLKPLAHQERWAEDVPY PTTRAVSLPP
2098	7595	A	2269	257	781	QELLSGLVNYFSLSWFLYVAQESIP SLPQSPMRETPSKAFHQYSNNISTLD VHCLPQLPEKASPPASPPPIAFPPAFE AAQVEAKPDELKVTVKLKPRRAV HGGFEDWRPLNKKWTGMKWKKG KIYIGTPNGTLKTPLA/EDEID/EFSKE MGHFLKPDGPCKIIGKVWHEKGM NDK
2099	7596	A	2270	271	404	
2100	7597	A	2271	2	5684	PTSPCGEGYGISLNLTFIISNMRVLR AHFIELQFPFMGQVVTGTQNSEQN LGPQAIPQDGSITHQISRPNPPNFGP GFVNDSSQRKQYE/EWPQETQQLLQ MQQKYLEEQIGAHRSKKKALSAKQ RTAKKAGREFPEEDAEQLKHVTEQ QSMVQKQLEQIRKQKKEHAELIED YRIKQQQQCAMAPPTMMPVSQPPQ PLIPGATPPTMSQPTTFPMVPQQLQH QQHTTVISGHTSPVRMPSLPGWQPN SAPAHPLPLNPPRIQPPIAQLPIKTCTP APGTVSNANPQSGPPRVEFDDNNP FSESFQERERKERLREQQERQRIQL MQEVDQRALQQRMEMEQHGM VGSEISSRTSVSQIPFYSSRLYLCDF \MQPLGFLQSQSPQHQQQMGQVLQ QQNIQQGSINSPSTQTFMQTNERRQ VGPPSFVPDPSIPVGSPPNFSSVKQG HGNLSGTSFQQSPVRPSFTPALPAAP PVANSSLPCGQDSTITHGHSYPGST QSLIQLYSDIPEEKGGKKRTRKKKR DDDAESTKAPSTPHSDITAPPTPGIS ETTSTPAVSTPSELPPQADQESVEPV GPSTPNMAAGQLCTELENKLPSNDF SQATPNQQTYANSEVDKLSMETPA KTEEIKLEKAETESCPGQEEPKEEQ NGSKVEGNAVACPVSSAQSPPHSA GAPAAKGDSGNELLKHLKKNKKSS SLLNQKPEGSCSEDCTKDNKLVE KQNPAEGLQTLGAQMGGFGCGN QLPKTDGGSETKKQRSKRTQRTGE KAAPRSKKRKKDEEEKQAMYSSTD TFTHLKQVRQLSLLPLMEPIIGVNFA HFLPYGSGQFNNGNRLGLTFGSATL EGVSDYYSQLIYKQNNLSNPPTPPA SLPPTPPPMACQKMANGFATTEELA GKAGVLVSHEVTKTLGPKPFQLPFR PQDDLLARALAQQPKTVDPASLP TPPHNNQEELRIQDHCGDRDTPDSF VPSSSPESVVGVEVSRYPDLSLVKE EPPEVPSPPIIPLPSTAGKSSESRRND IKTEPGTLYFASPFGPSNPGPRSGLIS VAITLHPTAAENISSVVAAFSDLLH VRIPNSYEVSSAPDVPSMGLVSSHRI NPGLEYRQHLLLRGPPPGSANPPRL VSSYRLKQPNVPFPPTSNGLSGYKD SSHGIAESAALRPQWCCHCKVVILG

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						SGVRKSFKDLTLLNKDSRESTKRVE KDIVFCSNNCFILYSSTAQAKNSEN KESIPSLPQSPMRETPSKAFHQYSNN ISTLDVHCLPQLPEKASPPASPIAFP PAFEAAQVEAKPDELKVTVKLKPR LRAVHGGFEDCRPLNKKWRGMKW KKWSIHIVIPKGTFFKPPCEDEIDFL KKLGTSLKPDVPVKDYRKCFCHEE GDGLTDGPALLNLDLDLWVHLNC ALWSTEVYETQAGALINVELARR GLQMKCVFCHKGTGATSGCHFRCT NIYHFTCAIKAQCMFF\KDKTMLCP MHKPKGIHEQELSYFAVFRVYVQ RDEVQRQIASIVQRGERDHTFRVGLI FHTIGQLLPQQ\MQAFHSPK\ALFPV GYEA\SRLLGGTRYANRRCRYLC SIEGGRDG\RPV\FVIR\IVGNKGHGR TGV\KVD\SPKGVWDKILEPVACV RKKSEMLQLFPAYLKGEDLFGLTVS AVARIAESLPGVEACENYTFRYGRN PLMEPP\AVNPTGCARSEP\KMSAH VKRFVLRPHTLNSTSTSKSFQSTVT GELNAPYSKQFVHSKSSQYRKMKTA EWKSNVYLARSRVSGGWGLLWL VRR\TLEETHHGSFEYIGTNHFETKL GQQGKEKLYESQNRGVYMF\RMND DHVIDATLTGGPARYINHSCAPNCV AEVVTFERGHKIISSSRRIQKGEELC YDYKFDFEDDQHKIPCHCGAVNCR KWMN
2101	7598	A	2272	1	2806	
2102	7599	A	2273	288	843	AGSGVLQGLFICPKAPGPRPTGAEG KR\KLQIGVKKR\VD\HCPKSRK\GD VLHMHYTG\KLEDGT\EFDSKPAPR TSPFVFS\GTGQVIK\WDQG\LCL GMCEGE\KRKL\VIPSELGYGE\RGE LPPKIPRPVQPLVFEVELLKIRADEL SCNQTGEGQGEKAPHQGPDCSKKK NKKQKPIKKT\KSPK
2103	7600	A	2274	80	308	VLTHLGNWILGSTEGPMGGP*FCTN LSEGLRFGISPSWREALYGWHA
2104	7601	A	2275	2	456	RSFFFFFCEVGSWVGSMRVVMARL LSEGEQGIPTACAFAQQPGGRPRR GLAGVGEGGPQCSWVNYRCTLEFL VSL\GTDLARGRGNSASGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCHVV QGWVSTSWGSSSPVPQFFPKLLEF TGK
2105	7602	A	2276	2	81	
2106	7603	A	2277	325	485	ELRVDPVNF\KL\LSHCLLVTLAAHL PAEF\TPAVHASLDKFLASVSTVLTS KYR
2107	7604	A	2278	291	529	LFL\CKVGTWHQGP\NHQKAPKAPG TPPTPSYPGT\PSRQLLWQVWQRP LPA\PLPAVGTSS\TSPGRQCPGFS AQHHLFP
2108	7605	A	2279	52	109	TVRLPR\HPGSRKNMASYCRIPACIA AERRYGTCMYQGR\WAFSS

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2109	7606	A	2280	3	452	
2110	7607	A	2281	26	526	NSTDSE RTHPWLLSPADKTTVK/AP AWGKVG AHAGEYGSEALERMFLS FPTTKTYFPHFDLSHGFCPGLRATG KKVADALTKRRGAPLDDMPNALV RPLASDLHAHKL\RVGPGSTFKLLKP LACL\LT LGPAHLPRPSFTPGGCKAS LGQSFLGFLKHRCLNLPNYR
2111	7608	A	2282	447	539	
2112	7609	B	2283	8	694	MQYNRRFVNVVPTFGKKKGTTFTK IFVGGLPYHTTDASLRKYFEGFGDIE EAVVITDRQTGKSRGYGFVTMADR AAAERACKDPNPIIDGRKANVNLA YLGAKPWCLQTGFAIGVQQLHPTLI QRTYGLTPHYIYPPAIVQPSVIPAA PVPSLSSPYIEYTPASPVYAQYPPAT YDQYPYAASPATADSFGYSYPAA VHQALSAAAPAGTTFVQYQAPQLQ PDRMQ*
2113	7610	A	2284	3	191	
2114	7611	A	2285	101	444	CSLFVPRPSRLQPLRRVTGQETGRP RSKAHVASTWRAFPEDQVVLLAG APLEDEATLGQCGVEALTTEVTG \RMLGGKSPWFPWPVLGKVMKVRL LKVAKQGERRKKKTGSG
2115	7612	A	2286	2622	2881	KKSKDNKTFFFFFETESCSALQAGV QWCNLGSLQTL\PGSNDSSHASAR VAGTKGMCHHARLIFVFLVETGLH HVGQACLGTPLDK
2116	7613	A	2287	41	655	TKLVMMQKLLKCSRLVLALALILV LESSVQGY\TRKPRHQWVPCNPDS NSANCLEEKGPMFELLPAE\STKIPR L\RTDLFPKTRIQ\DLN\RIPLSEDYS GSGFGSGSGSG\SGS\GSWFPNGKW EQDYQL\VDE\SDAFHDNLR\SLARI LASASRDWQHGLAEFNVIKEDL PTLTTRQM\VKQYFNVPMVNMINS WDKEFYRNF
2117	7614	A	2291	163	703	READMGTMKTQRDGHSLGRWSLV LLLGLV MPLAIIAQVLSYKEAVLR AIDGINQRSSDANLYRLDLDP RPT MDGGP\DTTK\PVSFVTKETVCPRP TQQSPKDGDFKRDGLNRMGMGTV\ TLN\QARGSFDISCDKNKRFALLG DFFRKSKEKIGKEFKRIVQRIKDFLR NLVPTES
2118	7615	A	2292	100	546	PPRTGQRQPLHSARRHGSPVS\ELAC \YSALISARTDEVTV\EDKINAL\K A\AGVNVE\PFWPWLCLQRPLA\NV NIG\SL\CNVRGPVEPAPSSLVAAP\ AGRSLPPPLACCSKLKEERKLEAKK RKNPKEVLNDDIGLLVLFELKPLL
2119	7616	A	2293	33	494	
2120	7617	A	2294	1	609	PLKRS DGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPEEKSAVTALW GKVN\DEVGGEALGRLLVVPWT QRFFESFGDLSTPD\AVMGNPKVKA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HSKKGLRGAFSDGLAHL\DNLKGT FATLASEL\HCDKAAPWIPEELQAPW ATCLVCVAWPITFGKRISTPPVAGL PNQENWLAWCWLNALGPTSNHLS LAFLAGPISN
2121	7618	A	2295	1	338	AALAWAVSRLHFSRLSFPPWAFRG AFAAVPTTAAMISLTDQKIGMGLT GFGVFFLFFGMILFFDKALLAIGNG\ FFPVVDGFIIRVPVLGSLNLPGIRS FVDKVGESNNMV
2122	7619	A	2296	67	283	LPFPGCFFLF*VLFVAGLAFVIGLER TFRFFQKHKMKATGFFLGGVFVV LIGWPLIGMIFEIYGFFLLFR
2123	7620	A	2297	3	209	
2124	7621	A	2298	3	544	TRAALAVAVSRLHFSRLSFPPWAFR GAVAAVPTTAAMISLTDQKIGMG LTGFGVFFLFFGMILFFDKALLAIGN VLFVAGLAF\VIGLERTFRFFF\QKH KMKATGFFLGWVYLVVLIGL/WPLI GMIFEIYG\FLLFRGFFPCRCWTFI RKECPVLGIPSPNLPGIRSFVDKVG SNNMV
2125	7622	B	2299	54	1731	XKLSRECEIKYTGFRDRPHEERQAR FQACRDRSEIAFVATGTNLSLQF FPASWQGEQRQTPSREYVDLREA GKVYLKAPMILNGVCVIWKGWIDL QRLDGMGCLEFDEERAQQEDALAQ QAFEEARRRTREFEDRDRSHREEME VHELEKSKRALETQMEEMKTQLEE LEDELQASEDAKLRLEVNMQALKG QFERDLQARDEQNEEKRRQLQRQL HEYETELEDERNERLAAAANKKL EGDLKDLELQADSAIKGREEAIKQL RKLQAQMKDFQRELEDARASRDEI FATAKENEKKAKSLEADLMQLQED LAAAERARKQADLEKEELAEELAS SLSGRNALQDEKRRLEARIAQLEEE LEEEQGNMEAMSDVRKATQQAE QLSNELATERSTAQKNESARQQLER QNKELRSKLHEMEGAVKSKFKSTIA ALEAKIAQLEEVEQEAREKQAAT KSLKQKDKKLKEILLQVEDERKMA EQYKEQAEKGNARVKQLKRQLEEA EESQRINANRRKLQRELDEATESN EAMGREVNALKSKLRGPPQETSQ*
2126	7623	A	2300	1	2448	
2127	7624	A	2301	1	2655	
2128	7625	A	2302	5	605	VDPDSGQIQVPCTPRGLKWSPNMN PARKTDACGEDTHPSLLGVFFSRPP LGILRFALQNPRSPGKESEMLPPPA WVYLKAPMILNGV/CVIWKGWIDL QRLDG/MGCLEFDEERAQSWPW*A HPQC*EGRRPSCRELGNVALGADG DSPGSIYTRRWKLSQRVPAPPPQE PKMPSLCCRNTSTTFSGRPSQSPRTK KQRPR
2129	7626	A	2303	1	588	MGFCHVDQTGLELLTQPLLALIGAA

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						LEGGRAGGAADLAPDFGRLALQIK YTGFRDRPH/EERQARFQACRDGR SE/IFFPASWQGEQRQ/TPSREYVDL EREAGKLNIPKGPAGDETPSSLSSM MIVLSSDSGPAVLAIPNLVTPPRYTP MVPCGGHHQAQRKRPLCTPPPSIQ QGSMSVKSMPTPVAAHKSFTSALC
2130	7627	A	2304	1	615	GLKGGKMPRVVPDQRSKFENEFF RKLSRECEIKYTGFRDRPHEERQAR FQACRDGRSEIAFVATGTNLSLQF FPASWQGDQQRQTPREYVDLREA GTVYLKAPMILNGVCAIWKGWIDL QRLHGMGCLEFDEERAQQEDALTQ QAFEEARRMTREFEDRDRSHRQEM EARVSQLLAVTGKKQLDPRPGSNL GGDDLKLR
2131	7628	A	2305	73	168	
2132	7629	A	2306	322	671	RLWASPAAPGKKKEMGNSMKSTP APAERPLPNPEGLDSDFLAVLSDYP SPDINPPIFRRGEKLRVISDERGWW KA\SLSTGRESYIPACVARSYHGW LLRGPG\KNMAEELLQLPD
2133	7630	A	2307	624	1581	KAATSENKIICCEWRTSQAALMLHR LWASPAAPGKKKEMGNSMKSTPAP AERPLPNPEGLDSDFLAVLSDYSP DISPPIFRGEKLRVISDEGGWWKAI SLSTGRESYIPGICVARVYHGL/W LFEGLGRDKAEELLQLPDTKVGSF MIRESETKKGFYSLSVRHRQVKTY RIFRLPNNWYYISPRLTFQCLAE DLV NHYSEVADGLCCVLTTPCLATQSTA\ APAVRACSSPVTLRQKTVDWRRVS RLQEDPEGTENPLGVVESLFSYGLR ESIASYLSLTSEDISSFDRKKKSISLM YGGSKRKSSFFSSPPYFED
2134	7631	A	2308	52	454	SQTQREPTMVLSPADKTNVCAA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNVAHVDDMPN ALSALSDLHAHKL RVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR
2135	7632	A	2309	3	452	
2136	7633	A	2310	26	502	NSTDSETHHGARLLPDKTKAQRPP RLKLGANA\GEYFGGPPWKGMFLS FPNPPKTYFRQFRP*ANGFAQG*RG HGQRKVA\DAL TQSPCRNVD DMPQ TALSAP EATLHG\HKL\ RVDPVNFKL \LSH\CLLG*PWP AHLPRPSFTPCGCT PSLEQSSW AFC
2137	7634	A	2313	43	595	LRNMWQLERN\IET\INTFHQYSVK LGHP\DTL\NQGEFKELVRKDLGQN FLKKENKNEK VIEH\IHEDLDT\NAA Q\QLSFEEFIMLMARAKPGALPTRR MHEGDKGPWPPPHKPGLGEGTPPR PQWPRSPVATAHGHKSWWPRPQA TNHGGQATLPLPKPGPRGLLCQTVL AVGLGGWGQIKSLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2138	7635	A	2314	3	419	SLYHNSSQKRHWTFSSSEQLARLRA DANRKFRCKAVANGKVLNDPVFL EPHEEMTLCKYYEKRLLEFCSVFKP AMPRSVVLTC AFLACKVDEFNVSN PQFVGNLRESPLGQEKALEQILEYE LLLIQQLNFHLIVHN
2139	7636	B	2315	324	487	MQRVRAGRIVITTAQRRLPDALG FREIFSSEQLARLRADANPNSDAK PWPTGS*
2140	7637	A	2316	1	1050	
2141	7638	A	2317	191	229	
2142	7639	A	2318	186	1232	CVWVLVCRPSGPGHDSIMYHNSSQ KRHWTFSSSEQLARLRADANRKVFR CKTRAH\GKVFPNDPVFLEPHEEMT LCKYYEKRVIEFCSVFKPAMPRSV VG/SRACMYFKRFYLNNSVM EYHP RL\IML\TC AFLACKVDEFNVSSPQF VG\NL\RESPLG\QEKALEQILEYELL PYTSNFNHFL\VHNPHY\RPFEGFLND LRTR\YPILNPEILRK\TA\DDFLNRI ALTDAYFLYTPSQ\IALTAILSSASRA GITMESYLSESLMLKENRTCLSQLL DIMKSVRN\LVKKYEP\PRSEEVAVL KQKLERCHSAELALNVITKKRKG EDDDYVSKKSKHEEEEWTD\DLV ESL
2143	7640	A	2319	152	371	DVLLATSSSEPSLFCPLCLTASTPKP LPPPG\PLPCPVWAMWGTGGFPLPG PPGQPRVRGPTAARGTPCCRPS
2144	7641	A	2320	4	474	PQYPAWHEGERAEWLCGRVSETGS ACSMADQL\TLKEQIAEFKEAFSL\F DKDGDGTITTK\ENLGTVNEILLGSN PTEAELQDM\INEVDADGNGTIDFP\ EFLTMMARKMK\DTDSEGRKL\EEA FRVFGLRVGNGLYL VACRNF RHV DGQTLGGGSLPD
2145	7642	A	2321	291	648	LTQLKTHCPLIKSKTMNKKRAIREP AQEPGPQKEENPKKHRSPSFTSTSPF GLEVPASYSPTKAEQPGQVRKAV QPAVRLEPRASHPAGPPVPPSGVLV SRRRPEPGQGKPPESDFDH
2146	7643	C	2322	155	316	MTGPVSGSFIHWVLFSGFSSMSSNA SNVFGLV RPSCTTGLSRMAADSAG CCSL*
2147	7644	A	2323	28	1323	PSGARVAGAGPCGGGGMFVQEEKI FAGKVLRRLHICASDGAEWLEEATE DTSVEKLKERCLKHCAHGLSKDPK SITHHKLIIHAASERVLS DARTILEENI QDQDVLLLIK\RAP\ SPLPKMADVS AEEKKK\QDQKAPDKEGILG\ATAN LPSNKLDRAAVQTNMRDFQTEL RK ILVSLIEVA\QKLLAL\NPDA\VELFK EGECNCWDEDGGMSVWDEACPA AFOREMGLFRENRA TKALQLNHMS\ VPQAIGSWL\NEHA\EDPTIDTPL\PG\ QAPPEAQG\ATAAASEAAAGASAT DEEARDELTEIFKKIRRKREFRADA

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						RAVISLMEMGFDEKEVIDALRVNN NQQAACEWLLGDRKPSPEELDK GIDPD\SPL\FQAIWDTRWVQLGLTN PKTLAFEDMLENPLNSTQWMNDP ETG\PVMLQISRIFQTLNRT
2148	7645	A	2326	307	412	SVQTIVFQPQLASRTPTGQS*SSCPY PLFATINAE
2149	7646	A	2327	50	247	
2150	7647	B	2328	276	779	MRTLAILAAILLVALQAQAEPLQAR ADEVAAAPEQIAADIPEVVSFAW DERAPLQVSGKSSPVCARLLLQET RDRGLLFALPLHSAYLEDLLRQSHF RQELMKLQPRSSLEQMIRKWLMPL HGMKVPLFRFPDKIIVLSTLIPTGD YSPHNLKNLFMRMVTSP*
2151	7648	A	2329	3	333	
2152	7649	A	2330	35	717	RRSSPSLLPLAERGGARARGRPERA PHPSTPATRTAPPPWARRMMKLKS NQTRTYDGDGYKKRAACLCFRSES EE\EVLLVS\SSR\HPDRWIVPWKEG MEARRKEAKCGKQVREVCEGRG VKGTLGRLVGIFENQERKHRTYV\ YVLIVTE\VLEDWEDSVNIGRKREW FKIEDAIKVLQYHKPVQASYFETLR QGYSANNGTP\VVAATTYSVSGFRA SMFRAFRWT
2153	7650	A	2331	104	381	IQGGSMTSSSFSTSICQKILNKEKQS CCSN*SKWSRNVSSNGKPNWTGTS LPALTEMARTTIWKKHIFTKKFSSV SIFQVFKSF*I*GSVLS
2154	7651	B	2332	228	445	METSSRELQAAEYLEKHQIKEVVSY LTSALLFLRPALKTLGLCTEDEDLQ DDGHKITLDKFKEEVNKRMEIX*
2155	7652	A	2333	3	1459	GSKQVSEGTDNGLPSYVSFAFIEKE VGNDLKSLKKLDKLIEQRTVSKMQ LEEQVLTISSEIPKRIRSALKNAEESK QFLNQFLEQETHLFSAINSHLLTAQP WMDDLGTMISSQIEEIERHLAYLKWI SQIEELSDNIQQYLMTNVPEAAST LVSMALDIKLQESSCTHLLGFMRA TVKFWHKILKDKLTSDFEEILAQH WPFIAAPPQSQTVGLSRPASAPIYSY LETLCQLLKLQTSHELLTEPKQLPE KYSLPASPSVILPIQVMLTFLQKRFR YHFRGNRQTNVLSKPEWYLAQVL MWIGNHTEFLDEKIQPILDKVGSV NARLEFSRGLMMLVLEKLATDIPW LLYDDNLFCHLVDEVLLFERELHSV HGYPGTFASCMHILSEETCFQRWLT VERKFALQK\MDSMLSSEAAWVSQ YKDITDVDEMKVDPDAETFMTHLL VITDRYKNLPTASRKLQFLELQKDL VDDFRILINTK
2156	7653	A	2335	46	1146	
2157	7654	C	2336	17	196	MTTLVTTTTMDMVIIATSRVVMGR YPGEVVIIKATNHTKLFHLQLIPNSG NFIAGPVS*

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2158	7655	A	2337	208	1504	FRFAAGGCSLGGSGGDTSTMSEEQF GGDGAAAAATAAVGGSAGEQEGA MVAATQGAAAAAGSGAGTGGGTA SGGTEGGSAESEGA KIDASKNEEDE GHSNSSPRHSEAATAQREEWKMF GGLSWDTTKDLKDYFSKFGEVVD CTLKLD PITGRSRGFGFVLFKESES DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGGLSPDTPEEKIR EYFGGFGEVESIELPMDNKTNRKR FCFITFKEEPPVKKIMEKKYHNVGL SKCEIKVAMSKEQYQQQQWWSR GGFAGRARGRGGGPSQNNWQGY NYWNQGYGNYGYSSPRLRWLWRI *LHWLPTTTYGYGDYSNSQSGYK VSRRGGHQNSYKPHLNY SICNL PTGGEAVFSNLKIQFESGS/CH*LLI AVQTKFLYQVPEWKYDVGSL
2159	7656	A	2338	208	1466	FRFAAGGCSLGGSGGDTSTMSEEQF GGDGAAAAATAAVGGSAGEQEGA MVAATQGAAAAAGSGAGTGGGTA SGGTEGGSAESEGA KIDASKNEEDE GHSNSSPRHSEAATAQREEWKMF GGLSWDTTKDLKDYFSKFGEVVD CTLKLD PITGRSRGFGFVLFKESES DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGGLSPDTPEEKIR EYFGGFGEWDPIELPHGQTRPNKRR GFCFITF*GVEEPPVKKIMEKKYHNVG LSKCELK\VA\MSKEQYQQ\Q\QQW DSRGGCAGRA\RGRGGDQ\QSGYG K\VSRRGH\HQ\NSYKPYLNY SICNL SPTAGTSLQALCRADFRFSQARSMR TG*RDAPRSRMLPFGGEAVFSNLKI HL\NGGSCHLLIAVQTKFLYQVPE WKYDVGSL
2160	7657	A	2339	1070	1238	PQRDFQFFLLWPPGGEA\VFSNLK\IP FERGSCHLLIAVQTKFLYQVPEWK YDVGSL
2161	7658	A	2342	1	456	RPRRPQREPTMVLSPADKTNVKAA WGKVG AHAGEYGAEALE/RMFL/SF PTTKTYFPHFDLSHGSSQVKGHGKK VADALTNAVGHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHAFLDKFLASVS TVLTSKYR
2162	7659	A	2343	2	512	GLEFGTSHRLRENPPWCLSPA\DKT NVKA\AWGKVG AHAGEYGAEALE RMFLSFPTTKTYFPHFDLSHGFAQ VKGATAKKVA\DALTKAVAHGRGT CPNALSALSGPATAHKL\RVGPGST FKLLKPLACLVDPGPAHLRPSFNP WRLQGFLGTFKFLGFLVEAPLLEPSK
2163	7660	A	2344	265	426	SFSISVFAACLALPMAQPQ*PCSQK V*QHCRVYMHAAHTWPLCLQDVLV ECCSQS
2164	7661	A	2345	56	341	IVTLDWSRNLKYNRCWSKCYILSSS DSSSFRDSFTNPAEF*FKSFILNFV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MYVYVNYFCNFFNDITAGHFFHLKL LYFRLCSLPGFADGTAPITV
2165	7662	A	2346	333	534	LMEDMKLFQKI*EKKQRNMLRNL* RKKMNQMM/YNM*HLLQHLLYFK FLL\HPM*LFSPGLYILSNFH
2166	7663	C	2347	117	386	MDILICTDFGSVNYFNVWRLPKSYL SLFYRSRIYIVHDEVKDKAFELELSW VGELTNGRHEIVPKDIREEAKEYAK ESLKEEDESDDDNM*
2167	7664	A	2348	2	359	FEDGVLLCHPRLEGSCTVISAHCNLS LPGFKRSSCLRLPSSWDYRNMPY PGYFCIFGFTNNTETGFHQASFKLL NSRDLPTLAPVKCWDYRHEHCTRP LKYIFYQRYSHCMLEQHLLN
2168	7665	A	2349	648	887	SWKLLLLLCLKNEHLPTKPATGHS NIADQTLKKSFCLEPFFHKV*KGLIF LTPRTTPSLHLPIAVLLFSTAFIAYS T
2169	7666	A	2350	306	449	EIKKKYLLPGVVAHACKPSTLGGR GGQIISGQEFETSLTNMAKPCFF
2170	7667	A	2351	1	625	NFALEAKNSARAISYVQTPMGHFT RGGPRLTITSLWGK\VNVE\ DAGGE TPGKGSLLVYP\WT\QRFFDSFGNLS SAFCPSWPTPKVKAHGK\KVL\TSLG DAHKSTWDDLKGHLLPKPEVNLHC \DKPAMWDPENFKAPGEMCLVTRF GQSLFRQKNFTPEGCRASLGKKDG ELQLASCPGPSQITTEASWPMNSEA FKDKAFILASNYK
2171	7668	A	2352	1324	1671	IVQTLSTLSKSSCRSTEPCTSLPDL QVGTTCTRPHGTCC/NRCHVGGLMN PLKPNC/GCRKCNCGYLYIYLGQR LHPRGKFQPGNNHRFSCTQSVHMDI THGSGMFSLCFPGSTMF
2172	7669	A	2356	8	564	SAQMAVTTADPRVRPRVRTQLCSL ASLIQTLVHLTPEEKSAVTALWGK VNVDE\VGKALGRLLVYPWTQR FL\ESFGDLSTPNAVMANPKVKAHS \KKILGALLVVGLAHL\DNLKGTF HTEVSLHCDKLHV\DPENFQAPGAT CLVLCAWANHF\WQKNFTPPV\QAC LFRKLVAG\VANALAHK
2173	7670	A	2357	23	679	GLLTSGGAHLSPSRVTQGIYYMSAL SEMPKPPDYSELSDSLTAVGTGRF SGPLHRAWRMNFRQRMGWIGV GLYLLASAAAFYVFEISETYNRLA L\EHQQHPEEPLEGTTWTHSLKAQ LLSLPFWVWDSYFFWVPY\QMFF VSLYSCYKELDPQNSGGYCYPSPIW LWAVYFGNRHHAF/VVKASNSDSA DLQLIDTVKSVTRFFPLRJTGTQS
2174	7671	A	2358	17	392	SFKMADQDPAGMSPLQQMVASGT GAVVTSLFMTPLDVVKVRLQSQR SMAS\DAFVKIVRHEGTRTLWSGLP ATLVMTVPATAIYFTAYDQLKAFL CGRALTSPLYAPMVAGALARREHR LGPLTS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2175	7672	A	2359	1	725	RFTGTMDAFVKIVRHEGTRTLWSG LPATLVMTVPATAIYFTAYDQLKAF LCGRALTSDLYAPM/VAGALAR/LSI VLGL*PPSVPTSAQTQSVAPSPNLC QPRDRGVF*VPRPGTAGR*CHVRPV ISLLPIVTPNPHTVGTVTVISPLELMR TKLQAQHVSYRELGACVRTAVAQGG GWRSLWLGWGPTALRDVPFSALD WFNYELVKS/WLNGLRPKDHTSVG M/SFVAGGISRTVAAELTLPY
2176	7673	A	2360	102	1573	SFKMADQDPAGISPLQQMVASGTG AVVTSLFMTPLDVGKVRQLQSQRPS MASELMPPSSRLWSLSYTKLPSSLQS TGKCLLYCNGVLAEPYLA/CPNGAR CATWF/QDPTRFTGTMDAFVKIGE ARGAPRTLWSGLPATLVMTVPATA IYFTAYDQLKAFLCGRALTSDLYAP MVAGALARLGPVELWISPLGALCS NKACRVQHVVRNRELGA CVRTAV AQGGWRSLWLGWGPTALRDVPFS VHPPQAL/YWFNYELVRSWL\NG LRPK/DQTSVGMSFVAGGISRTVA AVLTLPF/DVVKTQRQ\VALGAL EA VKSEPPCNVDSTWLL/LRRIR/AESG TKGTLLQASFPRNKGCPSCA\MIQ HLIEFRQKAFFPRGLNPGTGFLGGL EKGPKEGKDPVSSQREWGRGQGGD PSQSAFSSALREGGLFSLPLPATKLP GQGCPSGRPSTSSRHNFLLLPVVG ITYPPPKFKTKSSELPFVFPCGLL
2177	7674	A	2361	1	215	QPMSEESDQYLAVLTFPRCVLV MIHTHAQVLNHVCIYVCVHMSVAV Y/ISACRATDPDTHTCVYMIQTY
2178	7675	A	2362	3	543	TRNTLGWEVSSFSPLLSSCLNMVRT KADSVPGTQEKVVAARAPRKGL/G SSTSAHLIRPSVSI EESLKNKYARRE PPFCVRP/TLPKWAKREIGEFFRLSP KDSEKENQIPEE\AGSSGL\GKRQRR KSMFLLQPGFTQLMEKGLGTLHFI FGLTSPLFYPGYSRKVKFTINGVWF QLGFG
2179	7676	C	2363	69	290	MCLWNCCRKTQLAADILWLTAPAS PRDLRLGCVAEVFLARWELFGEDSF REKFFGFFFRDGWQPFLLSAGER*
2180	7677	A	2364	663	793	DGDSVMVLPTIPEEEAKKLFPGGVF \TKELPFGKKYLRYTPQP
2181	7678	A	2365	1	726	MPGGLLLGDVAPNFEANTTVGRIRF HDFLGDSWGHSFSQ/RGGFTPWCA PRSFARAAKLAPDFAKR/NVKLIALS IAVFEDHLC/AESKDIHVYHCE/ESPT EKLPIIIDDRNRELANPVGACWIP AEKDEKG/LCPVTASVWCFVFGP** RKLKAVYPSYPSYPLAGNFE*RFLR VVHLLSQLTA/EKKRVAHPQLIWKD GD\SVMVLPNPSPEEEAKKLFPEKE SFTQKELPNLAKKYL\RYTPQP
2182	7679	A	2366	3	452	
2183	7680	A	2367	1	627	TLLVPQDSERTHPWLLSPADK\TNV

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						KA\AWGKVGAAHAVRSMCAEALER MFLSFPTTKTYFPHFDSLHGSAQV KGATGKKVADALTKRRGAPLDDM PNAL/SSALEATLHAHKL\RVGPGST SKLLKPLACLVDPPGAHLPRPSSTP GGCNVFPGTKFPGLFVEAPLLEPSK LPLKLGSLRLAIVFLPLWGFPAPPP LSCTRTPVVFEIKS
2184	7681	A	2369	1	467	GTSACGVASLSVDCVPAPFSQQQP LPEGERTLGGRHRLRTRARALHPAP ACFCHASLCVCM/CA/CVLVCGLLC EHQSDSIHCLCHLCLCKCNLYLCIRA ASSQHLKCHWVGGNKTCFGPDDL GGRSEPTFETLSGEPATPADGKTGS CTGPERYQM
2185	7682	A	2370	131	406	EAMGILKLQVFLIVLSVALNHLKAT PIESHQVEKRKCNTATCATQRLANF L\VHSSNNLGGILSSTNVGSNTY GK RNAVEVLKREPLNYLPL
2186	7683	C	2371	257	422	MQVCFRQGFTLPKGHHGLIATLGA POLYMFLVLRASLFLWLSXFXRSX KLXXXRN*
2187	7684	A	2372	621	1202	GVPEPRARPSTSGMNGDRIRLPCWR NDRQK\THML\DVMDHFSRASSIH RRALSRRDRFTREPQ\DTYHYL\PFQ PCPHRRP\HFFPKSRNRPA*\CPFSS \TKPLNFHAMFQPFLEMI\HEGSAGP WDIHFHSPAFQHPPTFIREGD\DDR DCCAGEN\RHNSTGLPCGLKDQVVT K\CREDLVLWD\CFHQQLPG
2188	7685	A	2375	154	1702	IGHRDPARGRSCRCSGYYSRMVCE KLAPQSEMASAG\VSLRATILCLLA WAGLAAGDRVYIHPFHLVIHNESTC EQLAEANAGKPKDPTFIPAPIQAKTS PVDEKALQDQLVLVAAKLDTEDKL RAAMV\GMLANFLGFPYMGMH ELWG\VHG\ATVLSPTAVFGTLAS LYLGALDHTADRLQAILGVPWKDK NCTSR\DAHKVLSAL\QAVTGLLVA PGRADKQA\QLL\STVVG\FTAPG LHLKQPFVQGLALYTPVVLPRSLDF TELDVAAETID\RLMQAVTGWKTG CSLTGAKADSTLAFNTYVHFQGM KGFSLLAEPQ\EFWVDNSTSVSVM LSG\MGTFQHWSDIQ\DNFSVTQVPF TD\SAFLLLIQPHYASDL\DKVEGLT FQQN\SFNWMRKLF\PRTIH\TMPQL VLQGSY\DLQDLLRPGSSCPFLHTE LNLGRISGN\DRIRVGEVLNSIFFEL EADEREPTTESTQQLNKP\EVLE\VPL TRPF\LF\AVY\DQGATALALSWGRV GKPA
2189	7686	A	2376	181	353	VGDRCEGNGNEARGHWKREVCCP GARSGASV*\GSSGRLGLCL*\VGTR AG*\PGYPASLVPT
2190	7687	A	2377	1550	1823	GRLLDEPQAAHKFLRGEMGGQSPG VRGTELLGAFSLPGES/GSPGRASPL PFPPNLEKTVTFQSLGLPKIPKEPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LKEIKLTNVKKSCTLP
2191	7688	A	2378	134	321	GCF*KGRDLFADKMQEHSQ*FTAL FQPTNQKISSWVC GPKVNFKAIKTG SRSGKAIQNVES
2192	7689	A	2379	1	602	RTRASTRPSRDYGNVAVLWTRTSH RPLTEPEPRATMSHGKGTDMLEPIA APVGFLLSLLRTRGCVSEQRKLVFS GALQEA\TEHYNNHWFPEKPSRG SG\YRCIR\NHK\MTPHSRVASQ\VG LSQAQL\HQLP\SELT LWVDPYEV SYRIGEDGSICVLYEAEPLAASCGA SFT/CARNQVACWGRSSPSK\NYVM AVSS
2193	7690	A	2380	28	423	SKPLKMADDLDFETGDAGASATFP MQCSALRKNGFVVLKGRPCKIV*M STSKTGKHGHAKVHLVGIDIFTGKK YEDICPSTHNMDVPNIKRNDFQLIGI QDGYLSLPQESGGGIRDPLNLQRPP PRAWPGSG
2194	7691	A	2381	1	930	
2195	7692	A	2382	171	695	NRQDDLDFETGDA\GASATFPMQC SALRKNGFVVLKGRPCKIVEMSTSK TG\KHGHAK\VHLVGIDIFTGK\KYE\ DICPSTHD\MDVP\NIKRNDFQLIGI QGWGTL\SL\Q\DSGEVREDL\RVSP EGDL\GKEIEQKYDCGEEILIP\VLSA\ MTEEAA\VAIKAHGKITGSPGVAVV ASK
2196	7693	A	2383	789	1380	IPYFLMVYGLQTL MCKHITRRIRDH LHEAMNYFLIPSSPFLEANPPPPTPG TICPAC/YPPPPRAGQQLACFLSIPPL FPNLPIPPQKKDYWVLLSLGAPKFK GYLVLCMLQEPCRKQPGKSTGWI RNYPSWMHLATSTPQLRRGSKEVH NYKTMGSRPQKRYETGPGTQGGAE RILLSKPGRWRGSPGQEQVLGLQ
2197	7694	C	2384	248	433	MSGILVLNLFLT LGSVGPSSSVTLV LSVHQLPACAKLEKGNLHPCPNSS FPPRDFCVHPP*
2198	7695	A	2385	1	1108	
2199	7696	A	2386	1	1528	MGTRAARPAGLPCGAENPARRRLA LGARQQIHSWSPRTPTSTRLTAPAGP ARGVARPAMAPDPVAAETA AQGPT PRYFTWDEVAQRSGCEERWLVIDR KVYN\INEFTRRHPPGGSRVISHYAG QDATDPFVAFHINKGLVKKYMNSL LIGELSPEQPSFEPTKNKELTDEFRE LRATVERMGLMKANHVFFLLYLLH ILLLDGAAWLT LWVFGTSFLPFLLC AVLLSAVQ\AQAGWLQHDFG\HLS VFSTSK\WNHLL\HHFVIGHLK GAPA SWRNHMHFQHHAKPNCFRKDPDIN MHPFFFALGKILSVELGK\RKKKF M PYNHQHKYFFLIGPPALLPLYFQWY IFYFVIQRKKWVDLAWMITFYVRFF LTYVPLLGLKAFLG\FFIVRFL\ESN WFVWVTQMNHIPMHIDHRNMD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WVSTQLQVATCNVHKSC/AFNDWV SVG\HFNQIEHHLFPTMPRHNYHK VA\PLVQSLCAKHGIEYQSKPLLSAF ADIIHSLKESG\QLWLDAYLHQ
2200	7697	A	2387	45	949	APWWWYHPERLLGYPIAATLPSRL VLPGEVEPSTQWCSPLRLEPQFHLL PLQHLRRDSSSLSPPLPALGRTRGRR SSAPAHGDESCSLLPRPLSLAHGEP GGRRAEACSRLSRSRGRHSMTEPR STSASAAHAAAFCCFCCCRPPRPRP LAPPPP*PCR*SRRGCAGIDGAAAD VALGHPPE/HCPVPDVQMTSRRLMF IQLSQSPGVHCTSPHFSAPPTWCRR GPGSPATSPPLHTLPAVVAAPRAL RRAADRGRGRGLDRGVACAAERL QRQQLSRQSQSRSEAQPDAMEQ PRKRW
2201	7698	A	2388	804	985	VGGDSQDLRDPVPPQTAPPPPNLSL PPALSPRCASPSYPQKCLP/PPVTHR SACLSSAHRTHKKGQELVTG
2202	7699	C	2389	258	461	MSVTFIAVARGKLFFENLGHSELPL SLEWQTS DGEVEARGSRGGEALPR PGSMQPCPADVTRRPTRP*
2203	7700	A	2390	1	370	GTRVTSGGSRPMAAWSPAAA APLLRGIRGLPLHHRMFATQTEGEL RVTQ\MLKRKVSRLQLIKVTDISGG CGA\MYEIKIESEEFKEKRTVQQHQ MA\NQALKEEIKEMHGLRIFTSPVK R
2204	7701	A	2391	1	1107	
2205	7702	A	2392	1	1230	
2206	7703	A	2393	1	908	
2207	7704	A	2394	177	934	PGLSQEPGSGMETVVIVAIGVLATIF LASFAALVLVCRQR\YCRPRDLQ RYDSKPIVDLIGAM\ETQSEPS\ELE L\DDVVITNPHIEAIL\ENEDWIEDAS GLMSH\CIAIL\KICHTL\TEKL\VCHD NGALGAKMKTSASVSDIIVVAKRIS PRVDDVVKSMYPPLDPKLL\DART\ TALLSV\SHLVLVTRNACHLVTG\G LDWIDQSL\AAEEHLEVLREAAL\ ASEPDKGLPGP\EAFLQEPVLQFSAY RPAA
2208	7705	A	2395	1	333	GTRGERKAGLARGQVCGLSPFPK TKESFPNSQLNPFWN\CGASLSLV SFSCPATRLCGNALLPSLFFSMRGF GLAVRIRDNDNRLLSRMTSMCSISR VPEHVEFPNPK
2209	7706	C	2396	7	279	MXKGS PRXNFLECEKKSGQNPWAG LLRPWWVGHPKAPLIPVFSSISFPL YNPHFPXILCNKLKSHVCKKASKY TNNPISQQWTLSEFIK*
2210	7707	A	2397	35	416	SRAVEFVRSCAGYGERKAGLARGQ VCGLSPFPKTKESFPNSQLNPFW NYVWGLGPCGASLSL\VSFSCPATR LCGNALLPSLFFSMRGFGLAVRIRD NDSRLLSR\MTSMCSISRVEHVEFP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NPK
2211	7708	A	2398	3	344	
2212	7709	A	2399	1	1359	
2213	7710	A	2400	1	463	LAQAACGPAALQLCPAGHGAAMA ATFFGEVVKAPCRAGTEDEEEEE GRRETPEDREVRLQLARKREVRLR RQTKTSLEVSLLEKYPCSKFIIAIGN NAVAFLSSFVMNSGVWEEVGCACL WNEWCRTTDTTHLSSTEAFCVFYH LKSNPVSFLCQCSCYVAEDQQYQW LEKVFGSCPRKNMQITILTCRHCT DIKTSESTGSLPSPFLRALKTQNFK DSACPLLEQPNIVHDLPAAVLSYC QVWKIPAILYLCYTDVIGLDFITVE AFKPILSYR\SLKGLV\KNIPQSTEIL KKLMTTNEIQSNIYT
2214	7711	A	2407	160	441	
2215	7712	A	2408	107	691	RTAILSRLMKIFLPVLLAALLGVERAS SL\MCFSCLNQKSNLY\CLKPTICSD Q\DNV\CVTVSASAGIG\NLVTFG\H SL\SKTCFPCLPAPFPEGRSMLGVAS MGHSAFCQSFLVAIFSCGPMAGLRG KRSPLLGARACCLSLAGRALL\RFG PLDRPEPCSPDPPAQEGKPSFWIPQ CMGAPDSSRALICALGPRSG
2216	7713	A	2409	2	432	GRPPPDVEVMTSLKVDNLTYHTSP DVYIPRDYTKESRCFAFVRFHDKR DAEDAMDAMDGAVLD/GSELRLQ MARYGRTPDSHHSRRGPPRSYGC VGYGRRSRSPRLRRMP/RSRSRSRSR SRSRSRYSRSKRSRSTRSRSRSTS
2217	7714	B	2410	1522	2003	MAIIYGVFSASNLITPSVVAIVGPQL SMFASGLFYSMYIAVFIQPPWSFY TASVFIGIAAAVLWTAQGNCLTINS DEHSIGRNSGIFWALLQSSLFFGNLY IYFAWQGKTOISESDRRTVFIALTVI SLVGTVLFFLIRKPDSENVLGEDESS DDQDMEVNESAQNNTKA VDAFK KSFKLCVTKEMLLLSITTAYTGLEL TFFSGVYGTICIGATNKFGAEKSLIG LSGIFIGIGEILGGSFLGLLSKNNRFG RNPVVLLGILVHFIAFYILFNLMPGD APIAPVKGTDSSAYIKSSKEVAILCS FLLGLGDSCFNTQLLSILGFLYSEDS APAFAIKFVQSICAAVAFFYSNYLL LHWQLLVMVIFGFFGTIFFFTVEWE AAAFVARGSDYRSIMLKSFLDSDGI LAQLCRRQQPRAPLTIRTSPDTLRR VFEKYGRVGDVYIPRDYTKESRGF AFVRFHDKRDAEDAMDAMDGAVL DGREL RVQMARYGRPPDSHHSRRG PPPRS*
2218	7715	A	2411	2	229	
2219	7716	A	2412	3	353	FPLPFFTLVIWPGIRKFKLVHADGSL CEIFLIGPFKNMAGWNISVPYWFDQ SLSKYVPETETMCTLMEGKLNFFLF KPRCIGKQCKRRTWGKRTT*SIRRR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SPWNKQLGYLKRLFW
2220	7717	A	2413	18	282	DPLKSGPRNRS*TRWTPSPRS\ARRS KSKSLSVSRSRSRSR\SRRESLPP VSKRESKIQVAMGEKREGSPSSP\EE EAGVLLRK
2221	7718	A	2414	2	830	LRSPSVLFCGKAFFVSPRGRQLPER RGVAPPRAEEAGASSRGSGPPLRA MSYGRPPPDVEGMTSLKVDNLT\Y\ RTSPDTLEGAVFEK\YGRVGDVVHP RGIRYTKGSSRGFAFVRFDKRD\AE DAMDAMDGA\LDGGELRVQMAR YGRPPDSHHSRRGPPRRYGG\G\GY GRRSRSPRRRRSRSRSRSRSRSR SRYSRSKSRSTRSRSRSTSKSR\AR RSKSKYSSVSRSRSR\SRCRCGYRSP PPVSKRESKSRSRKSSPKSS\EEGA VSS
2222	7719	A	2415	1	320	RGRASKECSGLSAHLVIHCGEKPYK CNECTRTSGTN/SSLTQQRSH\AEKP YTRNECGKVFG/HIARHQIH\STKP YKCN/NTLKAFSKHSG\MAHLLIDR PEKLCHYS
2223	7720	A	2416	733	1005	NPQTPMKNCWP\LEKKAEP\PLGSG SMPLGFCPHGPPCSCDFLETH\FLDE \EVKLIKMGDHLTN\LR\LDGPEA GLGEYLFERLTLKHD
2224	7721	A	2417	148	1057	
2225	7722	A	2418	87	241	EGGLGNDPMTTDCSMAA*LFK**SP SS*ALGSFCEAQIIQSSKGLFSRGSC
2226	7723	A	2419	1	924	
2227	7724	A	2420	1	1004	MPVGAGRRAKGDPATLGALAVFTV GAKRSKGHSPKHPAGRLPPLPLR QRSTPMIDTLRPVPFASEMAISKTV AWLNEQLELGNERLLLMDCRPQEL YESSHIESAINVAIPGIMLRRLQKGN LPVRALFTRGEDRDRFTRRCGTDTV VLYDESSSDWNENTGGESVLGLLL KKLKDEGCRAFYLEGGFSKFQAEFS LHCETNLDGSCSSSSPPLPVLGLGGL RISSDSSSDIESDLDRDPNSATDSG SPLSNSQSPFVEILPFLYLGC\AKDS TNLDVLEEFRGSSPYMILFHYGEIG TSYVPITSHFRQKLAQGFPVSTGTP GFIYSAK
2228	7725	A	2421	686	1812	TCPVARASLTRGEDRDRFTRRCGTD TVVLYDESSSDWNENTGGESLLGL LLKKLKDEGCRAFYLEGGFSKFQA EFSLHCETNLDGSCSSSSPPLPVLGL GGLRISSDSSSDIESDLDRDPNSATD SDGSPLSNSQSPFVEALALPSYLGC A\KDSTNLDVLEEFGIKYILNVT\nL PNLFENAGEFKYKQIPISDHWSQNL SQFFPEAISFIDEARGKNCGLVHCL AGISRSVTVTVA\YLMQKLNLSMND AYDIVK\KKKSNISP\NFMG\QLL GLSRRDAGDSAGPCGQQGSRHSRL YFYHPFPTRNVLPGWDFLQSTWKD

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PTPFLAGMCLALQQFLLAASAGAA FFVCGPRCQNDTKLSVLRQGYQVR ELG
2229	7726	A	2422	66	187	WGGGGSAAAAMEANWTAFLFQAH EASHHQQQAAQNSLLPLLSSAVEPP DQKPLLPIPIQKPGAPETLKDAIGI KKEKPKTSFVCTYCSKAFRDSYHLR RHESCHTGIKLVSRPKKTPTTVVPLI STIAGDSSRTSLVSTIAGILSTVTTSS SGTNPSSSASTTAMPVTQSVKKPASK ACKKNHACEMCGKAFRDVYHLNR HKLSHSDEKPFECPICNQRFKRKDR MTYHVRSHGGITKPYTCSVCGKG FSRPDHLSCHVKHVHSTERPFKCQT CTAAFATKDRLRTHMVRHEGKVSC NICGKLLSAAYITSHLKTGHQSQSIN CNTCKQGISKTCMSEETSNQKQQQ QQQQQQQQQTHVTSWPGKQVET LRLWEEAVKARKKEAANLCQTST AATTPVTLTTPFSITSSVSGTMSNP VTVAAMSMRSPVNVSSAVNITSP MNIGHPTITSPLSMTSPLTLTTPVN LPTPVTAPVNIAHPVTITSPMNLPTP MTLAAPLNIAMRPVESMPFLPQALP TSP\PWRPTGPRCSRPMKLPITNSR QHRTACCPs
2230	7727	A	2423	3	777	RTSLVYDYPLRRRWLRRQRGGGGF CFGCGGRSPGPGFGLSPTVVTLAEL LVLLAALLATVSGYFVSIDAHAEEC FFERVTSGTKMGLIFEVAEGGFLDI DVEITGPDNIGILPTRLYNLSGKYTF AAHMDGTYKF\CFSNRMSTMTPKI\ VMFTI\DIGEAPK\GQD\METEAHQN KL\EEMINELAVA\MTAVKH\EQEY MEVRERJHRAIQRTTQNSRVVLWSF FEALVACCHDIWGQIYYLEGDFFEV RRSCFKKPLPG
2231	7728	A	2426	89	136	
2232	7729	A	2427	1	916	MFYHLVPDGKKPGATLKATSAPKG KANGGRQAHAPPRWASAGDVTHS AISELRESATAAASASSESAGSGPR MKSVIYHALSQEANDSDVQPSGA QRAEAFVRAFLKRSTPRMSPOARE DQLQRKAVVL\EYFTRHKRKEKKK KAKGLSARQRRELRLFDIKPEQORY SLFLPLHELWKQYIRDLCSG\LPD\ TQPQMIQAKLLK\ADL\HGGLFISVT K\SKWPLLMLGITGNPFYQETK\HIF QNLSPKGRPALKVIPPSLNCRVPLW KPDGFIPPTFTGSKFPSLGQVNR\SA KKFQSEGNRLTL
2233	7730	A	2428	2	484	PDSSGPHRLRENPPWCLSPADKTNV \KAAWG\KVGAAHVSRMCAEALER MFLSFPTTKTYFPHFDLSHGFCPGL RATGKKVD\EALTKRRGAPLDDMP NAL/SSALEATLHAHKL\RVGPGSTS KLLKPLACLVDPGPGPPSPAEFHPL RCNVFPGDKVSVWVSC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2234	7731	A	2432	197	332	
2235	7732	A	2433	1	1788	
2236	7733	A	2434	3	111	
2237	7734	A	2435	220	423	HEELKSGPYLLTFRDCFLHFWALV SKR/LALNFM*TSAPT*KALSKRNIC LVNKNRNIPYPKKKKK
2238	7735	A	2436	273	499	RSGVRDQPGQHGKITSLLKIQLAR RGGACL*SQLLRRLRQENRLNPGG GGCSEPRSCHCTPAWETEQDSISKIK
2239	7736	A	2437	1	1176	
2240	7737	A	2438	245	394	
2241	7738	A	2439	458	701	GPAPTRRGPAHGAHTR**PAGTAR AACGSA*SAGTASPAHKGKGHPG SRASGTGPGPCQRRRRSDHSSAGK WPLREASL
2242	7739	A	2440	365	814	AALRSSSENSRHRSLVKMSDKKAK DPVN\KSGGQGPKRKNWSKGKSSG TSFNNLVLFDKATYDKLCKEVPNY \NLITPAVGSERL\KIRGSLGQGKPFQ ELLS\KGFI PNWFSKHRASSYFTPGIT KGG\DAPSLLGEDCMNRSNPPVHLE K
2243	7740	A	2441	41	565	APSPRRPWGHFTEED\KATIKNLWG KGEMWKDAGGKNPWERPWLSTYP MGQRFFDQLLANLSLCLPIMGNP PKVKGTWPRKVLTSLGSAHKSTW DDLKGHLLPKPEVNLHC\DKPAMW DPENFKAPGEMLLVTRFGQSHFRQ KNFTPGGCRASWGRKMGDLELASA LVPSRYH
2244	7741	A	2442	3	284	
2245	7742	A	2443	1	3339	VEGMTQCQSCVSSIEGKVRKLQGVV RVKVSLSNQEA VITYQPYLIQPEDL RDHVNDMGFEAAIKSKVAPLSLGP DIERLQSTNPKRPLSSANQNFNNSET LGHQGSHVVTLQLRIDGMHCKSCV LNIEENIGQLLGVQSIQVSLENKTAQ VKYDPSCTSPVALQRAIEALPPGNF KVSLPDGAEGSGTDHRSSSSHSPGS PPRNQVQGTCTTLIAIAGMTCASC VHSIEGMISQLEGVQQISVSLAEGTA TVLYNPSVISPEELRAAIEDMGFEAS VVSESCSTNPLGNHSA GNSMVQTT DGTPTSVQEVAPHTGRLPANHAP\D ILAKSPQSTRGSGHRRKCFFTDSKG MTC\ASCVSNIERNLQKEAGVLSVL VALMAGKAEIKYDPEVIQPLEIAQFI QDLGFEAAVMEDYAGSDGNIETIT GMTCASCVHNIESKLTRTNGITYAS VALATSKALVKFDPEIIGPRDIKHIES KTSEALAKLMSLQATEATVVTLGE DNLIIRREEQVPMELVQRGDIVKVVP GGKFPVDGKVLEGNTMADES LITG EAMPVTKKPGSTVIARSINAHGSVLI KATHVGNDTTLAQIVKLVEEAQMS KNPNKHISQTEVIIRFAFQTSITVLCI ACPCSLGLATPTAVMVGTVAAQN

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GILIKGGKPLEMAHKIKTVMFDKTG TITHGVPRVMRVLLLGDVATLPLRK VLAVVGTAEEASSEHPLGVAVTKYC KEELGTETLGCTDFQAVPGCGIGC KVSNEGILAHSERPLSAPASHLNE AGSLPAEKDAVPQTFSVLIGNREWL RRNGLTISSDVSDAMTDHEMKGQT AILVAIDGVLCGMIAIADAVKQEEA LAVHTLQSMGVDVVLITGDNRKTA RAIATQVGINKVFAEVLPSHKVAKV QELQNKGGKVAMVGDGVNDSPA AQADMGVAIGTGTDAIEAADVVL IRNDLLDVVASIHLKRTVRRIRINL VLALIYNLVGPIAAGVFMPIGIVLQ PWMGSAAMAASSVS VVLSLQLKC YKKPDLERIEAQAHGHMKPLTASQ VSVHIGMDDRWRDSPRATPWDQVS YVSQVSLSSLTSDKPSRHSAADDD GDKWSLLLNGRDEEQYI
2246	7743	A	2445	14	503	NNDFIVIGTGTEFGIPGPTHAYEKT IYDDYNCL*QCELETENQNLQRQF YDKRKLEAMLQGMVTTETMKWEK ECERRVAAKQLEMQNKLWVKDEK LKQLKAIVTEPKTEKPERPSRERDR DKVTQRSVSPSPVPLLFQPV*NAPPI RLRHRRSRVSGDRWV
2247	7744	B	2446	226	347	XGKIIVASCFFPFSSRKRRSSTVAPA QPDGAESEWTDVETR*
2248	7745	A	2447	8	2985	WIQYSSTTLPNWDNKRKKKEKKA MLSARAKTPRKPTVKKGPKRTLKT QLG/YPCRVRPLGFPDQECCIEVINN TTVQLHTPEGYRLNRNGDYKETQY SFKQVFGTHTTQKELFDVVANPLV NDLIHGKNGLLFTYGVTSKGKTHT MTGSPGEGGLPRCLDMIFNSIGSF QAKRYVFKSNDNRNSMDIQCEVDAL LERQKREAMPNPKTSSSKRQVDPEF ADMITVQEFCKAEVDEDSVYGVF VSYIEIYNNYIYDLLEVPFDPINPNL HNLNCFVKIKNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRRIANTHL NRESSRSHSVFNIKL VQAPLDADGD NVLQEKEQITISQLSLVDLAGSERTN RTAEGNRLREAGNINQSLMTLRTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAIC\GLTPRRRYRNQPRGP\IGN EPLVTDVVLQSFPLPSCEILDINDE QTLPRLEALEKRHNLRQMMIDEFN KQSNFAKALLQEFDNAVLSKENHM QGKLEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIYEEDKRNLOQ ELETQNQKLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLWVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFQPDQNAPPRLRHRRSRAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKGDYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAES\EWDRCR\NKVFCGL WEMR\AGSQLGTWISASRHNPSAKS HETDSPSTERTFSFVWMISRKPCQK QSSRSSCRTPALVENHEPQLHHTLT PEQSFPYGSQKTTSIQ\QNVYSVCFA \SNINSRGRRLRVSSL\YEF\FIMFFLK YISCILIN
2249	7746	A	2448	20	349	SFCLEFP CRPGELLALQDSAQNSTF DKTALPLPCLAPCPPPLGPQS\THIQP CFPHTGPCAPFFTTDLLQGQRLSLSL HTPLHPVPAHWALPARRALARLTD RPNARLTP
2250	7747	A	2449	3	384	PFLSVVSSQVAGHGRIFQCTYLMND CQTKQPCWSGATWPHPWMQVKGT PALRAHPQTLSESRLPEGTRGSRPE DCPKPQPADPPSLGT\QCPPPWQLSP TQQKMSPTFAAAKGASQGLMWAH AVLSRA
2251	7748	A	2450	1	1503	
2252	7749	A	2451	1	855	NPRRRLRGRCRASASSPRRVRRRGQ RPRHPAPRRPQAARPSAAPRARRFL SQRPA\AAAAAQRAALMQAIKCAG GWKAEAVGKTCLLISY\TNA\FPGE YIPTVFDN\YSA\NVMVDGK\PV\NL GLWDT\SGQKDYDRVTPPYPA/Q ADVFL\CFPFVSPAS\FENVRAK WY PE\VR\HHCPN\TP\IILVGT\KLDL RD DKD/TRIEKLKEKLT\PI\TPYQGLA\ MAKEIGAVKYL\ECSALTQRGLKTV FDEAIRA\VLCP\PPVKERGRENCLPV VNVSAPSFLGPVPLEPL
2253	7750	A	2452	41	556	APSPRRPWGHFTEEDQGLLSTSLWG KV\NVEKCWKEKTPGKGS\LVVP\ WT\QRFFD\SFGN\LSSAFAHHGQTP KVKAHGK\KVL\TFLGRCQOSTLDD LKGHLLPKPEVNCTVDK\PAMWDPE NFKAPGEMLLVTRFGQSHFRQKNS PPEGCRASWAERWVT\GV\ASALVP SRYH
2254	7751	A	2453	2	454	RSFFFFFCEVGSWVGSMRVVMARL LSEGEQCIPTACAAFAQQPGGRPRR GLAGVGE\GGPQCSWVNYRCTLEFL VSL\LGTDLARGR\GNSATGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCNVV QGWVSTSWGSSSPSV\QFFPKLLEF TGK
2255	7752	A	2454	94	218	
2256	7753	A	2455	266	547	
2257	7754	A	2456	2	494	RGPVMAESWSGQ/SFLQALPATVLG ALGSEFLREWEAQDMRVTLFKLLL LWL\VSLLGIQLAWGFYGN\TVTGL YHRPGLGGQNGSTPDGSTH\FPS\WE MAA\NEPLKNPTENKGRQQRVSKGI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HWVCWLLHWVLLLPRPQQGPAGG SGLVAGSTQLPTGLGLILPS
2258	7755	C	2457	12	356	MGDSFMDEVAPRLASVDSRFFSFSQ GAHIKXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX X*
2259	7756	A	2458	764	1135	LLQTTSRNFKNLNQCTKSPICKKK GSVFFFFFFFETESCPVAQAGVQWR DLRSLQAPPPG\SRHSPTSASRVART TGAHHYTRLIFVCLVETGFHHVSQ DGLDLQDQFLESFLFCLLVRLRT
2260	7757	A	2459	1414	1761	SAINFFFLFETESRSVAQAGVQWH DLRSLQAPPPG\SRHSPAPASRVAGT TGRHHARLIFFFFFFFFFLVETGF HRVSEDDDLFTSGDLPTLTSQSAGI PGMSHCAWRIDGI
2261	7758	A	2460	63	542	TALPNQLHGGRHLCPSHAFGSQGA ARPKRPQPGPG\ASPEWVQLQSHH PLPPPTPQSPEGGEFLREQRPKPLSF KPLLHPRGPLCPAAPKLPPWPCPLR VPQFPHPPLPPSGRKRDRERGMEEGE GGWAAGERRGGKEETLGRGPFTQR ERPRNQEGEGG
2262	7759	A	2461	2341	2443	GRVWWLTPVIPALWEAEVGRSLT ARSLRPAWPTL
2263	7760	A	2462	28	403	NTTTCVKGLQTQSYKTSPDGNTTK QTNKVKHTHTII*II*NAPPAVSTTAIR NKFSKNGEQRFIEPYTNRPNIHSLK *RTIQQYASSSKNLEIKDFSWKKLQ* FLENRNKHECFQFPKVNVGAS
2264	7761	A	2463	727	1156	ETTLSEARRGRSAAASCRGSALRRG RFPESRRGREAAPVCPRHVLL*GAQ SKQAAVAGKRSCTRHASRWPKSLF TPRRRISLKRALHFWQQSADSPS VSRAPGSTWVGPKAPTEVTSVAPSR MMWQNEKKKVGGERQDWRK
2265	7762	A	2464	10	302	MERFEAGLSHISPWLC*CCSHCGD CCLGSRSWGVLVGGGSCGALGPWG RCVCAGGEFPDRASLPVDPALAKLE CSHKFPTPKDFHPRDRSPSRFL
2266	7763	A	2465	303	531	VLRickVSEENSLFPLSDITYLASIPN KTQTHCPEPAQKPSCKAQ*FWPKC KPHPPCCHWALPPGCCWACHRW E
2267	7764	A	2466	6	100	
2268	7765	A	2467	2998	3570	QDRKQGSSAPATPSRA*AAAAARAP RRPAGRWRG*DAPQSPAEPAPRSPP WRRAD
2269	7766	C	2468	125	404	MMARPPPWLESHCTRVVRADGQV RXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX ADAW*
2270	7767	A	2469	1348	1807	CPTVDPLLQKNCNDGSATALARVP LHACREGRWASPSGFFCCCCCFLR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WSLALLPRLKCKGPISTHCNLRPLPG SKDSPVSAS*VAGITGARHHAQLIFF VFLVETGFHQVVGQAGLELLTSGDPP ASASQSAGITGVSHRARPVSWFNSQ SMNP
2271	7768	A	2470	538	676	VKRNPEAGAVAHTCNPSTLGGRGG WIS*AHEFDTSMTGNMT*PHLYK
2272	7769	A	2471	40	336	EYLYRHFKNKLFLYANILCSSGIWR HYVLILRTVSELDD***GCRWGLSRS FDYLSNTGWV*VLLDISSFAFVTGP LIHGTGGLSAFDLHCEALSFYRD
2273	7770	A	2472	2063	2406	SQKKKIQWYLRMFRQFDIYVCFLEF SVVLLMIGGLLSHRLIPVKQYIKLHL ALLRTGAGAHACNSSTSGGQGG*II RGQEFETSLGSSNPSASASQSAGTT GVSHHAQPIFFF
2274	7771	A	2473	22	273	LTQKMDHNQVKFKSTTFYSILGKSV LSLSRPEYISGKSDTYSENIYPLSIKS EIEPIETRCLNRSNASLVQK*YGHKT GLWWLP
2275	7772	A	2475	1269	1511	INFFFF*IIDRFLCHPGWTA VAQSR LTATLLPSRFKRFLCLSLPSSWEYRP LPPYPANFCSKLLICLSTFYKDCG NSA
2276	7773	A	2476	1411	1827	LHTCCLRRRPSGRGRSQQGHCSQSG SSPPRRRPSPAPEGPGFHAP*LCIPDL GHGSRKRGCWPPCGPRTGWADLV ASAQAACGCQPPPPSGSCSL*GRG PVGGSGHGSPCWQLVELCGRCWSW PGVAGSTWQWRRHPH
2277	7774	A	2477	1345	1642	WQQFTGAVIHLAYVVLVCLVAFS SVSLGLNFFHKNFSFDFQRERCWLF SPFKGCC*RCFFTQSLYCYQVCEFT KTLIILLIQDVPEIFWSLFCFFHGP
2278	7775	A	2478	113	584	WQDYIYKEVRVTASEKNEYKGWV LTDPV SANIVLVNFLEDGSM SVTG IMGHAVQTVETMNEGDHVRVREKL MHLFTSGDCKAYSPEDSVREKEQP* INGFRRTHIPITEQGDA PRTL CVAGV LTIDPPYGPENCSSSNEILSRVQDLI EGHLTASQ
2279	7776	A	2479	658	785	KTHGWVQWLTPVIPAL*KAETGGW LEPRSSRPAWATQRDLIS
2280	7777	A	2480	2	598	PLGKGKFTGQSAQLTTGTGRGLILA KGSHATLQKHRINHTLTHKNPFL FWESPPSLNLALIKGLNGFCLGTEK LFEQMTYGGKKVKCPIGYFALQS WEFHPPPPTLFLSLPLAILWPGGENR GPRVSTKTGIKTRWPAPFLGPLSNR LGNPQPNPAPAAVPSLGLSPW*RG RGLPWGWAKPRCALWTPVSLPST
2281	7778	A	2481	253	286	NDDDP*LPCLGQPPRSCQPSLP*S LLWSKMTTTPAQRSG
2282	7779	A	2482	407	587	QAGRGRARGVSEEARNKPVPPTET PQPTLSPQ*MGPAQDPAPQQDYRG KKSLNAWCGRS
2283	7780	A	2486	246	519	FQFGIHNTNYQRQGA KVFFKNKGV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WGGPRSLPYSC*EGLPLGESYQFEP QSLRDA*DIP*GSVGKNPVGSHWW VSGVIGGFIITGDYSQH
2284	7781	A	2487	470	977	TPPPAGLRQRGYPPPGNRLEARNW ARAKGGKTSAGRVFTQP*FPEQQLP PGRPWWPRPGCPHGLPTRACKWSG GVLAPESPEPPSLPEGSHSWLGDG LLASRKLRAGGSVATFTSPQLCPLG PHEDREAREGEGRLAPAQPVSSPSA PAGHSLSHPSRTGKLALVPGH
2285	7782	A	2488	393	618	IREWVNIFWNIHTEEYYTVIKKN*V CQTWWLTTVIPELWEADVGGSLP RSSKLR*AMILPLYTSLDHKARLSL
2286	7783	A	2489	308	626	IRGTSNMNRKNVEKAYYAEA*LSL
2287	7784	A	2490	1222	1374	AQQVKRLEGQRGWKLGRGRWL TPVIPAL*EAEAGGSLEARSSRP AWAKK
2288	7785	B	2491	60	378	NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIHFI SPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX*
2289	7786	A	2492	1	437	DPRATEGMVVADKTCQKSTGRLPE LVTAIRMLKQMLFRYQGYIGAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISKNKLDLFRP YTPVNKKGTRLGRYRCEKGTAVL TEKITPLEIEVLEETVQTMDS
2290	7787	A	2493	2288	2668	FGRGHYCRRSVSQEEEAKNLVSEAI AAGIFNDLGSGSNIDLCVISKNKLDF LRPYTPVNKKGTR*VKETKFFLGPL ASWPPLVSPWHLDGVLVLSTLSTS SVPKSTSHDLRLVTCFMTVGCCQ V
2291	7788	A	2494	3	861	FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKLPKVRKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIHFI SPNIYCCGAGTAA DTAMTTQLISS\NLKLHSL\STGR/LP RV\VTANRMLKQMLFRYQGYIGAA LVLGGVDVTGPHLYSIYPHGSTDK VP\YVTHGFLAPLA\AMAVFEDKFR PD\MEEEEAKNLVSEDSPPQFP PPS WRIFNGPGLPEANIDLCVISK\NKL G FSPNTQLPNKKGTRLGWRYRCEK GTTAVLTEKIPLWST
2292	7789	A	2495	466	607	KKKERSCLWCPS*SLKNYGLSCR KKKKGAVKKIILVQAWWLMPVITV LWEAEVGGLEARGLRPTRATW
2293	7790	A	2496	449	694	ILRILGTPISFPVNKISFLPFKCLFPDS YIENLMNIYQPIKKNEIHVPLQ*PW MHLETHLSELIQEQTKKHKFSLIR GS
2294	7791	A	2497	52	298	YNIEEQQNKRTQRQSNRHRPTPPPEPP NPEW/TPKPTPPTK/PSSPQGE G/P GW TGGPAPHAGAAPPFAPSPANPTLFPS LTTGGKV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2295	7792	A	2498	112	485	YNIEEQQEQTYSKTE*SAQTHPSPGT AESRMEPKPTPPTKRLPPTGGGGRG GTWGDPPGPCWGGHPPVFPSPCPTP TLFPIFDPLGGQSLAQLGSMVVEPT LQRATTLSTFLKMGKKETVAPPQI
2296	7793	A	2499	32	392	RPTFGIWFYPPQVFPELLELKAKYIG KHCFSIHSLPDTGPLPGCP/SPPGRA ALGIIPGNLPAPEQKPCWDP/SPSSTL VWRMLNSASTSPSPAPSYISPPFPGQ SYFPAHPPTSSLSLGGIY
2297	7794	A	2500	914	1417	PQCLLPNRGGSVQVRLWGATASLS GWGFLASFHPIHPFGKFSSLPDTPW GLCLGCPFPQAERPWA*YPGTLPAP ELETLLGSLPSSTLVWRMLNSASTS PSPAPSYISPPFPGQSYFPAHPPTSSL SLGGIYHQLLPL*PLPSTDPPCAPLL TSPPLTFLKSPRP
2298	7795	A	2501	1120	1159	ERAVCGC*CIFVM
2299	7796	A	2502	1145	1367	IFFSFLHIYIHNTHMYIYYTLCVC VCCVYGMVCVACVYSSSKPKQVC VWIEGNLNY*LQVVCLWYLDFFHS
2300	7797	A	2503	155	454	GGFSVWHTETPPRMLMHQVQFNL EYLTTPESTQKGGPTPLCIYGYVFFK SDYLYSLSLFFRFLYFSSLL*YLML VNFLFRMLFSLFMSFCYLFFIIL
2301	7798	A	2504	901	969	RWPGMVAHACNPSTLGG*VGDP
2302	7799	A	2505	903	1339	DKTVQSIRSMGGWKMDASDSKFV DLWIAEGIGTSWRNPGYQAPRPFLH HGCWGDGKSPPLPKPVSHITDVG WLRMMVSTGLSHLW*VPSQGQSSQ GPHPPAPGVQPPQTPPPASLKGKSL HLQGACSEGGAPFSIELFAGRS
2303	7800	A	2506	433	548	PSEYTLGFKNPBKILTFNGGNSMSG VHF*TGFTFLFL
2304	7801	A	2507	637	906	RIKKLSDGSYFLPGVSQIA*GSNYF* SKLGPDDGASRLQSHHLGRPKVGV FHHVGQDGLDLLTLVIHPPSAFPEV LGFTGREPPRPSLHL
2305	7802	A	2508	211	575	RENHDLESQCKRGAPVPAGVPSSAL PQGPVSLLPGAGALCPFERSQQASP QVSPQGVDPKICSLQTTSLCSFCDR CTGMGSL/C/SSCPPCSSS/CHGRSHS SPC/CL*SRTSSVVGDEVCNNTL
2306	7803	A	2509	274	488	SGDKTMQLRGPCGGWGSPAGLGT CTAGSP*LCHHKGHCSIHSTSCFCLA TVSPCAIFNSTSKAGRGAQP
2307	7804	A	2510	83	442	NFTMVMYTDHILRNAHLMYTSGR RLSVPKIACHITDHSHTCYMPYL RD*Y*TMFSQGFHYAPYLHLHT*EH PFECLLAGRTFTDALFEPTYPTLTL LTPSHWQDGPPLTGSQMPG
2308	7805	A	2511	2	270	ARLGLPKCFFCVFVKTASRSVSQA GVQRCDHNSLQ*PPGLRSSLASR VAWTTGSHHHAQLIWLKCFKQYFV SSGFYLLLVALLWWGG
2309	7806	A	2512	234	409	KGFYAHEKNARTWWLTPIIPTLSEA *GGKMA*ARSLRPAWATIRDPISAK

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						SKKKKKKS
2310	7807	A	2513	78	460	NVCRKMPPSDRLAGAYILQCNPVE VVGPEREDAPQNRVQVRHGCVAW PLLAPPPRHLOGEGLTSARKRVL LGVTSGL*RTDSHNPPGPPQREQTE PRARPPALEHRAQQ*PGPGLGGHRG AGCHQ
2311	7808	A	2514	67	279	SHRVSERDAACGAAPAAARLAGGQR NGRAISGRPGLSS*GAGGGNVFKVC LLLKNKRTGGGRGHGYLYSLQR
2312	7809	A	2515	683	933	YTSELIGKIISGQEVVVGAWCEDLG *GPRKSRGREGKG*G*EGSGNAGRI VGFKQGRGEDAHSWSQRGRQEFV FYLKSTRNW
2313	7810	A	2516	2	208	SKIALLVHLK*ENRHQLFFELIPTVF FLFIFETGSHSVTLQECSGVIMVHCT LTSWAQASSPLSLPTA
2314	7811	A	2517	426	601	PSFRIFTQYSSFLKNSLKRLGAVAH VCNLSTMGG*GGRTA*AQEFETSLV NVVRPPSL
2315	7812	A	2518	55	489	HSALIQASVWFRYKYPGGLGASLP TN*GKKGSQVGSSAHFATTFTIPNG DNA*GAKSGSGCPGGECHPG*GPIS SCPLSEGQTCALNPLSCGSPGPDWLI LGKLGPLGCSKPKGSHFAFPLVPIF HPCSKTKLFPREELFVVR
2316	7813	A	2519	52	286	MMPCLRQRQREREREREREH MRTQRKQLK*WITRFKNSSKRQR TEKNSKKPPVPHRGAGHSNGKLC FRPAAS
2317	7814	A	2520	3	296	TNTTRYTIGDPALQDMNSRRAHSH TYGHTLLWEGICDLTRPPKLGSCRE KECPRPHPSLDR*SSGFWDPAARGE LMQWEMPQPCSPQPLPKPCRSSI
2318	7815	B	2521	83	241	SEWQKKLTPEQFYVTREKGTEPPFS GIYLNKEAGMYHCVCCDSPLFSV KLI*
2319	7816	A	2522	19	629	YFVLISPLLTFTSTHGFDCYLICNTV HKTPCVFRSLWDIQKEVFSIKGSRSP SPSKGNFGDSEGPVRTIPGGLTVE*L GMGSGRGEWDRILLPGTTHRGTSW HVNDVVISSCSIVYVFHSSEKKYCSG TGWPSFSEAHGTSGSDESHTGILRR LDTSLGSARTEVVCKQCEAHLGHV FHDGPGPNGQRFICINSVALKFKPRK H
2320	7817	A	2523	1	707	MGAGAETGRGQRAAAPERRHGRL LWLLRGLTLGTAPRAVRGQAGGG GPGTGPGGLGEAGSLATCELPLAKSE WQKKLTPEQFYVTREKGTEPPFSG IYLNKEAGMYHCVCCDSPLFSSE KKIYCSGVTGWPSFSEAHGTSGSDE SHTGILRLRLDTS\LGSA\RTTEVVCKA /QCESSILGHVFPADGPGPNGQRFICI NQCWLWKFKPKGNHWTIFQESAFP CHPFHVAPSIFHNSLE
2321	7818	A	2524	303	743	TGAQWGRGLGHVCWSMGFVSWE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						CSGNGLSQAGLVKLKLLIHLSTVQK GLTPRWGGMNLTQLPGGVGGP*FP KMPGATL*PFEGKSPAPQLFPCQPW AGAAHGGAGGPPSSGSPVPGPPQCPV KALPVLRA GWATQPPGSFLWPTPS D
2322	7819	A	2525	102	421	VQYGSNWNKPYWNRVGP*SHTTG ELKKRWPHPRSCCPHGAAGQGAER CGRERGPEDTSDLLNK*QW*RRFPS GPAECGA AVAGL*GAAGCRGRSRP LKSRDAGLKS
2323	7820	A	2526	225	448	TQEGRGIDFGPW WPQLLPSSSPSG L*SPATPPQAWVPPLPSSSSSPALILS GPNRKPEPPPGIPPQFYLTSL
2324	7821	A	2527	43	390	GDVPTVTGECPPSYRAMSPSYR*MS PQL*GKSPQL*GDVHQL*GNVPPVT GLCPPITGQCPLIVSPSYTVLSPHYK VVSPTVR*CPPVTG*CPPIAGQCPL *CPQAISWSPPVTG
2325	7822	A	2528	525	635	HIQQQLWWMPVISALWEA*EGGL LDPRSLRPAWAT
2326	7823	A	2529	66	432	TRGSWHKHALAPT VHRAGLWGGK AGTQASPGAADNVPPPY*TSGFCG WKAGTDFPTSKKPCPFLPHNPPLP PCKWQKGLSLFVISHSLICKVGMQL PRGSQVRLLLTKIQIHRLSLGRAE
2327	7824	A	2530	5	95	
2328	7825	A	2531	1	123	
2329	7826	A	2532	118	363	
2330	7827	A	2533	23	250	YLIVVWICISIGLYTY*LIIRALYILR KLT LFKYIPISH*SLSFIVIFCSLVYIY MYIYIYVYIYIYIYIYIYIY
2331	7828	A	2534	346	611	TSVEAQDATDRLWPDSPPAHGAC TRTVWPKPPYFPVKKMESCSVAQ AGVQ*CVLSSLQPPSPRFK*SPASAS GVAGITDFQKLFQ
2332	7829	A	2535	267	682	HFSSLRMQARPPSFRPYLVLPKNC WIFILINDSWMVLFEEASLPTVPSLV QTTIFLLGILQQPLTDLPSSTSTPF*S LHLSAV*VFRKFLSWPGMVAHTC NLNTWGG*GGRTA*AQEFDTSLGNI VRPCLQKKKS
2333	7830	A	2536	45	280	
2334	7831	A	2537	1560	1885	QLGVLLAGPFTSSPYGGVSPGLKRP WPAPRSYPLPAL*PLPAPYGVQRS LPNPKLGKNPLGPPISSQKPPCGGPV KTSIVAHNYSALSLSLTPQPSA PQALS
2335	7832	A	2538	60	341	VTLSLVILFSAHICRIKLNITNLQM YSVVHPNFHLDVTIPKIVVALCFRK KYAFFCFMQQKYRM*SEIHIFILS VVLNVNEINSIIQMY
2336	7833	A	2539	442	686	TSYNNLLNNLKNITFRKELSSLSHL CNRGQGILKSLIAWLGAHAHAGNP STLGGRRRIA*AQEFKTS LGNLRP VSPKK
2337	7834	A	2540	459	603	GFLLEIIDKAEGGAHACNPSAFGGQ

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						DGRTT*GQEFKTSLSNVTRPHLY
2338	7835	A	2541	1	188	PEQVLWQTKVTYSGKKKKKATKRP GAVAHTCSPSTLGG*GGWIT*GQEF KTS LANMVKPCLY
2339	7836	A	2542	582	825	GLSNMVHLWIEHHPAARSRDCHSG RLRREACLG YRKIS*HWP G MVAHA CNP GTLGG*GRRIT*GQEFKTS LAN MVKLCLY
2340	7837	A	2543	775	1019	DRSSPKKPPDDLPEFTEPQWFTLKHI KQCFSDISRLRVGPGMVAHAYGVA YLSTLGG*GRRIT*GQEFETSLANM VKLCLY
2341	7838	A	2544	303	429	AACVLPSPPSAHSSTHTTGSTHLG* GPPCSGPAPT WGSWKT
2342	7839	A	2545	853	867	NP*NLACFCV LLEFPSSF*RGFRRLG AVANICNPNTLGGQDGWITSGREFE TSLGNMVKPCIY
2343	7840	A	2546	357	560	KGSLVGLSLEERIFVVA VQPSLFHK KCLWQGTVAHTSNPSTLGGQG RSV A*PQEFKTS LGNIVRCL
2344	7841	C	2547	486	728	MWVG VWEV FSGVVLGWGVPV ML QSDG SWKLPVHLHELLPFHMSWYP PQDDPNISL KQLGLPGCP LLSLC DVS YMVSSA*
2345	7842	C	2548	240	332	MACFSFTSAQLKDRLRSPATH TPL LNAPL*
2346	7843	A	2549	2	603	SLPYLPQHPLEFGPLNLHRDQRAG AQTLTQPMSLCCSKSLQLPNA LTK RPCWVLFPA GLSSLLRND SAKLPFR NKSGFPPAQGLCPGGSRLTTWHLSF HGLFLLHQ RSAQRSTS QIPSNHTLT *CPTVTTETVPCLK*PRLSVVSVCF C SGSP*RALQCTPPGKPSF LSQLSLT DPLPSTNLLFHPVGT PRAPGWA
2347	7844	A	2550	132	419	
2348	7845	A	2551	1083	1563	PENQSSLYFLPANLLKMPFCFFVFF* DGVSLCCPGSAVAQLQPPAS*VQSD SPA FSLTSRWDCRRVPPRANFCIFS SDRGFSMLVRLVSNSRPQVIHLSQP PKVLGLQVETGPQKREWVPRELTA SGQWK GQEPDQGEDSGTEGRWLPL LPSAGHSGED
2349	7846	C	2552	173	501	MPSPSAPSIVPVLHGCWVHICQADV YHTLLKGFLFLRQSPTLSPRLECS GTILTHSNLRLQGSSDPAALASQEA GLKLLVSSDPPTSASXXXSAXLXCQ TGV SXXRP*
2350	7847	A	2553	174	364	YDAEFPRCSFGLIYPRLSVKEASRLS AVAHTCNPSTLGGQGRWIT*GQEFE ISLANMVKLHLY
2351	7848	A	2554	61	283	GGRIA* TQHSILDNRVRLHLKKKKK KKQYLKKVHLPGAVAH/TYNPSTL GGQGGWIT*GQEFETSLANMAKLC LY
2352	7849	A	2555	1140	1313	HVENSEGASGERKLTQRLGVVAL ACNPSTLGGQGRIT*GQEFETSLA NMAKPHLY

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2353	7850	A	2556	99	296	WVLIVHVISSKCLVLEICVYRLGAV AHACNPSTLGGQGRWIT*GQEFETS LTNMVKSSLYLKYKN
2354	7851	A	2557	175	332	RNPIFSLRKWPLRPGGVAHACNPST LGGQGWIT*GQEFETSLANTVKP RLY
2355	7852	A	2558	667	772	ARCTNPSTLGGQGRWIT*GQEFENS LANMAKNRLY
2356	7853	A	2559	7155	7302	IMKLKMYIWPAGAVAPACNPSTLGG RGGWIT*GQEFETSLANMVKLRLY
2357	7854	A	2560	227	410	FQVDPDTWLFIEVTLFIFMAIFYLW QVLLVFHFTA VR*CSLFQGSYGIFGI EGRIPYSEL
2358	7855	A	2561	275	685	LKPLFTPSPGPA GVP RGLCWKEAPT PGSLLGEEETELNVY*GPPPGSLRPA SHWAPPEGLRPTSPLFVAATSTIGPL PVLVTLGPHLSPLFGQFINKGRDDT VLLPPQSPGCRESLACQGEETSRLCF VSHTSPSSL
2359	7856	A	2562	20	354	PLYSQSFPIIYPFITLLPE*SF*NNNYC SFVNIPSLTPSHQLYKVHSPHPHPVF HTWAHPAPALCSSWVAMLT VYQG AVLYQCLSTAVSVQGPLRLLGFSNR DTLPSKGLS
2360	7857	A	2563	374	585	GNLINC*LHTHTHTHTHTHTHTHTH NLTNYPDFLYLLVTFPGDIVIQESAF IFFTKSPKHCGLGAIRNA
2361	7858	A	2565	918	1096	HCHSNSEFD TETLGMVAHTCNPSTS GDCGKQII*TQEFGTSLGNMVKPHL YQKKKKKSR
2362	7859	A	2566	101	327	LVKNQQSTQKLAKHGWACL*SQLL ERLREENHLNAGGGGCSELR*RPCT PAWATETVDSL PIMCLVLQPFLSLS R
2363	7860	A	2567	347	478	RDHCRLGTVAHAYNPSILGGQGRRI A*DQQLSIGNTVRPLY
2364	7861	A	2568	622	761	KSVEVFYLSIGQEECLPHIQFIFHAT IFIIGRAQWLTPGIPAFWETEAQEFK CIHICMQVWWHTSV*SVRNKSLYE ELLQARDPGKFVILHYHYWLFHGK A
2365	7862	A	2569	70	316	ISHPSPSTRWEAVTWALG*LFPCPC HLQGGGRQAPLPLPYPLPIVAPPLI SRLNPDGDL SAKTILDVTLYISSTTV GGSWG
2366	7863	A	2571	145	331	IFHSMKPISEWKLV*TLWQFFKELKI ELPFDPAIPLLGI*PKFQRLKNTNGIC HYFYM
2367	7864	A	2572	918	1135	GFISASLCNWILTHLKFFKEMGSRG VAQAGVQWLLTGAVMAHCNLKLL GSSNPLASAH*VAGAICMYDHWHA
2368	7865	A	2573	590	936	QLAACGGGSCLSQHFERPR*EDCLN PGVQDQPEQNRETPISTKIILKSWA WWHIPVVPGTWRADVGGLPEPSRP KATVSCDCATALQPGRRRARLCLK NKYIKYSVQKCVIFFLF
2369	7866	C	2574	34	670	MXVFLSSAGNMPVTCWCWEAPRC

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						NQKCTDPAARRPDPQTCASQDRLR CAPCTCHQPLXSRYTQHPGLVPLPH HDRQSVPPQGPVVQTDAAAXMVE VSVXVVLEGWGXPTTRMKLSLLG IKMLRRGGTVRGAPGAGSALRCGW RWRPPAWRPQMSTSRVSGVQARS TSSSPXPXXSGXLWVHVLLXLAQL DSQQGFDLLLAGRRXSGSNLI*
2370	7867	B	2575	70	165	EQIEALLESLRQAQQNMDPKAAEE QEEKEE*
2371	7868	A	2576	1	390	FFFFFFGVLPVLFDFHVCFLVFCWK HAGYMLVLGSAAVQPEMHRPSRPP PRPI*RRQTQK*LWFEVDVSWLQGR WVENQHFINRVLTCLERV*NRIYYG TSSSSPLRSGSEGVGPGAFSRPLYPC LGPPN
2372	7869	A	2577	435	861	RASLITVCVPGHLQAADQKNLHPLR AHVVGPCLAGSSCARRPSRA/RGPP RPTPPEHGSRLPQPS/CAAASV*TTR GP*GTLCLS*WGKGTSPGCCGIERP KAGGKCTGHSVCVPVTRKSNHSLC ARSPTSCRPKFAPAAAGPRGGALPG RVILCSKAISGTGPPRPTPEHGSRLP QPSWLRLSEPRGGLEGRFVCRDG ARAQVLDVVCIERPKAGGKCTGHS GVCVPVTRKSEGLGGGRLGLCISGCT AALPSTNM
2373	7870	A	2578	38	398	PVLFLDFHVWLFVFCWKHAGYML VLGSAAVQPEMHRPSRPPNYIAK MCKLSILSLSFLKEGAGDKNSSEPN LG*VP*FSLHPCLSNQMTLGNKQA ESMSLCGFFLPDCFFLTYSRIYL
2374	7871	C	2579	42	443	MKPAHSAVCPGHLASCETKEFAPR CGPTWLGPCPGRVILCSEAXSGTGP PRPTPPEHGSRLPQPSWXRRLSEPR GGLEGRFVCRDGARAQVLDVVCI RPAKAGGKCTGHSVCVPVTRKSEGL PAEDKKTNMKV*
2375	7872	A	2580	871	1253	PRLPPGLPGADRSPAGSQACA\GPA EHGPQGRRGGRGGGGGGGPGPLPHP PTCGTWTSEGA\SRRAPPPAAKGG AGPRCSPDSPSPEHFDQKQGLHS PCCWLFPPLLFPPSISDLSKRKRLPK NCL
2376	7873	A	2581	222	754	YPP*HVAPHPAPLPWQVQGPDPW PRYLWKVPPASLWPRGTEKSPCWA WLVGAGLGLPPFSLPNLSDLGTS FPLPQTLPLCPAPQGDLLKPKLGPK KGGSVLSTSPSSFPRGLVGGEAPPN LSPSHTHLGSNVCWTKKQEHTLLV PTFSQSSQNPPPLSPSPIGAVKALFAS TMG
2377	7874	A	2582	2	431	PÉGAAPAAMAVTALAARTWLGWV GVRTMQA\RGFGSDQS\ENV\RG G\SIREA\GGAFGKREQAEEERYFR/ ALQVML*DLFGVKD*N*TLSHRVL VEAQSREQLAALKKHHEEE\VHHK \KEIERLQKRNLRSRHK\QKDSKLLKH

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2378	7875	A	2583	1	232	RETACCGRDARGAAPAAVTA AARTWLGWGVRTMQARGFGSDQ SENVDRGAGSIREAGGAFGKREQA EEERYFR*GSDQSENVDRGAGSIRE AGGAFGKREQAEEERYFR
2379	7876	A	2584	3	399	LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLGWV/WGVRTMQA \RGFGSDQSENFPTGPRAPHP/RKAG GALGKREQAEEERYFRAQSREQLA ALKKHHEEEIVHHKKEIERLAEKK FERHKQKIKMLKH
2380	7877	A	2585	3	316	LLQILGTEPQKAVIVLVENFY*YVS KYSLVKNKMSKSSFREMLQKELNH MLSDTGNRKAADKLIQNLDAHNDG RISFDEYWTLLIGGITGPIAKLHEQE QSSS
2381	7878	A	2586	3	469	
2382	7879	A	2587	434	815	TQVDWTQRRARPGPWRHHPFPDD DSLGCCTSHLPPHGD*L*NPSSNGA NPRLSPAPHPPPREAQTPPGAGHR TPLSRACLGLAFPAQPVRLRRDTKR DGRKEQRETVPPTFPDARGTRLIL RHK
2383	7880	C	2588	204	354	MWLQMTRAVLSSNLDPYVCRRRA RGRSSPSGSLXXKGESWGPRHCY SP*
2384	7881	A	2589	390	681	RERGRRAGRRETA VRSREKERER EGLDRSSRKR*PELVKGSRAH*PQ SGRWSHRPRPAIVPTSFQPCDVRAG QPNGPSDLPDHLPTRRRKACDRR
2385	7882	A	2590	598	769	YPQCPTPCQAARVWWDShLAIPAL LGGRGRWII*QGEFETSLANMAKPH FYQKKKKK
2386	7883	A	2591	359	775	KKTQPLHQGYPKINFRSPSPPIVPV PLLALPK*GHSPFVSPPLQKIPPKG SPHDPTQRPSIAEGRAGTQLSSPL WMAGTLTEALHHKNRQYPLGSHN QLNLGSTGRTFSKRKGKDGPFDAAQ LQHLKGTFFFF
2387	7884	A	2592	585	780	TFSLPRLDFFFLKARKPRIKNTKNRP GVVAHACNPSTLRGQGRIT*VQEF ETSLANMVKHHL
2388	7885	A	2593	436	1645	GMSALVQSRVSHLHRVSLTRLTA RAQETSSPNTVTPPNQTLSTAQNK RTIPGPARE*VTLTRLSKEPLLVEK AAPTPHPQ*GPAPRPLQASALPLYE QHRRAPSSSEDPWRPLTPPSH*GVS TWT
2389	7886	A	2594	1	373	TCSCPWLAPLTLQKNCPPHCHILSL LRKTKQNDAPKKSPPRGLPAVSGM KQDTVTLGRMEKPPRSIPQRQWD GEATRSIPRRPRVPPVEPNPGHWQ NSPPG/EDQSILSTSNPRGPTPFKSGS
2390	7887	A	2595	502	798	SPKVQRHSSQAALRQAGGALS CLPSQRRPRTVSSREGPHPGKGV* GGVQRSKGPPLPTCPQGLTCLTPT DPGSAWNPPTPT*NEKGNSEIIRH

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2391	7888	A	2596	1	136	HPCVHEPMSFEWPWQYRFPFFFT*G SDPKKHGWASLPSGPWAQP
2392	7889	A	2597	429	1003	VAYVIGFKSNMPAKHMIKNTSVRV FICPPSMEGKHG*SQPR*NNSPLSPQ NNLSPTLCPLFLPQLKQESMC*SFFN FYQPALAFSLYSIIPSDVDLPSSPFE TRVSWEQFAYLLLESAYLLVQAIE *ASSFLLKHSTSLWIPLHCLFYITFD ICWSLYMNIIFFRGSHCSLQYDPGFL TLNAPSITI
2393	7890	A	2598	367	463	SGHGAHAYNPNTLGGRGRRIA*SQE FNTRLDN
2394	7891	A	2599	436	833	CLTSALLGCVYVYFFSPHPALFFLRI RTSAYNLLKQLFFRYWNSAKSDLS GHSKTLMCPKSGGGKACAVEPSC SLDTYLCPEIICQALFFICLFVHLLL FYCYWRGHEL*YSYCP*FNVKLIM MNSIACY
2395	7892	A	2600	53	95	DSILLTQAGMQWCELGSLQP*TRP PIVCFFCLFIYLLRQHLAPHPSWNAV V
2396	7893	A	2601	432	825	NFKDTAKGFLHFDHQKILDPCPLPG SRARFGTYPECPHVPSVTEAQETGL SVPSFGFHFHFLTYFLLLEYFYFH*G TLYLHLDLHQK*HCQAMRNFLYKS RIQRHHIYHSLDAYANLGHDAKDPF FSLDF
2397	7894	A	2602	83	111	
2398	7895	A	2603	1	71	
2399	7896	A	2604	215	758	LPLQYHRKNIHANTVALADARAPR TASRNRLGVRASGLASSPRLGLQ GSISSASRGRPAQHVPGRPATLSPP AGAGPSR*ERSRAGARGRWVLLDH AGERPAVRELSRPDPRQVSFGPRNIS EIGQVLSPETSSCELPGIGDLLWQL EVYDARKHSLVGPESLSHRELGSPA GGRRP
2400	7897	A	2605	211	323	LDSLQHSASTLAQHSASKPWKPD FHTQFFHTVWKLQWCRAVVPATQ EGDAGGSLEPRSLRL*CVAGTTALH HCDSFHTVWKNVCVWKLSGFHGFE AECCASVEAEC
2401	7898	A	2606	75	232	TQPGHKGETPFFPKTPKISPERWWG PIPASWGVKAGKLF*PRGERFPLIW F
2402	7899	A	2607	325	566	FNDKYFYYPRGQIQCHITLFLNLKI TSDFFFCFKKTG*VAHTCNPSTLGD *GGGIA*AQEFKTS LGT**DPIYKN
2403	7900	A	2608	1114	1367	AIARTLIIMINLTVNFSAINENCTTT *RYFDLL*YTTGMFRKIVRKLKVTH LKWNN*RYTFCIRKFNNLSEPF NHVCKVF
2404	7901	A	2609	100	450	FLEENYKVKFSCFSPFEELKKKGRL N**NFIS*I*IGPKIFSQTNS*NSNFYQ YLCILSGLIQDK*NFKILS*FYYK*V GNFDILYIHTCVCVCVCVCVCVCVF VCLWSTLRMTDTV

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2405	7902	B	2610	50	382	XGEQLVRQDL DAGVSEHSGDWLD QDSVSDQFSVEFEVESL DSEDYSLS EEGQELSEDEDEVYQVTVYQAGES DTDSFEEDPEISLADYWKCTSCNEM NPPLPSHCNRCWAHX*
2406	7903	A	2611	1665	1787	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2407	7904	A	2612	1431	1553	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2408	7905	A	2613	1	752	DL DAGVSEHSGDWLDQDSVSDQFS VEFESL DSEDYSPSEGGQELSDE DDEVYQVTVYQAGESDTDSFEEDP EISLADYWKCTSCNEMNPPLPSHCN RCWALRENWLPEDTGDKDKEISEK AKLENSTQAEFGDVPDCKKTIVND SRESCVEENDDKITQASQSQESDY SQPSTSSSIYSSQEDVKEFEREETQD KEESVESSLPLNAIEPCVICQ/GST*K WLHCPWQNRTSYGLLYMCKEAKE KE
2409	7906	A	2614	426	813	SSRRFVWRAKLLCERAQSGTVYEI* QCAHRHPRHRHPGCCRHRLGYAGT AGPLAGYRPFROHQRLWRAASAI CVD AISMRTSRSTVRPLWPPPSPA RFATWSHYRLRDHGDHTRPVDLPT SQFTILL
2410	7907	A	2615	1740	1862	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2411	7908	A	2616	1174	1354	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPLRPAGLFKH SPGLYSQPILT
2412	7909	A	2617	2271	2393	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2413	7910	A	2618	1029	1197	FFFFFFFFFGLVETGFHRVSQDSL DLLTS*SSRLGLPKCWDYRHEPPRPA EEGI
2414	7911	A	2619	402	990	
2415	7912	A	2620	1326	1716	KAKKKKRLFFFCIFLCFLWGLPASL LEPGNVWKHLVWNSLHWSTARVL SSPHLTSCNSWQKHPEHPKGAPKN HLGAGCSGSCL*SQHFGRRLRQEDGL RQGV*GCSKP*LHHCTPAWDKHL KNSNNSNH
2416	7913	A	2621	148	420	LSLSLCRFLGRFCSGSSFSIFVLFHF SFL*FMFSFSLETQKFHTSCVCVC VCVCVCVT*RILSFGIK*SSIQI*AQH LINFIFLSEKWR
2417	7914	A	2622	565	916	VPRARTQHSREKGRAGAWFGLHY QGSIICGSNSTW*NPPQRGPKLLVRL MS*GHCPPSSTQSGSTTTGKEEVKS SSGSDVALALYNDYFSLFCSSSVSKI KREPQLYKQTERETGHT
2418	7915	A	2623	1132	1245	KWHLGKIQNYSTGKCNRIYIYIYI*I YLF*CHLSIGNC
2419	7916	A	2624	209	326	
2420	7917	A	2625	808	1010	EETEGRARWLTVPNPNTLGGRGRW IT*GREFETSLTNKEKPPSLLKNAKK

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						KKKRKKEIKPGMVATCL
2421	7918	A	2626	1602	1940	PSGNTSETSKGLNIRSHTRLFEDIKG VNHRSSQLFQKKPKNRDRIFQERYV RLLSK*VHPCDICKRPTSFLTTL*Q QKHHHF*QKALENIKEEQTDKLILS CKRVLPFVKK
2422	7919	A	2627	2565	2748	KSLKLGMSLKIKFIFLIKGH LGFPHF LKICPKTNSIFNTHVS*YIYVCVYIY VYTYTHIY
2423	7920	A	2628	1032	1292	MYIPLNNGTVGVDSQMHLVDVQIDY RVLFSYDDWCRNV*FGWAFTSCLP LHGNIGGFFKMCVSYFFWEGELFSS VYFLESSYRKPNL
2424	7921	A	2629	1640	1815	NSKGESSAPLFLPD SHLEKRKSYGT HPLYISLLKNYEK*NNSNLKAVIFK ALLKNKQT
2425	7922	A	2630	1089	1226	IQIQNKLLKKECP SWVW*HMPVISAT QEGEVGRSLQPRSLRSAWAT
2426	7923	A	2631	197	430	SSFLLVYFFIFYFILFFETESRSVSRLE YSGAISAHCCRLFLGSSDSSCLSYSE G*GGSIDRAQEVKAAASCRTTAL
2427	7924	A	2632	343	596	GYSLLYIQKQPTPLKTKARIGCSYY VNCIFLWNFWKAHTSCFPLCSFVGD FMYICCLERNPEVGSAQ*DN GKQM PCYYRAASEG
2428	7925	A	2633	1143	1553	QCRRVPRGKRLELGVHSSSTG*QAPL LPSASATSSGFLADRRVGTGLRTPL RSRRSAGPYLARPASSAARGPPVGR RGPPWGWAAASAAISARSSPPSAAGS GPDWRRPGKRHSPRPTAAASAHTS PSQSPAIPAGGR
2429	7926	A	2634	158	585	ALTWVHLSSVSFFFDLKLTPSRSP ANPSTQQPPHPPHPAPKP*WEAGRI AAS*LPSKAGSWKPLL VNP KAKLW SHVGRMEGDLQCPLCLWLHLPILW FFGGSCFPQTEHSPVQSPDGLIIAWN CPASDAGIKDCLPKYFC
2430	7927	A	2635	1348	1540	SCCWACE*QCNWYVYISVCACVYT YICISTHIYIYTYIHVHLMGYVKIKQ LFNACDSMEHLQAH
2431	7928	A	2636	263	615	LVNSEGNIWVKLCHELQHGPLNSSP FLILLSHSEKINRASIMLKRYKLN NYILSAFNPPPGKIHTHTHTHTHT HTHTESQKVKST*EIT*IFPQQYTNL CQREEHCYFLSHSE
2432	7929	A	2637	270	665	KLKGVAHVPHYCQPARTLAPRLALS EGSFRATCPG*ELSGLRCSPICCPPRS PPALPLCPLKTKLPKC*KQTQYPGS GF*PSHPSCSGPKPLMGCPPTGGG QVDEWIVIYNKIYGRNTGLRRLHRP LYQFK
2433	7930	A	2638	54	311	SQHFRPRQVHHLRSGVRDQPGQH GEMPSLLKIQKL AGHGATHL*SQLL GRLRQENHLNLGGRGCSEPIVPLH FSLGKQSEALS
2434	7931	A	2639	26	229	CRMTMSRLVTMGVAVFLVVCERC DAVCPSGQSPSP\PWASPECCRDH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ICPHPVGPPGPPSLALPAW
2435	7932	A	2640	133	586	THVMLCAQVGSHHPALPWASPEEC CRDHICPHPVGPPGPPSLALPAWDT HTHTHTHTHTHARTRATHAHILPS HAVFYFPDQVQSGSLAGSPYPRGGG GGWFLGGAKKGRECPGG*MGPP MTPSSFQKQLLLPPSQGPTPKPEGG PCLQ
2436	7933	A	2641	186	609	RVGHHPPSVRHPHQGHGWLDPV QLHLWSSCVAFPPGGAPAGLPPSDQ DPGPPLAISPTHWPPCGQPKTIAA HGNGHTRTGGR*RPRRL*SRPAEWP SAPKGRSGGLPGSFQEPADSYPGCG TWCSSACKGRQPSYS
2437	7934	A	2642	989	1790	NYTPFLPCSASAEFCELWGRPLVV FCYFYFQPPLAVEPFFNVIVICWVR VKVGPAGAFPRGLRRDVQRADFSRS SEGLLMGWVRDFDNHQSTCALDPF SGGIGSLLVPGGSDLQIGCFQKSFOA LIEN*CLNRHNSLG*TPKRSIKILWA E*ISRAGLCNSSPEHPACGHPPPR*G QWEAGPTAARTCFSPPTSNPPNSG PQAHEAQVSGDHSIHIGGS*GSPSPPL AYNLSTRKAQPKCGKKCMVLPSTC KNCTYCKPFALWNCMP
2438	7935	A	2643	92	330	RQVCLPPSERNVASLRTPHPRGAQ KSQEGPPGRQSPSELKSRVWCVENS TWVSRAPQGTGWPGWALPFPHQ* GWLGP
2439	7936	A	2644	1137	1290	HGQINQMEVNLPMDRKV*THHTH THHTHTHTHTSSTSCPYTLKRNVK S
2440	7937	A	2645	96	357	
2441	7938	A	2646	2648	2953	DWGYLPFKTLTYPGMVCHCLPLKS FPLFFPPLFSK*WMGPKLYPPKPHL YQNISPQYLCQKTPQTKMPILKKG VFFFRM*APQESGTNVFCMFLCPS TL
2442	7939	A	2647	201	377	QTVFVKLCVYTHIYN*VYMLIHI*A PLSVY*YIAYI*AHILSYIYVHLVIYI TEKYDF
2443	7940	A	2648	1917	2056	QSHAKEWIFLLTCFIF*KLLRNIIYI YIYTHTHAYIYIYIYIFQ
2444	7941	A	2649	246	717	KRQSEEGVFSCCQGWNESLLKSK VLEYP*FLHFPFSFDLYLFNYVFIY LFIYFCSIQSQTQSKAERAYIYIYLY MCCRQNTVNFTTTTKQLFCHLNIH LRRRNEKRWGCHFLVYAFAERSMF IYFFSLCINENDPEWRLAERSMYWS KHHKSC
2445	7942	A	2650	191	657	SGGERRNSSAPSAMSPSGSATTSPG T*PRIIDSERTPAFHARASTVKPPAGI NTREHPPLPCTPKPCTKTHTFTAPPP PQRCTHTSSPPRNLIQIFTRDTHPPPT HTHRHTHTQEPGWWSFDWVGCLR GFSFECTHFHFPQNKGTFFKMSYIA TY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2446	7943	A	2651	1108	1282	PPLWAPAPAILFLQERKRGNDPNW DARRGN*TKNKNKNKNKNKKTETL LRRPVFGAAN
2447	7944	A	2652	2	479	FIIAHPDVTVLGELSYFVTEKMISIHLE CSCNVWRVLYYGFNLYIIRYIICN YIS*YILYIK*YT*VFF*TMGVYYKIN NNMQTVVPVYLNVIQVCCY*QIYL TFIYYGSHFLIELRNY*TRMHMLLYI DLLPVFTLPLPFMLSMMLNMGGIFN GPNF
2448	7945	A	2653	341	622	YQNRLFPNQCFCTCLLVWLWDSPAP PPRPWQPPPPQGAHT*DRKEEGDPI GIWAPEGKSCTPKPPPSLPTSPGW KRALQKGDGTGCPGPSTAST
2449	7946	A	2654	597	785	NNSPSQ*CHFGTDSIICILKQRLGAV AYACTLSTLGG*GGRIA*AQFEAS LGNIVRPCLYI
2450	7947	A	2655	237	656	RGQGWVGDSSQGRGGAKEGLLPSPH GLPTPNPIHPTSPIPPENYVQRNTEK SWSWREGGRWKEIGRGRMRGKPS VLPDPGDRVMEGGPPTPLQHRSPH PGERHGFSS*SKFPPPPGSRPQKERR KGQRGMCVRVQGQIN
2451	7948	A	2656	109	290	NKLLNIYMD**IICQILLKLYLVPIKL MDTVYMSIYLSLELCFVISPFLLTGI YLNLYIY
2452	7949	A	2657	122	359	
2453	7950	C	2658	133	315	MQWLYIATLIPFFWTQRKGTFSGK SQLLDLFLQALAILSPDPHPGILHR SLWAHLPA*
2454	7951	A	2659	1399	1644	CERGLPGPFSPMAHQG*TRAGDTG QPASSLPLGLTAGPYFPPSGCLGPFT LDGCGLSPPPLYLPVFFPGGLLKSSR PLSCLN
2455	7952	A	2660	592	943	RTGCGQTLTVSHPDQARHWPGPGF ALILLYPAQGFHLLPEAGPEGGRG SLLTEEGSREANSRSSLISAAQLPPA APPQGLGV*MQESSRWGGKGRSKG SLPINLGLNSKLKKTTPP
2456	7953	A	2661	181	401	
2457	7954	A	2662	1163	1457	HPRICWHHSDLHTITKTSHT*SESQ NPHSESPGPRGCEPPGPRGSEPPSL *LSLPPPLPFAFCSSCPGLMAGFPPK QALSITGPFSPSVALWLGH
2458	7955	C	2663	275	327	MPFRLSQDCHHSAGAQQ*
2459	7956	A	2664	70	191	DLLQKPQV*DPSRTECVSM*CFLSPP *AETTSILPCFPRI
2460	7957	A	2665	40	142	THIHILGFLI*G*GLAMLPSLVNSW AQVILLPQHPKVQLQAGSTVNQPA HRC
2461	7958	A	2666	479	722	YCHIFLGGFFCCCSQHILNVFLCLAS FFE*MISQL*KILLGLGAVAYACNPS TLGV*GGRIT*GKKFKTSLGNIVRA HLC
2462	7959	A	2667	265	518	VKTVFLSGLDPLSLNENNMVLIMTS IVIFSHPLHFRFETLIGEWPFNLILG QV*WLTPPLIPGLWEAKVGGSLPRS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LRTAWET
2463	7960	A	2668	626	695	GPAARARPGKGIRPFRL**HHFGCS LWMGWKMGSQCRSPVESIPLGRAR WLTIVIPVLREAEEAGGSLEPRGSIPG WATRVPRPLYIEKKKKK
2464	7961	A	2669	66	610	TNNGSKSFCLKEHRGSCGCCSSKDF GVPQRLVLGLVLEDLILGELQVLA FGALSGSISIFPSIPPHSAIIKKNSHLR KIPPVPPRQPFRRVWTSGPAPRAS PSFCFSPPLAPRPPGLRTRPPPS*APA APQSRRTGGPARCPRGVPSPRSQPE *TPCKKNFLMEKISYDFHSQRSSD
2465	7962	A	2670	1077	1598	YVCHTSLYTSKSAHSSPWKFSWDV NPTPLAIHVTTSTKTVSFHTEEVVW SVHSTLKRFGFGAGGGE*GISEKGG HMAQTGTSRRPIAGRDPGPGRPGL LAEYRRPGEEAEVAPEPEDPH*CH HQHTGGPQAPSAQVKVQSSPRRPH QLPVSVSPWIPGGCRGPITTVGTS
2466	7963	C	2671	40	180	MSFEAEIVLSPDRTTALHPGLQIETL SHIIIIILSTISFHQLLH*
2467	7964	A	2672	1818	2154	PTPVFVPSLFPSHKHLPQALCGLCG LMSMATKGLSPYTSPLNLWRDTH QRLDFSSSYIIFKTNRLGAVAHTCDP STLGG*AGKIV*G*EFETSPCKKRD VSKIIFFKKEQK
2468	7965	A	2673	137	1610	EENIKSYKEYKCHNLVIRKELLGG GAVAHACNPSTLGLQV*AIPQKIKK YLNFKL
2469	7966	A	2674	1	490	GNRSRARRLASSPGSAAAAYRRPLP AGPSVYPQHERPCASTARRATGFRE IKVPSKSEVTRILDGKRIQYQLVDIS QDNALRDEMRALEQPQGHPTPDL STGDQYCGDYELLSWRLWKQNN AGVS*KLGLKSSPVPEFPLAGTPITN TPPQPFNLANERTF
2470	7967	A	2677	2	215	
2471	7968	B	2678	63	203	SFRRPMASASTHPAALSAEQAKVV LAEVIQAFSAPENAVRMDEAPG*
2472	7969	A	2679	433	895	VFHLPSAEPRASDALMASASTPNRR PLSAEQAK\VVLAEVIQGVSPRRJA VAHGTRKAR\DNAC\ND\MGKMLQF\ VLP\VA\TPRSQQEVIK\AYGFQLPTG EGVP*SFAPWSSSYEA\QD\PEIRQA LSGKLEGACFCRP*TLTPWGLLVG GSVAAS
2473	7970	A	2680	235	442	RPTFFYIPFKISKIKPSKIST*RPPSLL VG*KSKEKASTQKCLTKIPVPSANL KDFLPKHDEKRELRH
2474	7971	A	2681	199	1061	RRSEPKGWNRAAFPPKVGCGCVW EKTGMGDQNPEETALPSSLHVSISQ RSPRSTQASPPTRGHPVQPRRVYTP FKAGRPRRQKQVTHGQTAATLQVE *ATLPTNT*TSTTRAPCENQRGGKQ RSGWLRATKPHTAERRPSLNRPLTP TEPNCKTTELKSYSLQSKTWRNKS* VKTCRSGK**VMER*WSGKHSVKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VSTFPPSPRGSSSRLKPEARVARKY GPSPQLKPRRWREKHHGKPREMGR SEKSESLEWDRSLPVLRLMVDGFSPG KQNRNGQGRGAQSMW
2475	7972	A	2682	415	575	ISGWGVGGSC*SQHFGRTRQEDHL NLGVRDQPGQHSENKVSIIKKKRN VISI
2476	7973	A	2683	457	549	VSTGNKVVPQGKVKACI**KVLLK MQIAFTFCPGTTLTPVDT*NVTHL NECNILASLWWLKHDLVFQLLATW LHFNLRSSISSENASAPSYCPTG VAT LSKPIFNYPHFIPFLHFSHMTLS*PY LAFFLPSPCNSKRNLDSHMVAIEAN RCLAN*NKNYDL*TADVSSFQNILQ FIVNHKIKLPT
2477	7974	A	2684	291	364	RLKL*SPHLRSYFEKSKEQLASRTP TGQS
2478	7975	A	2685	2	361	TETLARPPSPLVTNMKLLAETVLLL TICLEGALVRRQAKEPCVESLVSQ YFQTVTDYGDLMKVKSPQLQAE AKSYFEKSKEQLATPLIQEGLGTGT WFNFFELFSVGTGLTTAWPPS
2479	7976	A	2686	425	678	LLGAISWELWGTQPCHPVEGVPGPF GLSNPQAGAFREQPTGPV*SSSFEK SKEQLTPLIKKAGTELVNFLSYFVEL GTQPATQ
2480	7977	A	2687	64	287	RQMA LLKANKDLISAGLKEFSVLL NQQVFNDPLVSEEDMATVVEHSMN *YMSYYSLQATGEPQDLRCCSCAL L
2481	7978	A	2688	983	1386	QEVRYRKVETLRCLLFSSCLVPVCA ASPVSRPGCRFLRSSLHWPTGRLVF RQRGETFLVPEKTVLRGVASAPAQ KAAGRTPVPGRPDARLRADARS*S C*RAARPRRGASGAVGARGCGRPG FPFLRSSGIFV
2482	7979	A	2689	473	706	NLTLASKISLKYCKQYLWILFRKRL WPGVVAHVCNPTLGGRRGGQT*T QEFETILGNMVKPISTKYQKKKKKK RAAA
2483	7980	A	2690	1400	1600	VGGGSGRSSKFPPLP*CPPPSCCSLPI SSPPPCSLTPGPSLLHVS KGTRRISRL LDRISKRFTH
2484	7981	A	2691	6133	7646	YMLFLFLSTKGWTVIQNRQDGSVD FGRKWDYPYKQGFNVATNTDGKN YCGLPGNEQACKIKSFYKWDFF*L KNIHCWKPVLS*EEFPDKNVEAK DKGRKAVFSFPKFYFW*EILFCFSFR VEYWLGNDKISQLTRMGPTTELLIEM EDWKGDVKKAHYGGFTVQNEANK YQISVNKYRGTA GNALMDGASH LMG\ENRDHDPFHNGHGSFQPPYD\ RD\NDGWYV\WHSLLL*KSH*YHY SESLTIFLIATTSWALTVSHCPKLFM HHSKAFQL*GRHSYSHFTDEI*RDY VICPM SHNYPEIKLEFEHSYFLNNEH LDKYL\LYILKCV*KLSFSFPGFSDT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	Sequence NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KGCKSYYSIK*QTQSLDGLPQRPS YLSFLL*GTGGLWCISVTLCIAPKKG TTVHTSVAVFYG*SAKRNLTTVVLF LITPNTFSFRLTSDPRKQCSKEDGGG WWYNRCHAANPNGRYYWGGQYT WDMAKHGTDDGVVWMNWKGSW YSMRKMSMKIRPFFPQQ
2485	7982	A	2692	711	865	VTMKTFSLRHKACGQVKNTLTI*Q PNSSIQPTSHYYPHCQPNTGMLIRK G
2486	7983	A	2693	26	351	ASLPDVTNMKLRAATVLLLTICSLE GALNRTQATDPCSENLCQYFQTVT DYGKDLMEKDMSPQLAEAKSYFE NSKEQLTPLITKAVT*LGNFLSYFV* LGIQPASQ
2487	7984	C	2694	10	123	MSTDRHQGQRRWLGRPPHCYQHE AARSNCATPHHLQP*
2488	7985	A	2695	6	409	FCPALSSSTALFFLRGLWFRGKRLG STDLT LHKPFNLTPQQLHWYEMG ESHIDPKMLKPESGRSKSLFPSAAFL DLQSSFLPSFLVVFPPPLSGSCRSLSL PSGTNPLLQLVPLPPSILLPLSTVLF* RATKG
2489	7986	A	2696	736	927	SVAHSSCVSHTHMHTLLGRRATINC LFRNGRGQVQWLTSAPALRKADV GG*LEPRSSRPAT
2490	7987	A	2697	2	251	FFLKPCLTQVATSGGCNFWPQAIPL SWPPNSISYRTQPTIFFQYNINILQAL A*FTLFACNPSSLGG*G*WIMWPRS RHCTPV
2491	7988	A	2698	1278	1515	SMVIRIMKVNHPMGLLTKRAKRS LNEMLNVDGKSGGYILGAVAHTCN PSALGGRGGWIT*GQEFKTSLSNME KPLLY
2492	7989	A	2699	139	260	
2493	7990	A	2700	268	388	
2494	7991	A	2701	233	400	HFLRAKVSVTQARVQWLDNGSLQP PTSMK*SSYLSLSKCWDYRHVPM APRHFNK
2495	7992	A	2702	602	758	IICLSVI*NPRYTLGTVAHTCNPSTFG G*GTWNS*GQKFETSLTNMAKLCF Y
2496	7993	A	2703	379	1160	LVDMQLWPPVFHENKCCLGPPPQT TH*RPAPAVPTPQAGPGTQGLATAS SVSMCLCDKLPSSDQPRV*PGDAE LSVLGVGRSSRKESPDQAPPLPVIC ELSFARVGGAPGEPLQRPVLS*TP GTLWSKEIA*LQAVLGQY*HEGCAT IMPADP*GRGPENSGSVTAQGQPL PGRP*NRTHLFFVPHPGQAASQS SSSP*QSERRA*IVSPNSGQRYFFPE TEARRQ*GEPRGEGGDLPPFPQPV LLAALVHI
2497	7994	A	2704	178	412	LLHSSLGHVARLPTLQNMKTLARD GSVCFQSHLLGRLRQEDHGCSKP*L HHCTPAWVTEQDPILLKTEIGIPVCS FKR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2498	7995	A	2705	67	398	ISLT LGRHHGKIN VYFLYLKMQG*Y FCCTFVS VVNCSDCLSGHSRRKTEG DKVRKEKQEA*AWCKTCETTLKTF PILLFTKKQAGHITPLMLPFLILHTV VTPYFNLEAD
2499	7996	A	2706	264	612	KHFSYNFFSFSFFLEGGGRVLLCPSG WSLAQCSLQLLGSSNPPTLAS*VAG TTGVCQRAWLILKFFCRDRVSLCCP GWSGNS*LQMILSPRP PKILGFQASA TALGPLTPFCLIV
2500	7997	A	2707	179	472	
2501	7998	A	2708	498	849	GSLLSRAPIPYPLNWVSFFIPEVRTPP DIHTIGSEFPRFLKYLKPTREKILVPA LSPPVQPGPSVPFPLPLSQDSSGQAK APWPSSLMH*PGALPLRTTSTQKCD SPSEQTSDASG
2502	7999	A	2709	768	1073	GVETGFDLIAFEDLHAVPRDSGISLF LQATSAPPPPGTARPHQESPLASHK* QARQAPEPLGYA*ARQAQRMEATK ARPRPKSSGARVGREPTCSKPAPRR
2503	8000	A	2710	5451	5678	
2504	8001	A	2711	396	687	TFCPRCGCPSGLAMRLFLSLPVLVV VLSIVLEGPA*GAPEVSNPFDGLE ELGKTLEDYTREFINRITQSELPKAM WDFSETFRKVKEKLKTD
2505	8002	A	2712	1	93	LPKRWNSCHEPLVPLFSPLLVNAVL GVLGSK*GKKIKDNEIGEEIKLSLFA YEMILFVLL*NPYS*PKNFTVKLL YQSLRK*SDTRLKSTIYLYTSNKLK LRELYSE*PKRWNSCHEPLVPLFSP LVNAVLGVLGSK
2506	8003	A	2713	376	469	NQLPGERWLTPVIPTLWEARA*GL FEPRSL
2507	8004	A	2714	715	1050	
2508	8005	A	2715	404	559	VNIFHFKTFYLGPGAVAHTCNPSTL GG*GGQIT*GQEFKTS LANMMEPHL Y
2509	8006	A	2716	3	180	FFFIGVLTLLPRLECSGAITAHCSLD LLGPGVYTT*TLQVLGITGVCHHGQ LIIFYFL
2510	8007	A	2717	1825	1958	LWTISVFWKAGVPLPC*QSPRWTKS ECLSFTPMFLNKS NFKKRI
2511	8008	C	2718	23	349	MPGRGSTAQRGFSKRYSRSGARSL CSLFLFLAKSLSRAMTSFSNISGAGL ASKKNAVFQHSPLSALIEQAGSFGF YGFISLLPWRQRDFNHVLLGICWA VTSVEASE*
2512	8009	A	2719	41	298	ASKVICQQRWHAGFAWLLSLEASL PREGTAGEAVVLAHCLSPSVLKEKR QPAVRAVRKASRP*ILQRHSRQNE GHRQEWCHTA
2513	8010	A	2720	277	651	KPSRARLLYESKKEGEMLENCQFFL CLFAKEHLQAH*QKSS*TSMDRLIN EPSNDWDIYYWGHRS*TSRNIWK MKSWALLERLCLKTKTKRQRLRGP SFWSTSLEKPRWSCAPRPGHGG SVC GW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2514	8011	A	2721	76	185	VWQCLPLYPLPNTLRAVAFRFLAIG YAFPLSCLCALWIFPQNLTSLVTDY *FGWSK*DPQ*FVICLCVCVCVCVC VCVISKLCSSSTDSSR
2515	8012	A	2722	1685	2124	
2516	8013	C	2723	299	577	MFCFDQSSLGSIVLESWITVKPLTLI SSTLMRRDDNFICCHAGRLFLTVP YRWHTLSGVALFPGPCCGIFFCHSG FQCGRLPYRVHAPQG*
2517	8014	A	2724	14	213	VDMGSHRVSQDGLELMT*P*SARLS LPKCWDYRRDTPRLALLVLLNLPV PLGASHVGHCLLRSYFCS
2518	8015	A	2725	1169	1404	SFLYFNGLMNFPRPGQAFEDSHEFKY KY*K*ARL*IAHTCNPSILENQQGQI P*AQVFETSLDHTPRPCIYPPKKKKK K
2519	8016	A	2726	44	417	CGCGLGEICLSHGVAQHNRRGNSNCQ KALFNAEPKCASSSSSGKGG/TILVP PAGGKGPNI*WNP GPPGARGFPGL TPPRGGKKGRAQPPENLV*EKTG FPIVQRGGLKPPPGPPKGGE*RGPP
2520	8017	A	2727	624	1023	CWLWSRGILPAPWSCAAQPWLQLP EGSF*C*TKMCSSSSSPKREFPFPGPP AGRQGPQSNKREPPAPRVKGIPPPPP PKTGEKEDGPTTPINLGFSSSRVPP VTGGGYKPPRPPKGGKEKTGGTPGT HHRAL
2521	8018	A	2728	36	211	KTKNISQL*WHTPIVAATWEARAR GSPEPRSLRPAVSLQTAPTALQPSRL EMFVRRYP
2522	8019	A	2729	640	898	VLLTCLVCLVSSKTKPNITKQHTKI KFPOSSRARWLTPVIPKFWEA*AGG SPEVRSLRPAAGLEFLVSHLGRKC WDYRHKPPCLA
2523	8020	A	2730	707	1164	SCIFLNQVFNKNLYFLFFKIKNNLYF LCCMRILICAYNG*RFYLCGMK*GL *SWF*CFSLPSLFTAVKFIKCFSVVF CSLSFTGYFFMYTFRIFCLLYPVVQ MISYILQMPFQFLFSFIKLPSCPINVQ FVSVCVCVCVCVNLIFKSARLPI
2524	8021	C	2731	270	371	MQNLQCFRAFELLTHNSASELPLSA PVTYTEDD*
2525	8022	A	2732	2553	2764	GIGPGWGIRPKRTRPRQVNSNVLKA QEWQAEYPGIFQRPYPSYEQSFPP* TPPNPIKTSFPPRNCNSP
2526	8023	C	2733	25	288	MSKVQTWGRQKTSHTRLSLHTWK VAQRPGRGAPHLPDGVAARQRCSS LSTRVCCHHVSPQPNLGWAASVG DHSQLACSHGPLQSPS*
2527	8024	A	2734	1043	1207	NMMTTHTLKKVGTGGRARWAHTC NASTLGG*GWWIT*GQEFETSLAN MVKLHLY
2528	8025	A	2735	74	233	MVTFNCFNLH*TVTKGFTRLIV
2529	8026	A	2736	11	151	ICHDAVDRPR/CCRSAMTPWIDRDL PGRPTRPEPAVQRMISYDDKNRMG SDDVCIFLILE
2530	8027	A	2737	214	369	QKDSPD*SCDCVLKENEISNLRCPIQ

MISSING AT THE TIME OF PUBLICATION

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2554	8051	A	2767	108	279	
2555	8052	A	2768	3	314	LLALVKEGPVPLFLLMKEREGVSSV RSLDTHGILSSTPPVHLPKTG/TEAS GSSWGPADPQDAEKSCRPTSPTLGG GVPACVRCACVLLCCHGALSRLAA SLFFL
2556	8053	A	2769	1	465	
2557	8054	A	2770	192	400	
2558	8055	A	2771	1414	1597	SGVYKRCKGGGRFVFLECATSGLSL ISS\GLSWG/RLWGHGGCRLAGGWG GGGGGSGGMALL
2559	8056	A	2772	673	988	
2560	8057	A	2773	749	1169	
2561	8058	A	2774	2	290	
2562	8059	A	2775	3	520	HERRVVAWAGRGFVCCARSSRSRV IFCSAPAGMAHKQI*YSDKYFEEH YEYRFVMLPRELSKQVPKTHLMSE EEWRR/LGVQQK/SLGWVHYMIHE PEPHILLFRRLPKSSTKMKFISGIV KSCFKFNVVVYKVVFWNTWRN GYKSFHPYLCMSCILHSNRARVKC NCK
2563	8060	A	2776	1134	1312	
2564	8061	C	2777	49	282	MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAARRPDPQTXESQDRLR CAPCTXHQPLPLDTHNRTLHNRL NIPQKL*
2565	8062	A	2778	1	306	
2566	8063	C	2779	54	212	MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAALIFLAMPVQSDDSGK RQTG*
2567	8064	A	2780	34	308	
2568	8065	A	2781	35	407	
2569	8066	A	2782	41	360	
2570	8067	C	2783	105	302	MXNLKRLQISMKPAHSGVCPVTRX SEGLGGGRLGLCIXWLQRGASQHQ HVTGMFPAEDKKTNMKV*
2571	8068	A	2784	3007	3541	KRVDYWGIKSSIICSTLLPHRSLC KYYFFFLSLSFKDSFWVIFFFCLSQR WKGERAKEKTTNNKENEAFPSGYQ NAPGEEGTVRGAPGAGSALRCGWR WRPP/SRCGWRWRPPAWRLRCPRP ARRWVCKPGPPPPPLPPRRPWGP CSAGPGAGLTPSRASICSWQARRQS GSHLITLERKRVRR
2572	8069	A	2785	272	801	
2573	8070	A	2786	659	842	
2574	8071	A	2787	156	203	
2575	8072	A	2788	441	785	
2576	8073	A	2789	2	28	
2577	8074	A	2790	5	1049	LRVAVLVAFKMSTKNFRVSDGDWI CPDKKCGNVNFARRTSCNRCGREK TTEAKMMKAGGTEIGKTLAEKSRG LFSANDWQCKTCSNVNWARRSEC NMCNTPKYAKLEERTGYGGGFNER ENVEYIEREESDGEYDEFGRKKKKY RGKAVGPASILKEVEDKESEGEED

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EDEDLSKYKLDEDEDEDADLSKY NLDASEEEDSNKKKSNRRSRSKSR SHSRSSSRSSSPSSSRSRSRSS SSQSRSRSSSRERSRSGSKSRSSRS VTGALLPHEKDLIQVHLLLRGTERE VVLDDLHLVIAKKDEQDHGHPKDA TGHHLDPILVPVQVQKRNNVLKFTS
2578	8075	A	2791	971	1106	
2579	8076	C	2792	291	444	MGCFFPNSWVRAGVLPVPVICLSV RLTWGREARQGWVCRCSQNWVIFAP*
2580	8077	A	2793	1	672	
2581	8078	A	2794	1	691	MDFLLSWVHWSLALLLYLHHAKW SQAAPMAEGGGQNHHEVVKFMDV YQRSYCHPIETLVDFQYEPDEIEYIF KPSCVPLMRCCGNCDEGLECVPT EESNITMQIMRIKPHQGHIGEMSFL QHNKCECRPKKDRARQENGSAALQ KRDNVRSRQLPTSSRP*SRRWRSW STSRPAPVTPRASPLRATSSRPSRT SASRSREASRPAAWWATTSWARS AAAARTCC
2582	8079	A	2795	312	394	
2583	8080	A	2796	490	2890	PVALTDRQTDAPSPSYHLLPGRRR TVDAASRGQGPEPAPGGGVEGVG ARGVALKLFVQLLGCSTRFGGAVVR AGEAEPGAARSASSGREEPQPEG EEEEKEEERGPQWRLGARKPGSW TGEAAVCADSAPAAPALALAS GRGGRVARRGAEESGPPHSPSRGS ASRAGPGRASETMNFLSWVHWSL ALLLYLHHAKWSQAAPMAEGGGQ NHHEVVKFMDVYQRSYCHPIETLV DFQYEPDEIEYIFKPSCVPLMRCCG CCNDEGLEC/VVPTESNIPMQIMRI KPHQGHIGEMSFLQPNKCECRPK KDRARQEKSVRGKGKGQKRKRK KSRYKSWVPCGPCSERRKHLFVQ DPQTCCKSCKNTDSRCKARQLELN ERTCRCDGSALAQKRDNVLFQAAT DEQPAVIKTLEKLVNIETGTGDAEGI AAAGNFLEAELKNLGTVTRKSA GLVVGDNIVGKIKGRGKNLLMS HMDTVYLGILAKAPFRVEGDKAY GPGIADDKGGNAVILHTLKLKEYG VRDYGTITVLFNTDEEKSGFSRDLI QEEAKLADYVLSFEPTSAGDEKLSL GTSGIAYVQVQITGKASHAGAAPEL GVNALVEASDLVLRMTNIDDKAKN LRFQWTIAKAGQVSNIPASATLNA DVR YARNEDFDAAMKTLEERAQQ KKLPEADV KIVTRGRPAFNAGEG GKKLVDKAVAYYKEAGGTGVEE RTGGGTDAAYAAALSGKPVIESGLP GFGYHSDKA EYVDISAIPRLYMAA RLIMDLGAGKEFH HHHHHAS
2584	8081	A	2797	326	1280	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2585	8082	A	2798	356	518	
2586	8083	A	2799	27	225	
2587	8084	A	2800	470	754	
2588	8085	A	2801	707	907	
2589	8086	A	2802	2	502	VLSPEEDKATITSLWAKVNVEINAG RKKPLGKAPLVVLPWPTRGFLWN SFGKTL/ASALLAPSMGKTPQKSK ATLAKKGA*TSLGEDAIKAPLDDSP RATFCPSLSEL\HCDKL\HVDPENFK A/LLGNVLVTVLAHFHFGKEFTPEV\Q ASWQKMVTGVA\SALA\SRYP
2590	8087	A	2803	921	1146	
2591	8088	A	2804	1170	1482	
2592	8089	A	2805	1492	1853	
2593	8090	A	2806	909	1180	
2594	8091	A	2807	105	248	CTCSRVSHNAPRNSLVSMVFRMHH PPPLDTFRQ/PQPSFNL*YP*PNYP
2595	8092	A	2808	662	843	
2596	8093	A	2809	263	408	
2597	8094	A	2810	701	950	
2598	8095	A	2812	1426	1525	
2599	8096	A	2813	1	1416	
2600	8097	A	2814	108	520	
2601	8098	A	2815	3	201	GRGLRSPDVTQQRGRSPSAAER *PTRPGVLRALPAPA*GKHCPWPRP GARRRPSSPAARPCP
2602	8099	A	2816	318	428	
2603	8100	A	2817	448	647	
2604	8101	A	2818	42	191	
2605	8102	A	2819	3	452	
2606	8103	A	2820	25	519	EFHRLRENPPMVAVSCPTKTNVKA\ AWGKVGAHAVRSMCAEALERMF LSFPT\TKTYFPHFDLSHGFAQV*G ATGKKVADALTNVAHVDDMPN\ ALSALSDLHAHKLRV\DPVNF\KLLS HCLLG*PWAAHLPRPSSTPGGCTPS LGTNFLGFLCLKHRCNLNPNL
2607	8104	A	2821	270	453	
2608	8105	A	2822	115	427	
2609	8106	A	2823	1	1656	
2610	8107	A	2824	1	1188	
2611	8108	A	2825	1091	1764	SIAYQPKRVQDQTDSPILPELISNF SKVSGYKIN/AKKSQAFLYTNNRQT ESQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTKKWK NIPCSWVGRINIVKMAILPKVIYRFN AIPIKLPMPFFTELEKTTLKFIWNQK RVRIAKSILSQKNKAGGVTLPDFKL YYKATVTKTAWYWYQNSMVLVPK QRYRSMEQNRALRNNAAYLQLSDL
2612	8109	A	2826	1	1449	
2613	8110	A	2827	2	1675	
2614	8111	A	2828	301	453	
2615	8112	A	2829	1	2139	
2616	8113	A	2830	83	1257	WQQTAVVDGGLKRLSLLNCRDGD CPSPQEPGPNSGRFQPAATDWLEFQ ARRRMKLKAILSKLTQEQTCKHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MFSLISGS*KMRIHGHK/VGEHHSPG PVEGVSMPTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENYKPLLNE IKEDTNKWKNIPCSWVGRINIVKMA ILPKGIYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIAKSILSQKNKAG GITLPNFKLYYKATVTKTAWYWYQ NRDIDQWKRTEPSEIMPHIYNLIFD KPEKDKQWGKDSL FNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVRFKTIKLEENLGITMRDIGMG KDFMSKTPKAMATKAKIDK WDLIK LKCFC TAKETTIRVNRQPTK
2617	8114	A	2831	1	1383	
2618	8115	A	2832	2	153	
2619	8116	A	2833	1	2436	
2620	8117	A	2834	1569	1835	
2621	8118	A	2835	933	2812	
2622	8119	A	2836	56	1692	KSKSKQHASKASRRQEITKIRAEKEI EIQKTLQKINESRSWFFERINKIDRP LARLIKKKREKNLIDAIKTDKGDIIT NPTEIQTIREYYKHL YANKLENRE EMDKFLD TYTL PRLNEEEVESLNT ITGSEIVAINSLPTKKSPGPDGFTA LYQRYKEELVPFLLKLFQSIEKEGIL PNSFYEASIIIPKPRD TT KKENFRP ISLMNIDAKILNKILAKGIQHIKKLI HHDQVGFIPGMQGRFNIRKSINVIQ HINRTKDKNHMIISIDAEKAFDKIQQ PFMLKTLNKL GIDGTYFKIIRAIYDK PTASII L NGQKLEAFRLKTGTRQGCP LSPLL FNIVFEILARAI RQEKEIKGIQ LGKEEVKLS\LFADD MIVYVENPLP SQPQNLL*GWLSNFSK/MSSGYKIY KIDVQKS\QAFLYTNNRQTESQIMSE LPF\TIASKRIKYLGIHLTRDVKDLAF KETYKPLLNEIK\EDTNK WKNIPCS WVGRINIVK\MAILPKV\NYRFNAIPI KLPMTVFTLEKKNYFKVHMEPKKE PALPSQS
2623	8120	A	2837	2	433	
2624	8121	A	2838	371	452	
2625	8122	A	2839	307	497	
2626	8123	A	2840	95	314	
2627	8124	A	2842	2	311	
2628	8125	A	2843	1	602	
2629	8126	A	2845	571	690	CQQGFSFLQAYGPAQHAIS\MRKFK AKYPDYEVTWANDGY
2630	8127	A	2846	130	943	
2631	8128	A	2847	45	405	GIPGRRNMAVADLDLIPDVADIDSD GVFKYVLIPSP LGIPAPGIRPAESKEI VRGYKWA\GHHADIYDKSVGATCR KQGLRTVSILGGGRIS/HTKSPGQER FTVY\GYSMGLWSCPRTPIST
2632	8129	A	2848	1340	1504	
2633	8130	A	2849	3	200	GSCACAGSCKCKKCKCTSCCKSEC GAISRN LGLWLR\CCSCCPLGCAKC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AQGCICKGASEKCSCCA
2634	8131	B	2850	1	384	MWESVELPRDLLSGFAQNADSDMD NKVQVSDGDKELVGNWSKEKELPT VALHHALHVFWLFSRLGTPVSPR VAMEPKWSCEAGCCSCCPVGCACK AQVLRRLQRGIGEVQLLCLMWEQLF SQNCNT*
2635	8132	A	2851	1	2880	
2636	8133	A	2852	584	1253	
2637	8134	A	2853	1	2736	QSRARADQRITESRQVVELAVKEH KAEILALQQALKEQKLKAESLSDKL NDLEKKHAMLEMNARSLQOKLETE RELKQRLLEEQAQLQQMDLQKN HIFRLTQGLQEALDRADLLKTERSD LEYQLENIQVLYSHEKVKMEGTISQ QTKLIDFLQAKMDQPAKKKKVPLQ YNELKLALEKEKARCAELEELQK TRIELRSAREEAAHRKATDHPHPST PATARQQIAMSIVRSPEHQPSAMS LLAPPSSRRKESSTPEEFSRRLKERM HHNIPHRFNVGLNMRATKCAVCLD TVHFGRQASKCLECQVMCHPKCST CLPATCGLPAEYATHFTEAFCRDK MNSPGLQTKEPSSSLHLEGWMKVP RNNKRGQQGWDRKYIVLEGSKVLI YDNEAREAGQRPVEEFELCLPDGD VSIHGAVGASELANTAKADVPIYILK MESHPTTCWPGRTRYLLAPSPFDK QRWVTALESVVAGGRVSREKAEA DAKLLGNSLLKLEGDDRLDMNCTL PFSDQVVLVGTEEGLYALNVLKNS LTHVPGIGAVFQIYIKDLEKLLMIA GEERALCLVDVKKVKQSLAQSHLP AQPDISPNIKEAVKGCHLFGAGKIEN GLCICAAMPSKVILRYNENLSKYC IRKEIETSEPCSCIHFTNYSILIGTNKF YEIDMKQYTL EEFLDKNDHSLAPA VFAASSNSFPVSIVQVNSAGQREEY LLCFHEFGVFVDSYGRRSRTDDLK WSRLPLAFAYREPYLFVTHFNSLEV IEIQARSSAGTPARAYLDIPNPRYL PAISSGAIYLASSYQDKLRVICCKGN LVKESGTEHHRGPSTSRSSPNKRG PTYNEHITKRVASSPAPPEGSPHRE PSHPTATARGGPSCAGTS/PWPPPG AREVPRPDAQHAERAVPREAV
2638	8135	A	2864	426	539	
2639	8136	A	2865	1	1134	
2640	8137	A	2866	766	1115	SARQIATFFNNGIKHLAIMGGDILH VAHIFVTPFNLEGAYTSINQRAEVG SLIVIFHRQQMFFIGNHPPLIV/YSMC MANGTPASNRHGWRYAPDR*RSVR RCDGDPLHPDVRRRSG
2641	8138	A	2867	61	390	
2642	8139	A	2868	627	1324	
2643	8140	A	2869	343	452	
2644	8141	A	2870	589	672	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2645	8142	A	2871	1	3000	
2646	8143	A	2872	2	191	
2647	8144	A	2873	251	505	GSSSRLGQRTD*ATASRRHFKNKV PGEAKNCSPEDDEIPLYLKGGV\AD ALLYRATH\MILTVG\GTSICPYEL AVASFPKKAGS
2648	8145	A	2874	1780	1914	
2649	8146	A	2875	1154	1256	
2650	8147	A	2876	1	2629	
2651	8148	A	2877	334	468	YEEEEEDYD*EEEESEPPLDENDL EEDVVFQPPQIEGEAVYDA
2652	8149	A	2878	2	416	
2653	8150	A	2879	1	4116	
2654	8151	A	2880	3	3080	EEELEASKSFGPGNEEEKEEKEYE EEEEEDYDEEEESSEAGNQRLQQV MHAADPLEIQADVHWHIREEEEE ERMAPASESSASGAPLDENDLEEDV DSEPAEIEGEEAENGHPGDTGAELD DNQHWYDSPSDADRELRLPCPAEG EAELELRVSEDEEKLPASPKHQERG PSQATSPIRSPQESALLFIPVHSPSTE GPQLPPVPAATQEKSPERLFPPELL PKEKPKADAPSDLKAVHSPIRSQPV TLPEARTPVSPGSPQPRPPVAASTPP PSPLPICSQPQPSTEATVPSTQSPIRF QPAPAKTSTPLAPLPVQSQSDTKDR LGSPLAVDEALRRSDLVEEFWMKS AEIRSLGLTPVDRSKGPEPSFPTPA FRPVSLKSYSVEKSPQDEGLHLLKP LSIPKRLGLPKPEGEPLSLPTPRSPSD RELRSAQEERRELSSSSGLGLHGSSS NMKTLGSQSFNTSDSAMLTPSSPP PPPPGEEPATLRRKLREAEPNASV VPPPLPATWMRPPREPAQPPREEVR KSFVESVEEIPFADDVEDTYDDKTE DSSLQEKFFTPPSCWPRPEKPRHPPL AKENGRLEPALEGLTPQKRGPLVVS AEAKELAEERMAREKSVKSQALR DAMARQLSRMQMELASGAPRPR KASSAPSQGKERRPDSPTPTLRGS EEPTLKHEATSEEVLSPPSDSGGPDG SFTSSEGSSGSKKRSSLFSPRRNKK EKSKSGEGRPPEKPSSNLLEAAAK PKSLWKS VFSGYKKDKKKKADDK\ SCPSTPFSGATVDSGKHRVLPV\VR AELQLRRQLSFSEDSDLSSDDVLEK SSQKSRRPRPTYTEELNAKLTRRV QKAARRQAKQEELKRLHRAQIIQR QLQQVEERQRRLEERGVAVEKALR GEAGMGKKDDPKLMQEWFKLVQE KNAMVRYESELMIFALELEDRQS RLQQELRERMAVEDHLKTEELSEE KQILNEMLEVVEQRDSLVALLEEQR LREREEDKDLEAAMLSKGFSLNWS
2655	8152	A	2881	1	4132	
2656	8153	A	2885	1898	2056	
2657	8154	A	2886	1	233	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2658	8155	A	2887	1092	1339	
2659	8156	A	2888	363	512	EPLEGLLCLEGKGVEIVTILQAETPG EPLPP*KPHS*PGLCLRYRGHTL
2660	8157	A	2889	1	136	
2661	8158	C	2890	12	236	MTPGGLFLPYHSLPQPDFLASCPT HLSTPFLVADNELRLPKGQICPLHV FVLANRVVLKLCANSVWEHSGKIT *
2662	8159	A	2891	1548	1849	
2663	8160	A	2893	1	1441	
2664	8161	A	2894	954	1194	
2665	8162	A	2895	2039	2207	
2666	8163	A	2896	680	757	
2667	8164	A	2897	361	476	
2668	8165	A	2898	226	293	
2669	8166	A	2905	265	396	
2670	8167	A	2906	250	447	
2671	8168	A	2907	632	1038	
2672	8169	A	2908	3	363	VKDDPNDHEQKGKRGHKPFLRELPR ATIFFLINL*VIAEVEVQDSCIDQAES EMLLRSGAPDPGVPL*GCFALVIT HTHSSRAAMAFVPTGKKASCYSQE PS*WQNSPNDTQDHSNDLSE
2673	8170	A	2909	57	448	
2674	8171	A	2910	62	371	
2675	8172	A	2911	398	789	VTGAPLMLPVLPKPGMPLAALVTG LSGLLWPPCAELVGTEFKLPALVHL PHCFFASLLESPVSPRLAMEPNCSC AAGVSCTCAGSCKCKECKCTSCKK SECCSCCPVGC\SKCAQGCVCCKG ASEKCSCCD
2676	8173	A	2912	577	896	
2677	8174	A	2913	2	184	
2678	8175	A	2914	1	459	SSNTMNGWFWIDKCSLWLSQSLPY TRATQVTIKIPPNPATGV/SSGFVD*F WIDKCSLWLSQSLPYTRATQVTIKIP PNPATGVRRALWIDSDLRCAPLGLS TGGGKSRIKLG LGVPKFRGSDRNR VLIGAFYNPLAGYRALIGAFYNPLP PHLLLQLLLSVLLQPLLCCGKCKL KAPEGEETEFYVSPKAAV
2679	8176	A	2915	440	620	
2680	8177	A	2916	2	987	FGLRWPRGAVRRWQLWEEAAWK AEGAQARTNPHVSWAATVTRCSVP GKRNPAGWAAEPESGTWSPPGAE IRMFRFMRDVEPEDPMFLMDPFAI HRQHMSRMFASGGFWILAPFLSITD WQHCQGTRPASRRIMQAGSCSPL FG/MCLGIFGWFSWDMFWGLME*H DLGNMEHMTAGGNCQTFSSSTVIS YSNTGDGAPKVYQETSEMRAPGG IRETRRTVRDSDSGLEQMSIGHHIRD RAHILQSRNHRTGDQEERQDYINL DESEAAAFDDEWRRETSRFRQQR LEFRRLLESSGAGGRRRAEGPPRLAIQ GPEDSPSRQSRRYDW
2681	8178	A	2917	121	329	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2682	8179	A	2918	323	457	
2683	8180	A	2919	1	243	
2684	8181	A	2920	147	321	
2685	8182	A	2921	1	2310	
2686	8183	A	2922	319	773	
2687	8184	A	2923	85	369	
2688	8185	A	2924	1	681	
2689	8186	A	2925	1556	1953	HGVAAASLPSSAGRLSRARGPGSEE PAAAPAPRWRWQHPRGPGGPVSRR RRPPHGGTPGTVRRGGGGDPAAPG SGCPSPAVVPPRCPGAPLRRATLPP ACCGSLACSPLTL*PAPS/TPPL*ADD SCSVGLPT
2690	8187	A	2926	322	376	
2691	8188	A	2927	365	666	
2692	8189	A	2928	310	448	
2693	8190	A	2929	908	1189	
2694	8191	A	2930	761	913	
2695	8192	A	2931	1188	1373	EPHLKKKKKISRWWCIPVVPVTW KAEVGGSLPRRWRLQ*AEITPAHS SLGNGLTLLKKKK
2696	8193	A	2932	240	475	
2697	8194	A	2933	1212	1424	
2698	8195	A	2934	403	539	
2699	8196	A	2935	436	594	
2700	8197	A	2936	1	570	
2701	8198	A	2937	1086	1359	
2702	8199	A	2939	40	361	
2703	8200	A	2940	12	337	
2704	8201	A	2941	232	339	
2705	8202	A	2942	951	1069	
2706	8203	A	2943	286	621	
2707	8204	A	2944	299	513	HKCYFTLAHVHLIISFCAATLE*A*P SWGTCNCSTPNFVNTTPLTLAYYLGL WRSRLRPFSDSVSFSFCGIL
2708	8205	A	2945	97	258	
2709	8206	A	2946	5	464	
2710	8207	A	2947	1	522	
2711	8208	A	2948	76	488	
2712	8209	A	2949	619	746	
2713	8210	A	2950	125	279	
2714	8211	A	2951	1300	1410	
2715	8212	A	2952	1867	1947	
2716	8213	A	2953	2	52	
2717	8214	A	2954	352	538	
2718	8215	A	2955	3	313	QEFGTRICPAACFPLESGTPGFSLAS KWTPNCSCSPVGS\CACAGS\CK\CN RVANRTVLTQTSCCSC\CPVGCABA LPRGCICKGTSD\KCRSRCLDARDSC ALQM
2719	8216	A	2956	1172	1914	HFSAQPWASPCS/LLLLGLEGGQIV GSLPEVLQAPVGSSILVQCHYRLQD VKAQKVWCRFLPEGCQPLVSSAVD RRAPAGRRTFLTDLGGGLLQVEMV TLQEEDAGEYGCMVDGARGPQILH RVSLNILPPGAVEDDVQAGRWRVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SRDDVACGSEEEETHKIGSLAENA FSDPAGSANPLEPSQDEKSIPLIWGA VLLVGLLVAAVVLFAVMAKRKQV TIQLLQGNNTALAKSKEELSMPKS YQY
2720	8217	A	2957	3	632	
2721	8218	A	2958	3	728	
2722	8219	A	2959	194	451	
2723	8220	A	2960	2	484	NVLTSHQTQPNQRGKAATVTPALWR LTDVRLVTKYKIHFERNVGSFENSM KGNSIYF*GPGHDP LLNMNIVY*KS LTINNHMHKIT*ESLTEVLFSQGIFS VTNPHPEIFLVARIEKVLQGNITHCA EPYIKNSDPVKTAQKVHRTAKQVC SRLGQYRMPFA
2724	8221	B	2961	65	391	MAEVRKFTKRLSKPGTAAELRQSV SEAVRGSVVLEKAKVVEPLDYENVI AQRKTQIYSDPLRDLLMFPMEDISIS VIGRQRRTVQSTVPEDA EKRAQSLF VKECIKTY*
2725	8222	A	2962	1	2148	
2726	8223	A	2963	816	1014	
2727	8224	A	2964	2	358	
2728	8225	A	2965	84	176	
2729	8226	A	2966	137	426	QACIMREYK\LVVLGSGGVGKSALT VQFVQGIFVEKYD\PTIEDSYRKQV EVDAQQCML EILGYLPGTEQFTSNE GFIHEKWTRICISLFHHSTVHI
2730	8227	A	2967	449	602	
2731	8228	A	2968	203	535	
2732	8229	A	2969	2	446	
2733	8230	A	2970	3	240	
2734	8231	A	2971	914	1291	
2735	8232	A	2972	188	266	
2736	8233	A	2973	191	306	
2737	8234	A	2978	1	440	
2738	8235	A	2979	3	670	TSRGRVGTQAGEPRDLRPPPCPSSPL RV\AVV\CLEQPERGAWEAHNIPQ NGDSA VRSFG\TGTHVKLP GPAPD\ NPNVY\DFKTTYDQMYNDLLRKDK \ELFTQNGILHIAGRNKRKIP\GPERF QNCKDLFDLILTCEERVYDRVGWK I*ISR\EQGDLPSPVHVVNLDIQDNH EEATLG/ARFLICEVCQCIQHT EYM HNEIDELLQEFEEKSGRTFLHTVCF Y
2739	8236	A	2987	367	492	
2740	8237	A	2988	49	332	
2741	8238	A	2989	582	923	
2742	8239	A	2990	523	668	
2743	8240	A	2991	942	1513	
2744	8241	A	2992	176	362	
2745	8242	A	2993	4937	5137	
2746	8243	A	2994	651	836	
2747	8244	A	2995	1686	1883	
2748	8245	A	2996	415	635	
2749	8246	A	2997	2	308	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2750	8247	A	2998	57	598	
2751	8248	A	2999	802	923	
2752	8249	A	3002	119	297	
2753	8250	A	3003	950	1314	
2754	8251	A	3004	1	579	
2755	8252	A	3005	27	483	RDAEDAIYGRNGYDYGGQCRLRVEF PRTYGGRGGWPRGGRNGPPTRRSD FRVLVS/GWQ/DLKDHMREAGDVC YADVQKDGVMVEYLRKEDMEYA LRKLDDTKFRSHEGETSYIRVYPER STSYGYSRSRSGSRGRDSPYQSRGS PHYFSPFRPY
2756	8253	C	3006	34	171	MPKSFRVIAERSMHSWYVCFLICFIL HISITLHSLVMVFVTWREY*
2757	8254	A	3007	1688	1871	
2758	8255	A	3008	1	688	MSGWADERGGEGDGRIYVGNLPTD VREKDLEDLFYKYGRIEIELKNRH GLVPFAFVRFEDPRDAEDAIYGRNG YDYGGQCRLRVEFPRTYGGRGGWPR GGRNGPPTRRSDFRVLVSGPSPASG SWQDLKDHMREAGDVCYADVHK DGVGMVEYLRKEDMEYALRKLK *PPKFRSHGETSLHRRFIPERSNQL MATSPVSGLGSRGRDLSIPKARGSP HYFSSFPGPPT
2759	8256	A	3009	428	579	
2760	8257	A	3010	1924	2043	
2761	8258	A	3011	131	395	
2762	8259	A	3012	910	1173	
2763	8260	A	3013	1295	1489	
2764	8261	A	3014	1477	1604	
2765	8262	A	3015	443	805	
2766	8263	A	3016	1	2109	
2767	8264	A	3017	1297	1408	
2768	8265	A	3018	3	314	
2769	8266	A	3019	5	340	GSGTSAKAFRSIWGPLPPVHRHGSP RSSVQR/DGPGLGTGEPRVYIRNKV ANTGVPGAPGPSIGGVTA PATDYCH RIAPILAARRRRRRRRRRRRRRRG GGGGVAGGGGGGG
2770	8267	A	3020	1	1973	DGGARARGRAAARRRRRPRRRRRR RRRRRRRRRRRRRRRRLGLERP QPSTRGRAPGASRAEEKMEELVVE VRGSNGAFYKAFVKDVHEDSITVA FENNWQPDRQIPFHDVRFPPPVGYN KDINESDEVEVYSRANEKEPCCWW LAKVRMIKGEFYVIEYAACDATYN EIVTIERLRVNPKNPATKDTFHKIK LDVPEDLRQMCAKEAAHKDFKKA VGAFSVTYDPENYQLVILSINEVTS KRAHMLIDMHFRSLRTKLSLIMRNE EASKQLESSRQLASRFHEQFIVREDL MGLAIGTHGANIQQARKVPGVTAI DLDEDTCTFHIGEDQDAVKKARS FLEFAEDVIQVPRNLVVGKNGKLI QEIVDKSGVVVRVRIEAENEKNVPQE EEIMPPNSLPSNNSRVGPNAPEKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HLDIKENSTHFSQPNSTKVQRGMVP FVFGTKDSIANATVLLDYHLNYL KEVDQLRLERLQIDEQLRQIGASSR PPPNRTDKEKSYVTDDGQGMGRGS RPYRNRGHGRRGPGYTSGTNSEAS NASETESDHRDELSDSLAPTEER ESFLRRGDGRRRGGGGKG\QGGRG RGGGFGKGNDDHSRTDNRPRNPREA KGRRTDGS LQNTSSEGSRLRTGKDR NQKKEKPDSVDGQQLVNGVP
2771	8268	A	3021	1	2116	
2772	8269	A	3022	656	883	
2773	8270	A	3023	303	589	
2774	8271	A	3024	2	478	MAGKQAVSASGKWL MGIRKWYY NAAEFNKLGLMRDDTIYEDEDVKE AIRRLPENLYNDRMFRIKRALDLNL KHQILPKEQWTKYE/EGLCCSSSAL CFLLR*KDQPIECPSRSQEELL*SKLS PL*TAFET*AKENFYLEPYLKEVIRE RKERE EWAKK
2775	8272	A	3025	323	400	
2776	8273	A	3026	2	396	RPPTTTKFAAARQMAGKQAV*STQ AKGLNG/IFKKWYY\NAARIQNKLGL LM\RDDTIY\EDEDVKRSP*EDFPEN LYNDRMFRRH*EGHWTLNLKHQILP KEQWTNFEEKNFY\LEPYLKE/VLF RERKERE EWAKK
2777	8274	C	3027	144	341	MYHSLEKFSSCFKHIPDNFLKMTKI KQNIYRDHFLNFLSFQGXQHKKNK TGQHFTSKCTEPFLQD*
2778	8275	A	3028	1070	1335	
2779	8276	A	3029	2	303	
2780	8277	A	3030	149	244	
2781	8278	A	3031	1642	1797	
2782	8279	A	3032	1115	1320	
2783	8280	A	3033	1240	1408	
2784	8281	A	3034	539	669	
2785	8282	A	3035	1155	1579	
2786	8283	A	3036	437	666	
2787	8284	A	3037	51	279	IKGRWEPPPLASFFLTSQGHCS DGP GP*GWGEAVSPRGRNTLSSSSWHW VPYSELRGRGVACRKEVYKIVQNT QH
2788	8285	A	3038	3	300	
2789	8286	A	3039	451	760	
2790	8287	A	3040	183	410	
2791	8288	A	3041	602	1145	
2792	8289	A	3042	2	496	
2793	8290	A	3043	710	896	
2794	8291	A	3044	143	601	
2795	8292	A	3046	120	280	
2796	8293	A	3047	2	424	
2797	8294	A	3048	3	452	
2798	8295	B	3049	240	420	XLKGHGQRKVAERADPKPLPQRGR TCPKRRCPLSDPARCTSFVRDPVN FQASLSHCLAW*
2799	8296	A	3050	310	401	

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2800	8297	A	3051	544	700	
2801	8298	A	3052	1	568	
2802	8299	A	3053	686	787	
2803	8300	A	3054	8	182	
2804	8301	A	3055	227	547	
2805	8302	A	3056	1	523	ESLRKQLGQEPFFDMHMMVSKPE QWVKPMAVAGANQYTFHLEATEN PGALIKDIRENGMKVGLAIPGTSV EYLAPWANQIDMALVMTVEPGFGG QKFMEDMMPKVHVLRTQFPSLDI* VDGGVGPDTVHKCAEAGANMIVS GSAIMRSEDPRSVINLLRNVCSSCS RNRSP
2806	8303	A	3057	919	1100	
2807	8304	A	3059	429	780	
2808	8305	A	3061	567	682	
2809	8306	A	3062	148	372	
2810	8307	A	3063	113	303	
2811	8308	A	3064	367	449	
2812	8309	A	3065	48	369	
2813	8310	A	3066	979	1254	
2814	8311	A	3067	173	776	
2815	8312	A	3068	1	111	
2816	8313	A	3069	33	494	
2817	8314	B	3070	100	154	MVHLTPVERVCRCYCPVGQX*
2818	8315	A	3071	559	775	
2819	8316	A	3072	744	940	
2820	8317	A	3073	1	255	
2821	8318	A	3074	1	1206	
2822	8319	A	3075	905	1823	
2823	8320	A	3076	36	689	
2824	8321	C	3077	215	325	MSVYPLDHIQKRIARRSSLTSCMRG TIAWPTNSLT*
2825	8322	A	3078	1	831	
2826	8323	A	3079	97	236	
2827	8324	A	3080	409	602	
2828	8325	A	3081	818	1095	
2829	8326	A	3082	528	714	
2830	8327	A	3084	91	242	
2831	8328	A	3085	75	430	VSPGLPAARLFQVAYLDShLKCPGC QHVPMTVTFISSKEKP*PRTVPRPP WMRLGHVILFSFLIPSNLSFSPVIFL CGPFKVVIICTELQNVSRSPQTTLAT VYCNKITSYICKKKK
2832	8329	A	3086	1000	1145	
2833	8330	A	3087	225	324	
2834	8331	A	3088	3	54	IHYSLIIV*CWVQF
2835	8332	A	3089	461	658	
2836	8333	A	3090	337	408	GIQDRASHCTQGPPPPPS*VPQASPA AGEGPCDPPGRYPLRDSGQSVTLH AGSSATTIQEPRGA
2837	8334	C	3091	155	453	MLGALGAEELSLDSLPEGLLNFSKP GSEGGRLGLVPAAGEGPCDPPGR YPLRDSGQSVTLHAGSSATTIQEPR GAGHALASXQECQWSRDRAAQAG E*

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2838	8335	C	3092	121	393	MALPGRLPHRKLGGTLEAPWPGIP SGAVRRHQPPPTTLXXWLGKVKK PLRKRIEAKFLCAEGPEHIRQGSAA VPGGGGRSRNCEQCLI*
2839	8336	A	3093	270	573	
2840	8337	A	3094	15	297	
2841	8338	A	3095	970	1098	
2842	8339	A	3096	127	296	
2843	8340	A	3097	875	1075	
2844	8341	A	3098	171	404	
2845	8342	A	3099	186	392	
2846	8343	A	3100	2	202	
2847	8344	A	3101	2	242	ARGNMAAATLTSKLDLSLLFRRTSTF ALTIIVGVMFFERAFDQGADAYFT DHINEGVRPCAIPDLGTRLRGDSGV EKL
2848	8345	A	3102	79	1137	
2849	8346	A	3103	374	519	LDSRRK**C*LESRPHE*TS/DLSSGS LLI*GIWSILFYPMFAF*KFQKEN
2850	8347	A	3104	1	1214	
2851	8348	A	3105	105	379	
2852	8349	A	3106	260	421	LLYGDCTWTSFHLQRLQLHCQVSQ PCREL*LVSSVLCFPFISEELHCVTG HF
2853	8350	A	3107	420	848	
2854	8351	A	3108	664	1059	
2855	8352	A	3109	73	269	
2856	8353	A	3110	307	566	
2857	8354	A	3112	316	410	
2858	8355	A	3113	200	403	
2859	8356	A	3114	258	377	
2860	8357	A	3115	1767	1893	
2861	8358	A	3116	1	389	
2862	8359	A	3117	3	569	RHGEERLQTRTLRAAELSARAPSHS LPAPRSAPTWQKFSSPTEIVERCVES LIAVFAQKYAGKIDGYNYNLSLRPE F/L*AFMNTLAAFTKNQEGPWVSL DRMMEETGTPNSDGSARISSGISLI WIGWALAMGLAWNFLPSRAVPFPR KAGPGGDPGPGGFQTPPFSSFGLS VLHLPQAHPSEAH
2863	8360	A	3118	362	712	
2864	8361	A	3119	2	152	
2865	8362	A	3120	134	760	
2866	8363	A	3121	670	891	
2867	8364	A	3122	44	63	SPSNRNTTEGTLTNIIHNLGMYVFL HAVKGTPFETP*PG*KARAP*PPLGN NWDYGDRTSFTGSFFTISPILYFL ASFYTKYDPTHFILNHSFSS*VVLNS PKWPQLHGVRIFGN*KSKQQE
2868	8365	A	3123	88	207	
2869	8366	A	3124	2	191	
2870	8367	A	3125	145	865	
2871	8368	A	3126	69	118	
2872	8369	A	3127	1148	1323	
2873	8370	A	3128	197	327	PLGKKFSCSKSLRLLGPFLQL*SLRF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RKTTY
2874	8371	A	3129	154	303	
2875	8372	A	3130	3	158	
2876	8373	B	3131	144	274	XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL*
2877	8374	A	3132	383	529	
2878	8375	A	3133	1981	2132	EKENEDQKLIHLFFFSLGVKPTPCL KNINFFNHFASFLCASINKKWKRI
2879	8376	B	3134	144	274	XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL*
2880	8377	A	3135	383	529	
2881	8378	A	3136	1979	2131	EKENEDQKLIHLFFFSLGVKPTPCL KNINFFNHFASFLCASINKKWKRI
2882	8379	A	3137	296	592	
2883	8380	A	3139	224	700	VLLPPTGKRYPKVYIGVFKGPRKM GSSEIPFQNPFSIFSKEGYFLCREDFP NGAQISLLEEPFQIHLKLTFMFKNTT NFIFTAELCDQCQGL*NLHLSSSP* KKRHLT/HNQTHPHIKTDFHC*FIHY LVV*KSQSTSQHLLFKSTMGKDQRQI DNNIMN
2884	8381	A	3140	761	963	
2885	8382	A	3141	475	715	
2886	8383	A	3142	381	698	
2887	8384	A	3143	2	235	YASLEPPDRPQVGASCPGTYY*GA VPPSPAGVGREAGKGTGGCTCDK PLSPCSLAG\RRGSFPRRPSWTSPL LCW
2888	8385	A	3144	49	353	
2889	8386	A	3145	174	495	
2890	8387	A	3146	73	226	
2891	8388	A	3147	326	421	
2892	8389	A	3148	1306	1444	
2893	8390	A	3149	53	246	
2894	8391	A	3150	228	271	
2895	8392	A	3151	419	599	
2896	8393	A	3152	1	322	
2897	8394	A	3153	151	375	
2898	8395	A	3154	2017	2191	
2899	8396	A	3155	3	234	LWSASSAQDATWADSQELSMARLP HVRKCVVVVLLQLSLLELLDFPP L/CLGPGCPCHLAHQHPCPRPLFQ LSGR
2900	8397	A	3156	43	408	
2901	8398	A	3157	3	374	
2902	8399	A	3158	1	823	MAVVAPRTL L L L L LSGALALTQTWA GSHSMRYFSTSVSRPGSGEPRIA GYVDDTQFVRFDSDAASQRMPE PWMEQEEPEYWDRTQTEISKNAQI DLESLRIALRYNQSED/VPPPKTH MTHHPISDHEATLRWALSFPYAEI TLTWQRDGEDQTQDELVETRPAG DGTFOKWASVVVPSGQEQRVYCHV QHEGLPKPLTLRWEPSQPTIPIVGIL AGLVLF GAVIAGAVVAAMWRRK SSDRKGGSYSQAASSDSAQGS D VSL TACKV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	Sequence ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2903	8400	A	3159	1	1264	MAVMAPRTL L L L L L S G A L A L T Q T W A G S H S M R Y F F T S V S R P G R G E P R F I A V G Y V D D T Q F V R F D S D A A S Q R M E P R A P W I E Q E G P E Y W D Q E T R N V K A Q S Q T D R E N L R I A L P L T Y N Q S E A G S H T L Q M M Y G L G R G G S D G A L S F R G L P P V T A Y D G K D N I A L N E D L R S W T A A D M A A Q I T Q R K W E T / A A H E A E Q W R A Y L E G R C V E W \ L R R Y L E N G K E T L Q R T D P P \ K T H M T H H P I S D H E A T L R C \ W A L S F Y P A E I T L T W Q R D G E D Q T Q D T K L V Q T R P A G D G T F H K G A S C V G P L G E E Q R Y T C \ H V Q H E \ G L P K \ P S T M \ R W * P S S Q P T H P P S W G I H C L A L V L L W K L * S L E A V V A A C E C G R R K S S D R K \ G G S Y T \ Q A A K P V T S A Q G S D V S L T A C K S V R Q L P C V G L R G K S C F L P F L V D L E E P W T L F P A K G T L H V S V F M
2904	8401	A	3162	1	342	G S R T V P S P S P S S G L A S P G S P T H R S L G P T T P P M A S A T E D P V L E R Y F K G H K A A I T S L D L S P N G K Q L A T A S W D T F L M L W N F K P H A R A Y R Y D G H K D V V T S V Q F S P Y G Y L M A A G / S R D L S V R L W I P V ** E Y S * N G K Q L A T A S W D T F L M L W N F K P H A R A Y R Y D G H K D V V T S V Q F S P Y G Y L M A A G L E T Y P
2905	8402	A	3163	1	583	D M E S R S V T Q P G V Q W C Y L G * L Q P P P P R F * R F S C L S L P G S W D Y R C V P P H P A N F F I F S R D G V S H H V G Q A G L E L L V S S D P P A S A S Q S A G I T G L S H H A R P D / Y T F L L T V F E P F H G T H V R P P V T C G T L A S N W T P T A F I S L A E N T K V L K V A L K E V P F G F D I A I S K A S G T V Q I R A M S F M K T T F L S P S F V R E C H T H D H V T L L Q S
2906	8403	A	3164	1	347	F F I L F F L R Q S H S V A * A G V Q W H N L D S L Q P L P P G F K Q F S / L S L P S S W D Y R R M P P R P A N F \ * F L V E T G F R H V G Q A G L E L L T S G D P P A S T S Q S A G I T G V S H G A Q S C P L L Y I E F P L S I L A A T
2907	8404	C	3165	13	399	M E K I P V L F R V A N L I S I I P A P N K S R L C G K T R I S R S A K S K A N T R V F L A C R F G L A G D N A I A N V H A P D A D L E A Q S D V E R T M D L K P C I W V P D T L G E A E Q T A P A D R L S M H T Q H F G R P R R A D H E V R R P R P S W L I W *
2908	8405	A	3166	168	414	N P L L L P N T F P A N G N T I L I K E K V L F L F F * D G S P V L S P R P D C G L Q W R N L G \ S L Q S P P P G F T P F S C L S L P S S W D Y R H P P L R P A N F F L Y F L V E T G F H R A S Q G \ G L D L L T S R S / I P P R A S Q S A / R G L Q G V S H P R P A Y M S L R Y N K P A H V P L K I K V K K
2909	8406	A	3168	28	123	
2910	8407	A	3169	2	123	E N R L M A G G E / H M L A A I L L F T A L R C L C K V K H K P G L H A H * G T A P
2911	8408	A	3170	1	402	Q G F S P P \ E S L R Y G \ S W E G K A L T F P Q P D T H K G S V L E D * * K R K A S L Q L R * E E G I C L \ C L S L G M E C L G V K P / V A Y I L F T E I G E S R L M A G G K / H M L A A I L L F T A L R C

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LGKVKHKSGLRAHRTAPFLKLIY DTESFAHMFSC
2912	8409	A	3171	1	399	SSSLQPPPP\GFK*FSCIGLPTSRDYR CVPPRP\ANFVFSVETGFHHVGQAG LELLTSGDPSTSASQSAGMTGVTTV PRPVLLISEAHFWCKNSLFTGENVI EANQNLLALRFISAMDLQSLRIVRN QTFFF
2913	8410	A	3172	1	451	LYGEGWSFALVAQAGVQWCDLRL LQPLLPGFK\YSPASASRVAG/HYR WSL/DSVTQAGVQWHNLGSLQPPPP SFKRFSCLSLPSS*DYRCTPPGLA*/F FIFLVEMGF\LLARLVSNS*PSGDPS TLGLPKVLGLQGVSHHALVPHLLIL QKR
2914	8411	A	3173	2	346	
2915	8412	A	3174	1	2430	
2916	8413	A	3175	576	983	GRSFIVSFLLVNSGKVPTDK/ERLFD RMMNSNWG/RSFAFKVNSNLST*Q FKYKNKGICAAQCFSLFPLK*PIRL FFAGEHTIRNYPATVHGALLSGLRE AGRIADQFLGAMYTLPRQATPGVP AQQFPKACETDAF
2917	8414	A	3176	1	2930	RRAGSVKRGEARLFGPTERQSERPL RPSAARRPEMLSGKKAASAAAAA AAATGTEAGPGTAGGSENGSEVAA QPAGLSGPAEVGPGAVGERTPRKK EPPRASPPGGLAEPGSGAGPQAGPT VVPGSATPMETGIAETPEGRRTSRR KRAKVEYREMDESLANLSEDEYYS EEERNAKAEKEKKLPPPPQAPPEE ENESEPEEPSGVEGAAFQSRLPHDR MTSQEAACFPDIISGPQQTQKVFLFI RNRTLQLWLDNPKIQLTFEATLQQL EAPYNSDTVLVHRVHSYLERHGLIN FGIYKRIKPLPTKKTGKVIIIGSGVSG LAAARQLQSFGMDVTLLEARDRVG GRVATFRKGNVYVADLGAMVVTGL GGNPMAVVSKQVNMELAKIKQKC PLYEANGQAVPKEKDEMVEQEFNR LLEATSYLSHQLDNFVNLNKPVS LG QALEVVIQLQEKHVKDEQIEHWKKI VKTQEELKELLNKMVNLKEKIKEL HQQYKEASEVKPPRDITAEFLVKSK HRDLTALCKEYDELAETQGKLEEK LQELEANPPSDVYLSSRDRLQILDWH FANLEFANATPLSTLSLKHWDQDD DFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVN TRSTSQTFIYKCAVLCTPLGVLK QPPPAVQFVPLPEWKTSAVQRMG FGNLNKVVLCFDRVFWDPVNLFG HVGSTTASRGELFLFWNLYKAPILL ALVAGEAAGIMENISDDVIVGRCLA ILKGIFRS\SAVPQP\KETVVSRRWA DPWG\RGs*SYVAQGS\SGNDYDL MAQPYHSWAPSIPGAPQPIPRLLC GENITIRNYPs/TPVHGALAEVGSRE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AGKEIARPSFWGAMY/TRLPRQ\ATP GCFLAQQVPQACETRCIPKGRGPM CPVSCPCKEGSSSNTRSPLEKSTPGI WAPDQLMELPDLTKGACLLNDLE HQGGTCPLVWNCVLRKD
2918	8415	A	3177	62	447	GDRAEESAEPRAWSHSDNSHRYTT LFICLTHTHVHNPVHS\HTHTHTHT HTHTHTHTVSRYRHTETPPLLLKQTG LKFY*NSRDDTPRSRPGSSGLQRLSS SPPVPFQPGTVEASADFCGDDLLTT VRLQ
2919	8416	C	3178	90	233	MRIGYKVKDGTFLDLQMGGLPGX XXSRPKRNHQLSKGEREINLGL*
2920	8417	A	3179	462	929	SLFHTWKADGFFLTGNSSSRPGNNT ICKSKKCPILYLISNHPQIMPLFF CDGSFTLVGPGWEWQWCDLSSLQP PTPR/FN*FSCLSLPSSWDHRHPPSCP ANFLYF**RLGFHHVGQAGLELLAS SDPPASASHSVGITGVSHHTWPMPL LLLI
2921	8418	A	3180	160	272	FFL*DRALLCLPDWSAVV*SWLTAA LA\YRRKRSSYLSLPSSWDYRHLPP CPANFSYFL*RQSLTVLPRLVNSW TQVSLLTQPSVLGLQA
2922	8419	A	3181	6	270	RDRVLLCHTDWSIAVESQLTASSN SW\VK*SSCLSLQTRDYRHEPPYL ANF*IFCRD/RGLTMLPRLV*NSWPQ GILPPWPPKSLGLQV
2923	8420	A	3182	92	549	VWQGLHPQLHPHFASQNLISLALS LKAGVQWHDLSLQPPRRFKPFS CLSLPSSWDYRRAPLCPANFFLYF** RQGFTMLARLVSNY*PRDPPASASQ SAAITGVSHCARPRLSSLLQCFNSNS RLEHTDGIHFLSEAMSAIHESFPHI
2924	8421	A	3183	16	661	DRVSVTQAGVQWCNLGSLQPLPPR FR*FSCLSLSSWDYRRPPPRPANFC IFSRD/MAFTTLARLVSNS*PQ/CDPP TSASQSAEITGVSHRAWPVLSPPQF FFFDMESHAIQAGVQWRHLGSLQ PPPPMFK*SSCLSLSSWDYRRPPPR PANFFVFL*RDGVSPC*PGWSRSPD LVIHPPWSPKSAGITGLSHCAQPYP QFSKHKDLRVSGKA
2925	8422	A	3184	288	489	CGLILELEKLLLWVIQIQMSLNKA TI*SNDIFCPLST*NQVWCVFKGRSL HFEQKVVPSSNKVTG
2926	8423	A	3185	3	166	WLYSANVAHAPYRGSAWCLRDS RPPAQYWSAQHYSL*PTQFPLEFT TKSLLS
2927	8424	A	3186	3	725	LALLGRVYDVLSARD/YVELGPQYS VSKMTQRRSHVYTTRLNT/ADIYDS DLVPLCPQLSAVPLHSRNSAPYPYN PLYSVP/LPG/VVTGRFYGEDGLPTP ALTQVEAAITRGLEANKLQLEKQ TFPPCNAEWSSARGSRLWCSQKSPK DADDTSIYMFYQKVGDNIDSWSKN AGRVFKDSKFDANDPILKDQTQE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WSGSATFTSDGKIRLFYTDYSGKHY GKQSLTTAQNGVKPEGTTETTMK
2928	8425	A	3187	1	1988	
2929	8426	A	3188	134	944	MLRCGGRGLLLGLAVAAAAVMAA RLMGWWGPRAFGRLFIPEELSRYSR GRPR/DPGA*YLALLGRVYDD/DPP GRRHYEPGSHYSGFAGRDASRAV TGDCSEAGLVDDVSDLSAAEMTL HNWLSFYEKNYVCVGRVTGRFYGE DGLPTPALQTVEACDSTRGFGGQT NYKLQEKQTFPPCNAAGGGAQPGAA RLWCSQKSGGVSRDW/ALAVPRKL YKPGAKEPRCVCVVRTTGPPSGQMP DNPPHRNRGDL/DHPNLAEYTGCPP LAITCSFPL
2930	8427	A	3189	1	312	AQPGVQ*RNLSLQPPPPGSKRLSC LSLPSS*DHRPPPCPANF/SVFLVE MGFHHVGQAGLELPTSGDPPASAS QSAGITGASHRTRPES*FY*LRLGIII FR
2931	8428	A	3190	2	176	
2932	8429	A	3191	3	67	
2933	8430	B	3192	1	1587	MVKLSIVLTPQFLSHDQGGQLTKELQ QHVKSVCPCPYLRKVINTLADHH HRGTDGFGSPWLHVIIAFPTS YKVV TLWIVYLWVSLKTFWSRNGHDG STDVQQRARWSNRRRQEGRLSICM HTKKRVSSFRGNKIVLKDVTILRRH VETKVRKIRKRVTTKINHHDKIN GKRKTARKQLSQHSISHVLAFSDPP FCKKGSLQLAPPSADDNIKIPAERLR IPLPPSADDNLKTPSERQLTPLPPSAP PSADDNIKTPAERLRGPLPPSADDN LKTPSERQLTPLPPSAPPSADDNIKT PAERLRGPLPPSADDNLKTPSERQL TPLPPSAPPSADDNIKTPAERLRGPL PPSADDNLKTPSERQLTALPPSAPPS ADDNIKTPAERLRGPLPPSADDNLK TPPLATQEAEEKPRKPKRQRAAE MEPPPEPKRRRVGDVEPSRKPKRRR AADVEPSSPEPKRRRVGDVEPSRK KRRRAADVEPSSPEPKRRRVGDVEP SRKPKRRRAADVEPSLPEPKRRRLS *
2934	8431	A	3193	792	1024	SHRKMFOQAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKALCNW RMIISRHLPSVVLHVPLYQPRTRPT LH
2935	8432	A	3194	1	1656	
2936	8433	A	3195	112	368	SHRKMFOQAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKPLCNW VSLLVFLAFEHSLPGQDMDTFFSLQ LCAQARTGRSD
2937	8434	A	3196	1	1353	
2938	8435	A	3197	1	452	
2939	8436	A	3198	1	510	
2940	8437	A	3199	2159	2958	

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2941	8438	A	3200	350	927	LFLVSPLKTISGSRNG\HDGSRDVQQ RA*SSNRRRQ\KKRVSSFRGNKIVLK DVITLRRHVETKVRAKIRKRKVTTK INHHDKINGKRKTARKQKMFQRAQ ELRRRAEDYHKCKIPPSARKPLCNW VSLFVFLAFEHSLPGQMDMTFFSLQ LCAQALQREMAERKAA\YRHHSPIP VGNRVVQKHLHPHPVGPLI
2942	8439	A	3201	1	277	FFFF*ERIWLCCPGWSALARTWLT AAPNSWAQTILPHSWG\YRRLPPCP AFILFYLF\CRDK\SLAMLRLVLNS\ WAQVILPLQPPKVLGLQA
2943	8440	A	3202	1	340	SIHLPKAPPPNHSTGVVWQHRNFFL RWHLTQC/*PGWSAVAQSLLTATST SR\VKQSSHLSLLSSWDHRCAPPHL ANFLYF**RRDFTVLLRLVSNS*A*V ICPRWPPKVLGLQM
2944	8441	A	3203	2	354	ESLTGVQWHEFASLKPL/PCLSLPR GWDYRRAPPRPAYF*FLVETGFHHI GRAGLKLLTSDPPVSASQSAGITG MSHRAWPLLKYFSALQTLNILQKN KNKNLIKTYFISLHVKIF
2945	8442	A	3204	166	373	EGALFCSQASELLSCGLLAVFTRFK LRGPHCCCAKKVYSLPRMGPH TTL H/TALNI*SCPCCLFIFLVC
2946	8443	A	3205	2	775	LHHLPGGGSVSHNKPALCGAVPAG RPDTGDNPAVPGRSNGSALTPVWV LIAKQSPPIVKILKFGWFPHLAMVIS SFGGLILSKTVSKQYKGM\AIFTPVI CGVGGNLVAIQTSRISTYLHMWSA\ LGVLPLLMMKKFCPNPRSTFC\SQKL NSMSCSRLLLLGGSQGH\LIFFYIY LGGGVVSQS*T/TPDLCGCSNLLGRA* SRVTNPAVTGAEEVLVRLTWHQGL WDPDNHCIPYLTGLGDLLGTGPPGDS AFSLTGY
2947	8444	A	3206	2	348	IAFGRYELDTWYHSPWP\EEYARLG RL\HMCEF*IKYMNSLTILTMHMVN CAFDPPLGLPKELSLETRMETFFPAL PSFHSIHCP\CVQPELGKAFGCLSVG AWGCRTHLRFTGLH
2948	8445	A	3207	1	1503	
2949	8446	A	3208	1	635	
2950	8447	A	3209	1	665	MQAIKCAGGWKAEAVGKTCLLISY T\TNA\FPGEYIPTVFDN\YSA\NVMV DGK\PVN\WGLWDT\SGQKDYDRVT PPYPYPA/QADVFLICFSLVSPAS\FE NVR\AKWYLNVRHHCPN\TPHILVGT KLDLRDDKD/TRIEKLKEKKLT\PIT YPQGLAHG*GRLGAVKYLG/CAPA AHTSEGLKTVFDEAIRA\VLCP\PPVK ERGRENCLPVVNVSAPSFLGPVPLE PL
2951	8448	B	3210	1	693	MYGVSAFVVLSP\TGRLPSVLQKEN QQQGV\PN\SPPLHEQM\QMDTGLCRL TPGLTLAGQWTRGSDSLPGAGEAG RTSFLPMYNANSAASSATHTGAAS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RESCGERECVQFSQRTARDRWCI RAELEQDILDSAAVTIIQKWHIKGR ALHPAGVLGHVEAPFSLVLQLERSR FLKNRWESAGARYPGREEGNEIRH RGCGDRGSQEA AVRCKGPPTPAV ELPPRLPVLS*
2952	8449	A	3211	1	627	FFFGKSILLFKKINVTDFIEKDILKMF LKGLKRHLFWPGMVAPAC*SQHSG RPRRMDHLRSGVRDQPGQVQGETPS LLKNIKKISRAWWQAPVIPATREG*/ E*GESPEPGEGKVCRRAEIAATCTP AWGVQSETLSSKKKKS FVLNVPHH PRQASVSFHC FHNQWGSPLWKKA RTFLLLGNGWLSCPHLSTQGNLSA PHLAEAQTLSP
2953	8450	A	3212	114	411	EREF RVPQVELQGPDLG*LNLLLP RLKQFFGLTFQRIWNYKLAPPPVN LEFWAKTGFSHV NQVGFELLT*GDP P/AWASQRVKMTGPTHQAHLGNF F
2954	8451	A	3213	48	1400	HPMTPI*STPLLYPL/PVTSGLASLSS LTLQNSDSLLQPLTSAM/PPSAIPTP QRTSTPGLALFPGLPSPVANSTSTPL TLPVQSPLATAASASTSVPVSCGSS ASLLRGPHPGTSDLHISSTPAATTLP VMIKTEPTSPTPSAFKGPSHSGNPSH GTLGLSGTLGRAYTSTSVPISLSAC LNPALSGLSSLSTPLNGSNPLSSISLP PHGSSTPIAPVFTALPSFTSLTNNFPL TGNPSLNPSVSLPGSLIATSTTAATS TSLPHPSSTAAVLSGAFCFSTSPAAP FPLNLSTAVPSLFSVTQGPLSSSNPS YPGFSVSNTPSVTPALPSFPGLQAPS TVAAVTPLPVGWPPQHPQLPVLPGF GSAFSFHFNRSRWLHKPGFIIWDFK AGRQFWFFRAFGPSRVS LGFLRLH NHPCKNYSIMRLHSQHCSRSIQLR LWESYPAQPDGVS
2955	8452	A	3214	2	694	QLLNYPAGPGGPRYVDCDLF*NGY HLWYHD\YGHLEF\RLQLATQFEN WYMKYQSPHQT KYGAETVSGFPR DPPSDVPVRCPRKSLLEQYVHLGLDS KPQKNTCLESPLWNF\ADFMTE\QSP \TKVLGNKKGIFTRAETTOQSA AFL LRERYWKIAQ*NP GIPHSVAR SQCL ENTACCSLSKTDTHLRVPSSPGGQR LPQQQNKCLDCSRQTRTFSGLGFV VIYSSREH
2956	8453	A	3215	2434	2765	GIILFWAQLFPASFFFFFFFF*DGVS LC CPGWSAVVRSQLTASSASRVQAILC LSLPSSWDYRHLPPCLANFFVFL/CR DGGFTMLARLV LNS*AS*VHPPWPP QSAGDYQA
2957	8454	A	3216	2	481	LFLFLRHSFTLSPSLDVQWRDLGSL QPPPPRFK*FSCLTLPSSWYYRHVPL CLANF*FLVETGFCHVGQSGLELLT SGDLPASASQSVWITGMSHGARLH GHFLGSWENWTCQAPGSSKSDCS

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						PHMANAVSAGGPGTLLIPSAPSCPC NLAGGRCPLR
2958	8455	A	3217	126	364	RAWAN\LS*LKVLPPGLKGFSGLTL PSTGNNGLVPPPRVNFSGFSKNGVS PCGP/GWF*TTALRELGPLSLLEIGIN PFFL
2959	8456	A	3218	132	342	SLSSLKNMYICLWNVFLFVFGYRAF LCHPGWSTVAQS*LT/IPGT/LWVKP SSLLVLPKRWDYRHEPLRPDLK
2960	8457	A	3219	2	264	QLTATPPPTGFKQFSCLSHPSSWDY RYVPPRPAKFCIFS/VRRGFTMLAR MVSIS*PCDLPTSASQSAGITGVSHR AWPVL*FVFLVETGFHHVQGQDGLN LLTLRSAHLSLPKCWDYRRKPPGLA CFMILNSYLV
2961	8458	B	3220	134	3038	PGMEDGSDMDMTSVEDIGGRSCVT RFVRTLLLIMEHGVKPHSKHLTEYF AFLYEFAKMGEESQFLSLQAIST MVHFYMGTKGPENPQVEVLSEEG EEEEEEEDILSLAEKYPAALEKMI ALVALLVQSRSERHLTSLQTDMA ALTGGKGFPFLFQHIRDGINIRQTCN LIFSLCRYNNRLAEHIVSMLFTSIK LTPEAANPFFKLLTMLMEFAGGPPG MPPFASYILQRIWEVIEYNPSQCLD WLAVQTPRNKLAHSWVLQNMEN WVERFLLAHNYPRVRTSAAYLLVS LIPNSFRQMFRSTRSLHIPTRDLPLS PDTTVVLHQVYNVLLGLLSRAKLY VDAAVHGTTKLVPYFSFMTYCLISK TEKLMFSTYFMDLWNLFPKLSEP AIATNHNKQALLSFWYNVCADCPE NIRLIVQNPVVTKNIAFNYILADHD DQDVVLFNRGMLPAYYGILRLCCE QSPAFTRLASHQNIQWAFKNLTPH ASQYPGAVEELFNLMLQFLIAQRPD MREEELEDIKQFKTTISCYLRLCD GRSCWTTLISAFRILLESDEDRLLVV FNRGLILMTESFNTLHMMYHEATA CHVTGDLVELLSIFLSVLKSTRPYLQ RKDVKQALIQWQERIEFAHKLTL NSYSPPELRNACIDVLKELVLLSPH DFLHTLVFPLQHNHCTYHHSNIPMS LGPYFPCRENILIGGKSNIRPPREL NMCLLPTMVETSKGKDDVYDRML LDYFFSYHQFIHLLCRVAINCEKFE TLVKLSVLVAYEGSKSKCFLEANC GQFGSALFITNLISQYQNLQSDFSNR VEISKASASLNGDLRALAFAPVSTH SQTVPSSNSNSARAFKQMQDLSA TEKLTTPRGKKPKERKTKDDEGGNS HLKGRAC*
2962	8459	A	3221	2170	3139	DLRALALLSVHTPKQLNPALIPTL QELLSKCRCTCQQRNSLQEQEAKER KTKALALWTTIITFRVGGGSNTLGV TGLRVVCSAEPK*YKC*KQN*LPTS PPNVILMTFREVSLLACVFTDDEGA TPIKRRRVSSDEHTVDSICISDMKTE

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						TREVLTPSTSDNETRDSSIIDPGTE QDLSPENSSVKEYRMEVPSSFSED MSNIRSQHAEQSNNGRYDDCKEF KDLH\CSKDSTLA\EESE\FPSTSISA VLSDLADLRSCDGOALPSQDPEVAL SLSCGHSRGLFSHMQQHDILDTLCR TIESTIHVVTRISGKGNQAAS
2963	8460	A	3222	3	344	PESHSAQAQGVQWPDGLSLQLSLP AFKQFSCSLSPSSRDYRRASPRPANF *FLVETGFCHVSQAGLKLLASSDPP VSASQTARITGVSHHAQPRATFYRH KSVLVLP LLKSPQ
2964	8461	A	3223	1411	1741	GYLQFSFSFFLFFFFFFFFLGESHSV T/RGLECSSVISTHCNLRPGSSDSR ASASRVARTRGMHHHTRQIFVFLV QMGFHVHVQAGL/DSS*PSVVHPP\ RPPKVLGLQA
2965	8462	A	3224	361	462	RHFLSTETYCNSFF/RHSSSKNYTK LKRYE*VS
2966	8463	A	3225	3	89	
2967	8464	A	3226	1	336	VCQVCGFRSRLHTNVNRHLLLNKP KIFPHVCDDCGKGFSSMLEYCKHL NSHLSEGIYLCQYCEYSTGQIEDLKI HLDFKHSADLPHKCSDCLMRFGNE RELISHLPVHETT
2968	8465	A	3227	951	2075	RTANLNFCKILDKSQALNVNCPAET GL*LRANSRWP/PINCELCEFNISKYF SDLKQHMILKHKRTDSNVCRVCKE SFSTNMILLIEHAKLHEEDP/N/YVCK YCEYKPVIFENISRHIADTHFR\DPPI HWCEQCDVQFSSSELYLHFQEHSC DEQYLCQFCEHETNDPEELA*\HVG K*GMHVN**ELSDKV/CNNGWNMG QYSLLSKITFDKCKNFFVCQVCGFR SRLHTNVNRHVAIEHTKIFPHVCDD CGKGFSSNTWKRKRGGQKTFPLLI NLELSTSLTNYRGSPWASELSTSVE VSMAMPLPAAEAETQGHDSGEREPF SQTPGLMQPFSIPVQITLQGSRRRQG RLPVLGDWRPFKLTCSPPALIIAQPI VGAQE
2969	8466	A	3228	2	415	LDPGSLAGFTSYIQFMYDEFVEEYE PTKADSYRKK/VAQDGEEVQIYIINT AGQEDYTAIKDNYFHCVFSTITES FAATVDFKEQ/ILRVKKDENIPFLLV GNKSDLEDKRQVSIEEAKNRAD*W NVIYVETSPKT*AN
2970	8467	A	3229	607	1317	
2971	8468	A	3230	260	535	
2972	8469	A	3231	246	985	KLRHKMAANKPKGQNSLALHKVI MVGSGGVGKSALTQFMYDEFVED YEPTKADSYRKKVVLDGEEVQIDIL DTAGQEDYAAIRDNYFRSGEGFLC VFSITESFAATADFREQILRVKED ENVPFLLVGNKSDLEDKRQVSVEE AKNRAEQWNVNYVETSAKTRANV D/KEWPFLKTRWWNTCKYISSHCPR

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						PAPVSRKTAHWAEVFFDLMREIRARKMEDSKEKNGKKRKS LAKRIRERCIL
2973	8470	A	3232	1	634	MAANKPKGQNSLALHKVIMVGS GVGKSALT\QFMYDEFVED*E\PTK ADSSRKVVLDGEEV\QIGYPLDTA G\QED\YAAIRD\NYFRSGEGFLCVFS ITEMESFAATAEFREQILRVKEDEN VPFLLVGNKSDLEDKRPGL*EEAK\ NRAEQWNVNYVETSAKTRANVDK VFFDLMREIRARKMEFEYYLNGTK NTKRLAERIREGGCIL
2974	8471	A	3233	314	373	
2975	8472	A	3234	1	2129	PSVAGAATLWFHVTL PFCARLCGR RSCTHSGIITEFHFFHL/ PFRPIPLAC GNDDCRIHIFAQQNDQFQKVL SLCG HEDWIRGVEWA AFGRDLLASCSQ DCLIRIWKLYIKSTSLETQDDDNIRL KENTFTIENESVKIAFAVTLETVLAG HENWVNAVHWQPVFYKDGVLQQP MRLLSASMDKTMILWAPDEESGV WLEQVRVGEVGGNTLGFYDCQFNE DGSMIIAHAFHGALHLWKQNTVNP REWTPEIVISGHFDGVQDLVWDPEG EFIITVGT DQTTRLFAPWKRKDQSQ VTWHEIARSQIHGYDLKWLAMINR FQFVSGADEKVL RVFSAPRNFVGKF LCHYR\KSLNHVLCNQDSDLPEGAT \APALGLSNKAVF/LREDKAPQPPDE EELLTSTGFEYQQVAFQPSILTEPPT EDHLLQNTLWPEVQKLYGHGYEIF CVTCNSSKTL LASACKAAKKEHAAI ILWE\TT SWKQVQNLVFHSLTVTQ MGLLT**GSFLLGCFPEDSNLVIVEK AWIQS/TPEFEPVFSLFAFTNKITSVH SRIIWSCDWSPDSKYFFTGSRADKKV VWGECDSTDDCIEHNIGLP PPSVL DRGWGCDQLSASAQCSHPSQRYVV AVGLECGKDLLIYLGKRLIKFQK*M T/ATHCVGNKSKPKVIHWAIQKIYC WEGICSGKT*TRREGRR*VVYTFA SCG*DHTVKIHRVNKCAL
2976	8473	A	3235	451	778	GSGRWKRSRVARAGMQISGAHLQL NCKPPPPGLKADPPWLS\ PSSWDP QMCPTPWLLFVCLVETGFTMLPQ AALQLLS*SDLSA*ASQNAGITGMS HHAGPDTVPLF
2977	8474	A	3236	1	186	FFFFEMESRTVTQAGVQWHDLG\SL QPP\PPG\SSDSPVSASHVAEITGAHH HTWLIF FIFLFL*GVQWHD LGLTAT SLLGSSDSPVSASHVAEITGAHHH TWLIF FIFLFL
2978	8475	A	3237	1	353	KIWLFFVFKTDV SILVHPRLECSGAI SAHCNLHLPGLSDSHTSAFRVAGTT GARHQAQLIFTFLVEMGFHHVGH GLKLPT*EIRPPRPPEVLGLHACAT VPGHKYVNEPIKMVLLK
2979	8476	A	3238	3	453	GQTGTWQGNTGQRPVQLPPHPPPIH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LVSRRHGKLRHGFRLRPMPEPRGLES GKTGSARGVAACTSP*GRSG/QGGG PRDIAQQGGCRGSACGRRSHEALRP RVWCGEGPQWTW\CAVCP\NRSAP GAGLAD\RQHPGESRAWGETRLCE AGGAE
2980	8477	A	3239	232	472	LHSFIHSFIHLFIYLFDRVLLCCPDW STVERSQLTVTLKSR\VK*SSCLS/LP SSWGYRSVPPCPANYFYFL*RQRLT TLPS
2981	8478	A	3240	2	345	MVHVAVAGLNGTHSCPPASSSVLTF GHP\PHEQLQQSVGPTSPHSPLL*PL SSLEVLGWGSEGVGGLQEIQKCSK ALPCKTPCGCFCIYLIFSPTQGDIFPH DPAPPLLLSASWV
2982	8479	A	3241	205	361	DAHSPAPAVSTPGQAWAAVLAMFP PGPWGEGSRL\IPHPAPPLLLSAS WV
2983	8480	A	3242	137	959	IPFPVMLDPAGRQQQRWGRIMGY KVSLLGA*NLGRCKNIHKGSCREGL CLISLRAWEGRVLGEGFAQN*HTA HPEPGKSSHS*KIPFQRESGL*PATH PVPSKTPPLPGESSRARAWCLKGE DPCPRKPPAP*SLPPGPWGE/P*QGL QPRLGL*TPGLGYEHLKPPF/PSA PAA*PPG\PAKAQAPRKSCAPTIVTH ALLPPNPLPTQLGWKWISADQSQSN PFPRAYP/REPSLFSPNAPLSPSPHP TTFPEFPCSPTPPPQIPHQDFPRS
2984	8481	A	3243	23	438	SRHLGLPKCWDYRQEPLCLALSFFF RVRVS\SVAQVVVQWHDGRSLQPQ TPGPK\YPPATAS*VAGARLIFFK*FL *RWDLTIMPKAGLKLPAATGDPPACL LLSFSLIPTGGFTRFEPTRHSLLEV GLSPMLVRHWLWA
2985	8482	A	3244	1	1061	ASRRALQLFGIPVRQLQKGACPLGL HQLSSPRYKFNFIADVLFKIAVAV HIELFLRHPLFGRNVPLSSSGSFIMS EAGLIITNAHVSSNSAAPGRQQLK VQLQNGDSYEATIKDIDKKSIDIATIK IHPKKKLPVLLLGHSDRTCRPGEVL WVAIRQIPSP*QNTVTTGIVSTAQR EGRELGLRDSMDY\QTDALINNYG NSGGPLVNLDEGIVIGINTLKVTAGIS FAIPSDRITRFLTEFQDKQIKDWKKR FIGIRMRTITPSLVDELKASNS\DFPE VSSGIYVQEVVPNSPSQGGIQQGGDI IVKVNGRPLVDSSSELQEA\LTESPL LLEVRRGNDDLLFSIAPEVVM
2986	8483	A	3245	1	268	QGSPSRDPSPGLGGPNGGIFLAP/AGP NPP/RGTRGNPVFS*NSKICPGWGGP PVGPGS/RGELG*RAALAPGGPGGL DWAPGP*PGGQRGAPF
2987	8484	A	3246	20	353	KEVGRLTHSVNHSGGREKYVWHP GNAL*YGKLPVLPCPIFIVNR*VQ*P *PERHMTVRGSGMNVWIMP/PGKPP RPAEVPVEVEGHLEWTAEDSSNHC QLQG*DQLQWGRWL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2988	8485	A	3247	2	322	KLDNSSKWLENGTFDLSILQDLDNF C*KMGKWSEVPYVQAFF\SIHSLPSL CSQCHL/CPDFPSFSP/YPLLSPPQT QSPLNPPFPLTPLTSLLRLLARLN QVPILP
2989	8486	A	3248	141	924	PFSSQTVKLSGGATRNPVSSPKASG GQPSEGWEVALEGDSCAALMRQQ CPGLLSRK/RAPGNPTASGSAPGA TKRSLGGRARRGLEFVVSFFGGGR AQSSLGNAHPHSGTIPKAPHASQQG LGLRLGGLEPSTPPWVHPPARPRAS PDPSRVAGSPRSLPNPPAAGKGGRG SGEEARYFDLS*ILKSLPYPGHERVY QEPQRGVKTSCSCSPF/HLPLLLFQS SPPPSTLVGAGLKIGFLRCPVGGILI GKGFFFNCLHST
2990	8487	A	3249	1	363	QVSLVINWDLPTNR*NYIHR*AYIW NTPLPLHTWPSLGLKLLIFLIPLEFQ VGRGGRDRKGGAINKGTEYDERT LRDIETFYNTSIEEMPFNVADHMLM GCPATQPLSGLIIGASDQY
2991	8488	A	3250	1	87	LNETVLLWHSWGMSTVVQTQLLPA ASTW/VKQSSHLNLSWDHSRVP PHWANFLIFCR/DRSFAMLPKLVSN PWAQAVLPPLPIVL*LNETVLLWH SGWMSTVVQTQLLPAASTWA
2992	8489	A	3251	3	270	CFNSAWTEPGARSPRPAAHSQPSV TSSPHPRTPAPPPPPLQR/SP*SPP*R PRPP/PHVRHNYPSGLKSHH*SAE*P GPLGPIPTVY
2993	8490	A	3252	3	452	
2994	8491	A	3253	1	477	TLLVPQDSERTHPWCLSPADKTNV KAAWGVKGVAHAGEYGAELERM FLSFP\TTKYTFPHFD\LSHG\SAQG* RAHGK\KVA\DALTKAVAHVDDMP KRRCPP*SDLHGAQAFGWDPVQLQ SS*SHLPCLGEPWAAHLPRPSFNW RLQRLPWGQISWGFC
2995	8492	A	3254	3	295	LFLFFFFFF*MESHSVTRLECSGTIW AH*NLHLPSSDSPALASRVAGTTG MCHHIQLIFFVFLVEKGFHHVG*/D MSLSLDLVIHPPWPPKVLGLQA
2996	8493	A	3255	306	519	GTRVERHSRERPSCHLLCEPSQRYS PLLFLVGL*CPPASPGKSPRTKENNF TADSKSQGQSEKSLWVTLA
2997	8494	A	3256	453	626	HGSCLLHHREQVPIPPGIPNLSDSIL* FPVLRWMLCLYTSCMWFSQSFWI AVMYFV
2998	8495	A	3257	1537	1909	NVLTVEDHPIPIPSKNRPFHNLDPVN LAFFFFFFLNRVSFCHLGWSAVARS HLTCNLLSPGFKQFSCLSLLSSWDY QACMHHTRLVFGVFSRDGGFTMLA RLVSNS*PQVILPPLPPKVLGLQA
2999	8496	A	3258	1	342	KTESHSVAQAGVQWCDLGSLOPPP PRFKLFSCLLSLSSWDYRGALPRPT DLFA/QFLVEMGFCHVAQAGLELLS SGNLFASASQTARITGVNHHTWPVL

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						*F*VKKIPPSLPGLL
3000	8497	A	3259	1	338	FFLRWSL/NSVAQAGVQWRNLSSL QALPPGFRPFCSLSLPS*DYRCPP RLANFFLYFLVETVFHRLY*RSRMV LIS*PGDPPTSASHSAVVRYLLRRRQ CLRQGLCRASVF
3001	8498	B	3260	188	1504	MRTLLPPALLTCWLLAPVNSIHPEC RFHLEIQEEETKCAELLRSQTEKHK ACSGVWDNITCWRPANVGETVTVP CPKVFSNFYSKAGNISKNCTSDGWS ETFPDFVDACGYSDPEDESKITFYIL VKAIYTLGYSVSLMSLATGSIILCLF RKLHCTRNYIHLNLFSLRAISVL VKDDVLYSSGTLHCPDQPSWVG CKLSLVFLQYCI MANFFWLLVEGL YLHTLLVAMLPPRRCFAYLLIGW GLPTVCIGAWTAARLYLEDTCWD TNDHSPVWWVIRIPILISIVNFVLFIS IIRILLQKLTSPDVGGNDQSQYKRLA KSTLLLIPLFGVHYMVFAVFPISISSK YQILFELCLGSFQGLVVAVLYCFLN SEVQCELKRKWRSRCPTPSASRDYR VCGSSFSRNGSEGALQFHGRSRAQS FLQTETSVI*
3002	8499	A	3261	1	1047	MVSISWPRDLPASASQSAGITGLIGA LVLSVGIYAEVER/HEI*NP*KCLPGS SHHPHPGRRHVHGLLHWCAGVPP *QPELLASRLSRGYGLVLSWLEP RYEKMISGMYLGEIVRNILIDFTKK GFLFRGQISETLKTGRGIFETKFLSQIE SDRLALLQVRAILQQLGLNSTCDDS ILVKTVCVVSRRAAQLCGAGMAA VVDKIRENRGLDRLNVTGVVDGTL YKLHPHFSRIMHQTVEKLSPKCNVS FLLSEDSGSGKGAALITAVGVRLRTE ASS
3003	8500	A	3262	178	568	IIFFFFFKMESCSVAQAGVQWWDL SSLQPLPPGFMPFCLSLPSSWDYRR PLLPANFLYF**RRGFTVLARMVSI S*PCDPPASASQSAGITGVSHCAQLE SKFYEGRDVHLFCSPLYFQKARKLP GIE
3004	8501	B	3263	776	5218	MLGDNSSMSVTAPKTFQWDMMW RRKGLILILALCRPKEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEDQLDT MLWDSSNTLNTALSKEKTMFSSR AKIVKPNGEKPDEFESGISQALLELE MNLDLKAQLWELNITAAKEIEVGG GRKAIIFVVPQLKSFOKTQVQLRR ILPKPTQKSCTNNKQKLPRSCTLTA VHDAILEDLVFPSEIVGKRIHVKLD GSHLIKIHLDEAQNNVEHKVEPFS GVYKKLMGKDVNFEPFQLMPGT PGSLEMGLLTFRDVAIEFSPEEWQC LDTAQQNLYRNVMLENYRNLAFLG IALSKPDLITYLEQGKEPWNMKQHE MVDEPTGICPHFPQDFWPEQSMEDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FQKVLLRKYEKCGHENLQLRKGCK SVDECKVHKEGYNKLNQCLTTAQS KVFOCGKYLKVIFYKFLNSNRHTIR HTGKKCFKCKKCVKSFCIRLHKTQ HKCVYITEKSCKCKECEKTFHWSST LTNHKEIHTEDKPYKCEECGKAFKQ LSTLTTHKIIKAKEKIYKCEECGKAF LWSSTLTRHKRIHTGEKPYKCEECG KAFSHSSTLAKHKRIHTGEKPYKCE ECGKAFSHSSALAKHKRIHTGEKPY KCKECGKAFFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTKHKIIH AGEKLYKCEECGKAFNRSSNLTIHK FIHTGEKPYKCEECGKAFNWSSSLT KHKRFHTREKPFKCKEKGKFIWSS TLTRHKRIHTGEKPYKCEECGKAFR QSSTLTKHKIIHTGEKPYKFEECGK AFRQSLTLNKHKIIHSREKPYKCKE CGKAFKQFSTLTTHKIIHAGKKLYK CEECGKAFNHSSSLSTHKIIHTGEKS YKCEECGKAFLWSSTLRRHKRIHTG EKPYKCEECGKAFSHSSALAKHKRI HTGEKPYKCKEKGKAFSNSSTLAN HKITHTEEKPYKCKECDKTFKRLST LTKHKIIHAGEKLYKCEECGKAFNR SSNLTIHKFIHTGEKPYKCEECGKAF NWSSSLTKHKRIHTREKPFKCKEKG KAFIWSSTLTRHKRIHTGEKPYKCE ECGKAFFSRSSLTTHKTIHTGEKPY KCKEKGKAFKHSSALAKHKIIHAGE KLYKCEECGKAFFNQSSNLTHKIIH TKEKPSKSECDKAFIWSSTLTEHK RIHTREKPYKCEECGKAFFSQPSHLT THKRMHTGEKPYKCEECGKAFFSQS STLTTHKIIHTGEKPYKCEECGKAFR KSSTLTEHKIIHTGEKPYKCEECGK AFSQSSTLTRHTRMHTGEKPYKCEE CGKAFNRSSSLTTHKIIHTGEKPYK CEECGKAFFSSSTLNGHKRIHTREK YKCEECGKAFFSQSSTLTRHKRLHTG EKPYKCGEKGKAFKESSALTKHKII HTGEKPYKCKECCAFNQSSILTNH KKIHTITPVIPLLWEAEAGGSRGQE METILANTVKPLLY*
3005	8502	A	3264	1	208	RDRVLF*HPHWSAVV*SKLTAASTS WVK*FSCLSFLSWCLAMLPRLVLN SWPQVTLLPQPPKVLGLQV
3006	8503	A	3265	78	359	RHSSKNLGNVDSECE*T*FPDIIPFH* KKLTEGEYQKSVNH/MTNAVAHST LSSQLLLALQKTLCLFLMLLTKL PTIIHRTVDAHSLADDDVE
3007	8504	A	3266	48	330	VCGCVWMLRVLCYPGWSAVAQ S*LTAALISLVNPSSSLSPSSWDHR RAPPRPANFFNL*RQELPMLRLVL/ NVWAQVILPPWPPKMLELQV
3008	8505	A	3267	200	1033	RSLAPRWHLGHKEKNVTTTSVWG WSPGRNASNSAGVGAGLPFVSTW LAVSSKNIDITEHIDFATPIQQPAME

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PLCNGNLPTSMHTLG\HLHGVSNPSPQCTYTGESQLTEVLQNLGQR/RNIHNSRLNRLAPRM/LQSFGKEPRPSWVL/CPAQALYWRV*RPKERRPIELPSAQLRLHYGPPQMKDVPILISLANILPQLPSSGNDVIVATHGQ*SLHHTLL*TPFHLGNVYVAMEEFKALVWYESTLASLQPEFVPAKNRIQTIQCHLM LKKGRALLP
3009	8506	A	3268	2	2956	LADSSPSNLQIIKELLSMHHQPDPA LTKEFDYLPVDSRSSSGFVGLRNG GATCYMNAVQQLYMQPGLPESLL SVDDDDTDNPDDSVFYQVQSLFGHL MESKLQYYVPENFWKIFKMWNKE LYVREQQDAYEFFTSLIDQMDEYL KKMGRDQIFKNTFQGIYSDQKICKD CPHRYEREEAFMALNLGVTSCQSLE ISLDQFVRGEVLEGSNAYYCEKCKE KRITVKRTCISLPSVLVIHLMRFGF DWESGRSIKYDEQIRFPWMLNMEP YTVSGMARQDSSSEVGENGSRVDQ GGGGSPRKKVALTENYELVGIVIH SGQAHAGHYYSFIKDRRGCGKKG WYKFNDTVIEEFDLNDETLEYECFG GEYRPKVYDQTNPYTDVRRRYWN AYMLFYQRVSDQNSPVLPKKSRSV VVRQEAEDLSLAPSSPEISPOSSPRP HRPNNDRLSILTKLVKKGEKKGLFV EKMPARIYQMVRDENLKFMKNRD VYSSDYFSFVLSLASLNATKLKHPY YPCMAKVSLQLAIQFLFQTYLRTKK KLRVDTEEWIATIEALLSKSFDACQ WLVEYFISSEGRELIKIFLLECNVRE VRVAVATILEKTLDLALFYQDKLKS LHQLLEVLLALLDKDVPENCKNCA QYFFLFNTFVQKQIRAGDLLRHS ALRHMISFLLGASRQNNQIRRWSSA QAAREFGNLHNTVALLVLHSDVSS QRNVAPGVIFKQRPPIAPSSPLLPL HEEVEALLFMSEKPYLLEVMFAL RELTGSLAALIEM/VVYCCFCNEHF SFTMLAFHLRNQLAETA/PPHEFKGI RFPTTFMEILVIEDPIQAERVVKFVFE TENGLLALMHHSNHVDSSRCYQCV KFLVTLAQKCPAAKEYFKENSHHW SWAVQRLHH\KMSDLYWTPLSNVS NETSTGKTF*RTISDHDTLPYATALL NEKEHSGSRNGSKSRPANENGHRH LQQGSQSPLDDWVSLRSDLDVDP
3010	8507	A	3269	68	301	NFRDLCDILCSETTRLNTINMSIL SNLTYRFSEIPF*IFRRLFVL*KL/ENS ILKYIWTCKGPRLVKTTFKNNSES W
3011	8508	C	3270	224	518	MINKGQAGANIKSNXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXX*
3012	8509	A	3271	342	724	NTYPWAVL/VFFFFFFLRWSLTLVAR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LECRAGVQWCDLGS LQPLPPQFE* FSCLSLQLALPRPAKFFVILVEMGF TMLAKMVSIS*PCDPPALASQSARIT ILDFMLAPACPLLIIPFTWTLFFRNTI
3013	8510	A	3272	3	367	
3014	8511	A	3273	58	553	VARSAPPDGAVCAGPGSRRTMAE QSDEAVKY\YTLERFQMHNVHKSST WLILHHKG\YDLTKFLEEHPGGEEV LREQA\GGD\ATENFEDVGHSTDA EMSKTFIIGVELHPVDRPKLNKASGT FKGCV*GNFLFTTI*FLVPSWWTNW \VIP\AISAVGRRLGCIRL
3015	8512	A	3274	41	400	KRLGPRGGVGPSPNGGNQGL*GPKI FPWPSTLGTK/GEPLPSSSSSSPPQK RGFPSSPEK\APGVPPPTPKGPSPPGG GVKKKGRA*KKKPLGLWEKGPNA PGGPGTPTFGGPPGQYPG
3016	8513	A	3275	3	146	WGVITMMVTCSV/A/CTLFWLIAIL AQCNP LYRP*LKDETTWY LKHHWP
3017	8514	A	3276	161	472	
3018	8515	A	3277	3	273	AAAPGN GRASAPRLLLLFLVPLLW APAAVRAGPDEDLSHRNKEPPAP SSCSRSLWAVQGPEPARVEVSGPG WGERGCRAGCAEYQAPGL
3019	8516	A	3278	124	672	FQRTKLLNGPGDVETGTSITVPQKK WLHVISPIFVQSLTLPFLAKWGDRL QLLQIELAAREVSDI*EETV*NETYL LLCSRKTLDTLKWAHSIPSYARLF YI**FSCSLKLAFSQFLLPADPYGVA VGGTVGHCLCTGLAVIGGRMIAQKI SVRTVTIIGGIVFLAFAFSALFISPD GF
3020	8517	A	3279	2	991	AAAAPGN GRASAPRLLLLFLVPLL WAPAAVRAGPDEDLSHRNKEPPAP \PSSCSRSLWAVQGPEPARVEKIFTP A\APVHTNTEDPATQTNLGIYPMQF VAAIIQLL\NVEIGVSRTFFIAAIMA MRYNRPGPCWAGAMLC/LAGLMT CLFS/VLFGYATTVIPRGLYILMFQP VLFAIFGIRMLREGLK\MSPDEGQEE LEEVA\ELKKKDEEFQRTKLLNG\ PGDVETGTSITVPAQKKWLHFISPIF GQALTLTFLAEWGDRS*\LTTIVLAA REDPYGVAVGGTVGHCLCTGLAVI GGRMIAQKISVRTVTIIGGIVFLAFA FSALFISP
3021	8518	A	3280	1	278	QHDLDQVDVAFTEEE*RLAGP\AQR KLYRDVIVENLRNLLSVGHPPFKQD ISPIERNQDLWIMTTATRIPGNLGKN QTVISSYSKLFICFASS
3022	8519	A	3281	263	588	DSALPQKEELKMNMFKEAVTFKDV AVAFTEELG\LLGPAQRKLYRDVM VEN\FRN\LLSVGHPPFKQDVSPIER NEQLWIMTTS/TPRRQGNLDTLSVK AL\LLYDLAQT
3023	8520	A	3282	1	1285	MEDSELPSARSVLP SKRIGVVQSQQ RPPLGERHYGPTTRDGALHSAYSPT

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						QARCVSHPTYEKYPHVWRGWPPFS PEKERQRLNLRKEEAEQLRRQK VEEDKRRRLKEEVKLRKEERLRKVL QARERVEQMKEEKKKQIEQKFAQI DEKTEKAKEERLAEEKAKKKAAAK KMEEVEARRKQEDARRLRWLQQ VRAQ/EGNRSREVK*HLKSHEPVCS GGDSRTHPQPLVHAWSQLP*RLLA RVLRELQEREKALRLQKEQLQRELE EKKKKKEEQQLAERQLQEEQEKKA KEAAGASKALNVTVDVQSPACTSS PITPQGHKAPPQINPHNYGMDLNSD DSTDDEAHPRKPIPTWARGTPLSQA IIHQYYQPPNLELFGTILPLDLEDIF KKSAPRYHKRTSSAVVNSPPLQGA RVPSSLAYSLKKH
3024	8521	A	3283	3	262	FHTEERSYECTECGKA\FKHSSTLLQ HRKVHTPERRQEDRAHGKVVC*H RVHQERSYSRKEVKESGRESAIRKK LNLAHPNTHPRE
3025	8522	A	3284	1	269	FFFFPQIGSHPITRLECSDAITFCCSL NLPGRDPPASAS*VAETTGLHHHA GLIF*FFVE/MGL/HQAGLELLDKVIL PPLPPKELGSQM
3026	8523	A	3285	3	1191	KSCFNAFFNFEDMQEITQHFAVCH VDAPGQQEGAP/SPFPTGYQYPTMD ELAEMLPVLTHLSLKSIIIGIVGAG AYILASRFALNHPELVERPLCSLMVD PC/ALKGWIDWAASKLSGLTTNVV\ EIILAHHFGQEELQANLD\LIQTYRM HIAQDINQDNLQLFLNSYNGRRDLE IERPILGQNDNKS\TLKCSTLLVVG DNSPA\VEA\VMADCGGLPHVVQPG KLTEAFKYFLQGMGYIPVCAAQSPE HRVST\SASMT\RLARS\THSTSSSLG SGESPFSRSVTSNQSDGTQESCESPD VLD\RHQTMEISLDDVLLSALLRNN GKSAQKKKISAKPKLEFLCPRPGTC DHGSRKFCYTVL\DP\PRERSKATAV ALGSFPAGGPAELSLRLGEPLTIVSE
3027	8524	A	3286	3	638	SSKLSGLTTNVVDIILAHHFGQEELQ ANLDLIQTYRMHIAQDINQDNLQLF LKS\YNGRRDLEIERPILGQNDNKS TLKG\STLLVVG\DNSPA\VEA\VECN SRLNPINTTL\K\MADCGGLPPG*FS PGKLTEAFKYFLQGMGYIPLVLCYS TSGSMTSVARS\THSTSSSLGSGES PFSRSVTSNQSDGTQESCESPDV DRQQTMEVSC
3028	8525	A	3287	1	407	FSIETESCSVAQAGGKWHDSGSLQP QPPRFK*FSCLSLLNSWDYRPAPP/* PG*LFFVFLVETGF/IHVGQPGKLKL TSSDPPTSASQSAGITGLRDRAQPPP EDSNVQFENHWQRECTMLLFTLGP LKLFP\TELML
3029	8526	C	3288	157	468	MHHIHNASRTFQLIFSSFPRGNAIVF MLKMGGFLELRGPRSGMDHHRGR GEANQPF\CTSPAACGQNLPIKHGL

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						PRWSTKGETTADTDSVDLENPILYK YFQL*
3030	8527	A	3289	14	348	EFHSCRPGWSAMTQSRLTLQPPPPG FK*FSCLSLLSSWDYRHTPPHPASF* LLVDTGVFLHVGQAGLKLLTSGDSP TSASQSARITGVNHCARPSTFLRLQ RKAGRCSTSL
3031	8528	A	3290	1	2201	MTNLAMVERDSEAGTAASRFPNGH AAKGKAQAHYKVWRPAEVRCLKL GPEWVTLRYTIKHPYKLCGKRQH VFFFTSRSDVGFMLTTLKPFGSVS ESKMNNKAGSFFWNLRQFSTLVST SRTMRLCCLGLCKPKIVHSNWNILN NFHNRMQSTDIIRYLFQDAFIKSDV GFQTKGISTLTALRIERLLYAKRLFF DSKQSLVPVDKSDDELKKVNLNHE VSNEDVLTKETKPNRISSRKLSEEC NSLSDVLDAFSKAPTFPSSNYFTAM WTIAKRLSDDQKRFEKRLMFSPAF NQLCEHMMREAKIMQYKYLFLSLH AIVKLGIPQNTILVQTLRLVTQERIN ECDEICLSVLSTVLEAMEPCKNVHV LRTGFRILVDQVWKIEDVFTLQVV MKCIGKDAPIALKRKLEMKALREL DRFSVLNSQHMFEVLAAMNHRSLI LLDECSKVVDNIHGCPLRIMINILQ SCKDLQYHNLDLFKGLADYVAATF DIWKFRKVLFILFENLGFRPVGLM DLFMKRIVEDPESLNMKNILSILHTY SSLNHVYKQCQNEQFVEVMASALT GYLHTISSIENLLDAVYSFCLMNYFP LAPFNQLLQKDISELLTSDDMKNA YKLHTLDTCLKLDDTVYLRDIALSL PQLPRELPSSHTNAKVAEVLSSLLG GEGHFSKDVHLPHNYHIDFEIRMAD TNRNQVLPL/SLDVGTTSAT\DIQRL LTYISFAGLSELKS
3032	8529	A	3291	3	485	LHTLDTCLKLDDTVYLRDIALSLPQ LPRELPSSHTNAKGGQRS*AALLGG EGTPPSKDVHLAPHNYHIDFEIQN GTPNRNPSAYPLSDVDTTSCQLQFK E*LCYVFPRSA YCLGSSHPRGFLAM KMRHLNAMGFHVILVNNWEDGQT RDGRCQSPFLKT
3033	8530	A	3292	1	530	LRKTFIPNRPLILLPPGNSLATHLFF ETVSRVAQAGVQWHHLGLLQSPS PGFKRFSCLSLPSNWDYRHAPPRLA NFYIFS*DGVSFHHVGQAGLKLLTS GDPLTLASQSAGITGVSHCTRPLIHK FGLSYRQRIENVSFLLPYTHASSLLQ LLLAPLVTNGQGQEQKPELVREVG
3034	8531	A	3293	115	463	VTKQLFNILSFIFFHTSILIFFFLKME SCSVA\RLCSGTILAHCNLCPLGSS NSPASASRVSWDYKVCATMPG*FL YF**EQGFHHVGQAGLRTPGPQGD PARPWAPKVLGLQA
3035	8532	A	3294	503	1055	DIDFSPV*LVNVQMRRHALLMNLW DT/QDSHTSLRNAEYCSLMEEDMAP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SNKTTWLRPLTQQF*NLPQKKTALA KK*KDFTHRVLFTA*MCLPQSSSLW HL*NWKQSKCPSVGDWEH*FVQW GTPYQKEE*GTPIDKGQSTYNIMQI YICFFLKQYKDKNLKWLLWRTGVS GGSETEIDSEVISGL
3036	8533	A	3295	3	304	FFLVETEFCHAAQAGVQWCDLGLS QPPPPGLQQSSHLNLPKS*DYRCEPP MPG*FLETGFHPSCPRLVPKLLGSSS PPASAS\QSIGIS\GVSHCPEKFPF
3037	8534	A	3296	324	650	KKEHRVTCFSFWEMESRSVA*AEV Q*HDLSLQPLPHGLKRVSLSLPSS WDYRHLPPCLTNVCIFSRNGVSLY* PGWSRTPDLVILPALAPQSAGITGG EPPCPATK
3038	8535	A	3297	2	564	FFFPPPPSPGFKQFSCSLTPSSWD YRCPPPRPANF*FLIETGF/VHVGQA GLELLTSGDLPTPASQNAITGVRP GTQPASCF*MWQGLIGQNKMTISLL LQSILL
3039	8536	A	3298	352	392	
3040	8537	A	3299	20	200	FTLIQNCFHEIQIEQCGLDAVAHTY NPSTLGGQGG*IA*AQEFETSLGNM VKPHLSLK
3041	8538	A	3300	971	9082	
3042	8539	A	3301	1	15447	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEES KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPNRHKSLRTVKTMDQA DDVSCPLLNSCLESPPVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSIFYSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGSFKN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSQNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTPVASFSFGIKK SIFRIRESKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNCTSNNTVIS QDLDYKEAKCNKEKLQLFITPEADS LSRKTSVSQTSLEAKKWLRGIFD GQPERINTADYVGNLYENNSNSTI AENDKNHLSEKQDTYLSNSSMSNS YSYHSDEVYNDSGYLSKNKLDGIE PVLKNVEDQKNTSFSKVISNVKDA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVGPPAFRIAS GKIRLCSHETIKKVKDIFTDSFSKVI KENNENKSKICQTKIMAGCYEALD DSEDILHNSLDNDECSMHSKVF DIQSEEILQHNQNMMSGLEKVS KISPCDVSLETS DICKCSIGKLHKS VSSANTCGIFSTASGKSVQVSDASLQ NARQVFSEIEDSTKQVFSKVLFS NEHSDQLTREENTAIRTP EHLISQKGF SYNVVNSSAFSGFSTASGKQV SILESSLHKVKGVL EEFDLIRTEHSLHYSPTS RQNVSKILPRVDKRNPEHC VNSEMEKTCSKEFKLSNNLN VEGGSSENNHSIKVSPYLSQFQ QDKQLVLGTVSLVENIHVLGKEQ ASPKNVKMEIGKTETFS DVPVKTNIEVCSTYSKDS ENYFETEAVEIAKAFMEDDEL TDSKLPSHATHSLFTCPENEEM VLSNSRIGKRRGEPLILVGEPSI KRNLLNEFDRIENQEKSLKASKST PDGTIKDRRLFMHVSLEPITC VPFRTTKERQEIQNPNTAPGQE FLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLIT TGRPTKVFVPPFKTKSHFHRV EQCVRNINLEENRQKQNI DGHGSDDSKNKINDNEIHQFNK NNSNQAAAVTFTKCEEEPLDLIT SLQNARDIQDMRIKKKQ RQRFVPQPGSLYLAKTSTLPRIS LKA AVGGQVPSACSHKQLYTYG VSKHCIKINSKNAESFQFHTEDY FGKESLWTGKGIQLADGGW LIPSN DGKAGKEEFYRALCDTP GVDPKLISRIVVYNHYRWIIW KLAAMECAFPKEFANRCLSP ERVLLQLKYRYDTEIDRSRRSA IKKIMERDDTAAKTLVLCVSDI ISLSANISSETSSNKTSSADTQK VAIHELTDGWYAVKAQLDP LLAVLKNGR LTVGQKIILHGA ELVGSPDACTPLEAPESLMLKIS ANSTRPARWYTKLGFFDPRPFPL PLSSLFSDGGNVGCVDVIIQRA YPIQRMEKTSSGLYIFRNEREE EEKEAAKYVEAQQRLEALFTK IQEEFEEHEENTTKPYLPSRAL TRQQVRA LQDGAE LYEAVKNA ADPAYLEGYFSEEQLRALNNHR QMLNDKKQAQIQLEIRKAMESA EQKEQGLSRDVTTVWKLRI VSYSKKEKDSVILSIWRPSSDLY SLLETEGKRYRIYHLATSKSKS KSERANMPAGRTV*K*SKKQK SFRYKRRGLGCSMSPSTTFKSGI Q*Y*LSIPEKSFI*S*KCQHSY FNSYFQGCSVKPSHDF*RQR IIQNVROAQR*QL*I*C*INQK YSHG KESRCMCFK*KL*KR*AV AT*KIHE SSITFKKGTINQNTN LRVIOKNQEE TTSISKITVNP DSEELFSDNENNFVFQVANERN NLALGNTKELHETDLTCVNEPI FKNSTMVLYGDTGDKQATQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VSIKKDLVYVLAEEKNSVKQHIK MTLGQDLKSDISLNIDKIPEKNNNDY MNKWAGLLGPISNHSFGGSFRTAS NKEIKLSEHNIKKSKMFFKDIEEQYP TSLACVEIVNTLALDNQKKLSKPQS INTVSAHLQSSVVVSDCKNSHITPQ MLFSKQDFNSNHNLTSPQKAEITEL STILEESGSQFEFTQFRKPSYILQKST FEVPENQMTILKTTSEECRDADLHV IMNAPSIGQVDSSKQFEGTVEIKRKF AGLLKNDCKNSASGYLTDENEVGF RGFYSAHGKTLNVSTEALQKAVKL FSDIENISEETSAEVHPISLSSSKCHD SVVSMFKIENHNDKTVSEKNNKCCQ LILQNNIEMTTGTVEEITENYKRNT ENEDNKYTAASRNSHNLEFDGSDSS KNDTVCIHKDETDLLFTDQHNICLK LSGQFMKEGNTQIKEDLSDLTFLEV AKAQEACHGNTSNKEQLTATKTEQ NIKDFETSDTFFQTASGKNISVAKES FNKIVNFFDQKPEELHNFSLNSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPKCKE MQNSLNNDKNLVSIE TVVPPKLLSD NLCRQTENLKTSKSIFLKVKVHENV EKETA KSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNLYEN NSNSTIAENDKNHLSEKQD TYLSNS SMSNSYSYHSDEVYND SGYLSKNK LD SGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNM SGLKVKSKIS PCDVSLETSDICKCSIGKLHKS VSSA NTCGIFSTASGKSVQVSDASLQNAR QVFSEIEDSTKQVFSKVLFKSNEHS DQLTREENTAIRTPEHLISQKGFSYN VVNSSAFSGFSTASGKQVSILESSLH KVKGVLEEFDLIRTEHSLHYSPTSR QNVSKILPRVDKRNPEHCVNSEME KTCSKEFKLSNNLNVEGGSSENNHS IKVSPYLSQFQQDKQQLVLGTVSL VENIHVLGKEQASPKNVKMEIGKTE TFSDVPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDELTD SKLPSH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEPSIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKERQEIQNPNTA PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSA TRNEKMRHLITTGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PTKVFPFPFKTKSHFHRVEQCVRNI NLEENRQKQNIIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEDYFGKESLW TGKGIQLADGGWLIPSNDGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWKLAAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRAIK KIMERDDTAATLVLCSVDIISLSA NISETSSNKTSSADTQKVAIHELTDG WYAVKAQLDPPLAVLKNGRITV GQKIILHGAELVGSPDACPTEAPES LMLKISANSTRPARWYTKLGFFPDP RPFPLPLSSLFSDGGNVGCDVIIQR AYPIQWMEKTSSGLYIFRNEREEKE EAAKYVEAQQKRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRALQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVILSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSEILFQI YQPREPLHFSKFLDPDFQPSCEVDL IGFVVSVVKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASNL QWRPESKSGLLTLFAGDFS VFSASP KEGHFQETFNKMKNTVENIDILCNE AENKLMHILHANDPKWSTPTKDC SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKKRRALDF LSRLPLPPPVPICTFVSPAAQKAFQ PPRSCGTKYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRTAPTSSE DYLRLKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI
3043	8540	A	3302	1	2163	
3044	8541	A	3303	1	5771	
3045	8542	A	3304	1	3395	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEES KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTS GNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FESGSDKISKEVVPPLACEWSQLTLS GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVS DIKEEV LAAACHPVQHSKVEYS DTFQSQK SLLYDHENASTLILTPTSKDVL SNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQM TILKTTT EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRK FAGLLKNDCKNSASG YLT DENEVGFRGFYSAHG TKLNVS TEALQKAVKLFS DIENISEETSAEVH PISLSSSKCHDSV VSMFKIENHNDKT VSEKNKNCQLILQNNIEMTTGT FVE EIT/EM*HAFT*GFC*HSE*RNFTT*P KYVWIGESF*NITL*C*FGNFRYM* M*YREAS*VSLICKYLDWF*HSKW KICPGIRCFITKRKTSVF*NRR*YQA SLFQSIV*K*RTFRPAHKRRKYCYT YSRTFNIPKRLFI*CGKFICFLWI*YS KWKASFHFRKFLTQS*GSVRGI*FN QN*A*SSLFTYV*TKCIKNTSSC**E KPRALCKLRNGKNLQ*RI*IIK*LKC *RWFFRK*SLY*SFSISLSISTRQTTV GIRNQLSTC*EHSCFGKRTGFT*KRK NGNW*N*NFF*CSCENKYRSLFYLL QRFRKLL*NRSSRNC*SFYGR**TDR F*TAKSCHTFSFYMSRK*GNGFVKF KNWKKKRRAPYLSGRTL NQKKLIK *I*QDNRKSRKILKGFKKHSRWHNK RSKIVYASCFFRADYLCTLSHN*GT SRDTESKFYRTWSRISV*ISFV*TSDF GKIFKQFSSFRTSILSSFCYKK*KNET LDYYRQTNQSLCSTF*N*IAFSQS*T VC*EY*LG GKQTKAKH*WTWL****

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						K*D**Q*DSSV*QKQLQSSSSCNFHK V*RRTFRFNYKSSECQRYTGYAN*E ETKATRLSTARQSVSCKNIHSASNL SESSRRPSSLCVFS*TAVYVWRF*T LHKN*QKCRVFSVSH*RLFW*GKF MDWKRNTVG*WWMAHTLQ*WKG WKRRIL*GSV*HSRCGSKAYF*NLG L*SL*MDHMETGSYGMCLS*GIC** MPKPRKGASSTKIQI*YGN**KQKIG YKCDNGKG*HSCKNCTSLCF*HNFI ERKYI*NF*Q*N**CRYPKSGHY*TY RWVVCC*GPVRSSPLSCLKEWQTD SWSEDYSSWSRTGGLS*CLYTS*SP RISYVKDFC*QYSACSLVYQTWILS* P*TFSSALIAFQ*WRKCWLC*CNYS KSIPYTVDGEDIWIIHISQ*KRGRKG SSKICGGPTKETRSLIH*NSGGI*RT* RKHNKTIFTITCTNKTASSCFARWC RAL*SSECSRPSLP*GLFQ*RAVKS LE*SQANVE**ETSSDPVGN*EGHGI C*TKGTRFIKGCHNRVEVAYCKLFK KRRRFSYTEYLASIIRFIFSVNRRKEI QNLSSCNFKI*K*I*KS*HTVSSDKK NSVSTTTGFR*NFISDLPATGAPSLQ QIFRSRLSAILF*GGPNRICRFCCEKN RTCPFRLFVRRMLQFTGNKVLDLP* *GHY*ASYVNCCCKQPPVATRIQIRPS YFICWRFFCVFC*SKRGPLSRDIQQN EKYC*EY*HTLQ*SRKQAYAYTAC K*SQVVHPN*RLYFRAVHCSNHSW YRKQASDVFS*L*DILSKSFITLYGQ KEVCFHTCLSPDDFKVL*RGERD*M PIGSKERPTFFEIFKTRCNKADLGPI LNWFEELSSEAPPYNSEPAEESHK NNNYEPNLFKTPQRKPSYNQLASTP IIFKEQGLTLPLYQSPVKELDKFKLD LGRNVPNRHKSLRTVTKMDQAD DVSCPLLNSCLSESPVVLQCTHVTP QRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPMDSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGSFKNV SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTL GQDLKSDISLNI DKIKEKNNDYMNK WAGLLGPISNH SFGGSFRTASNKEIKLSEHNKSKK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF R
3046	8543	A	3305	1	5771	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEE LSSEAPPYNSEPAE ESEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTD S ENTNQREAASHGFGKTS GNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCR TKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPN DTDPLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLT L S GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSEN SLPRISL PKSEKPLNEETV VNKRD EEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFAEPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NKNSVKQHIKMTLGQDLKSDISLNI DKIEKNNNDYMNK WAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEV PENQM TILKTTS EECRD/C/S/YLMIRKLIEAEDRL*KR *WKGMTQLQKHLFSVFLT*FH*AQI YLKLLAIKLVVQIPKKWPLLNLQM GGMLLRPS*ILPS*LS*RMAD*QLVR RLFFMEQNWALLMPVHLLKPQN LLC*RFLT TVLGLLAGIPNLD SFLT DLFLCPYHRFSVMEEMLVVLM*LF KEHTLYSGWRRHLDYTYFAMKE RKKRKQQNMWRPNKRD*KPYSLK FRRNLKNM KKTQQNH IYHHVH*QD SKFVLCKMVQSF MKQ*RMQQTQLT LRVISVKSS*EP*IITGKC*MIRNKL SSWKLGRPWNLLNKR NKVYQGM S QPWGSCVL*AIQKKKKIQLY*VFGV HHQIYILC*QKERDTEFIILQLQNLK VNLKELTYS*QRQKKLSINNYRFQM KFYFRFTSHGSPFTSANF*IQTFSHL VLRWT**DLSFLL*KKQDPLSSICQ TNVTIYWQ*SFG*TL MRTLLSLIC*L LQATSSGDQNPNAFLLYLLEIFLCF LLVQKRATFKRHSTK*KILLRILTYF AMKQKTS LCICYCMQ MIPSGPPQLKT VLQGR TLLKSFLVQETSF*CLLLIVR YIIVLYHFVWPKGSLFPHLSQPR*L QSLVKGRKRLMTKRTAKREEPWIS* VDCLYLHLLVPFVHLFLRLHRRHFS HQGVVAPNTKHP*RKKN*ILLR*LH LKNSMKFLFWKVIQ*LTKNLH**IP KLFCLVQQEKNNLYLSVNPLGLLPP VQKIISD*NDVVLHL*SKNRRVPRP VRKNVRKISRTQLQLKNIS
3047	8544	B	3306	16	10899	MPNVLEDEVYETVVDTSEEDSFSLC FSKCRTKNLQKVRTSKTRKKIFHEA NADECEKSKNQVKEKYSFVSEVEP NDTDPLDSNVANQKPFESGSDKISK EVVPSLACEWSQLTSLGNGAQME KIPLHHISSCDQNISEKDLLDTENKR KKDFTLSENSLPRISLPKSEKPLNE ETVVNKRDEEQHLESHTDCILAVK QAISGTSPVASSFQGIKKSIFRIRESP KETFNASFSGHMTDPNFKKETEASE SGLEIHTVCSQKEDSLCPNLIDNGS WPATTTQNSVALKNAGLISTLKKK TNKFIYAIHDETSYKGKKIPKDQKS ELINCSAQFEANAFEAPLTFANADS GLLHSSVKRSCSQNDSEPTLSLTSS FGTILRKCSRNETCSNNTVISQDLDY KEAKCNKEKLQLFITPEADSLSCLQ EGQCENDPKSKKVSDIKEEVLA CHPVQHSKVEYSDTDFQSQSLLY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DHENASTLILTPTSKDVLNLVMISR GKESYKMSDKLKGNNYESDVELTK NIPMEKNQDVCALNENYKNVELLP PEKYMVRVASPSRKVQFNQNTNLRV IQKNQEETTSISKITVNPDSEELFSDN ENNFVFQVANERNNLALGNTKELH ETDLTCVNEPIFKNSTMVLYGDTGD KQATQVSIKKDLVYVLAEEKNSV KQHIKMTLGQDLKSDISLNIDKIEK NNDYMNKWAGLLGPISNHSFGGSF RTASNKEIKLSEHNIKKSKMFFKDIE EQYPTSLACVEIVNTLALDNQKKLS KPQSINTVSAHLQSSVVVSDCKNSH ITPQMLFSKQDFNSNHNLTSPSQEQI TELSTILEDGSGSQFEFTQFRKPSYILQ KSTFEVPENQMTILKTTSEECRDAD LHVIMNAPSIGQVDSSKQFEGTVEI KRKFAGLLKNDCKNSASGYLTDEN EVGFRGFYSAHGTKLNVSTEALQK AVKLFSDIENISEETSAEVHPISLSSS KCHDSVVSMFKIENHNDKTVSEKN NKCQLILQNNIEMTTGTFFVEEITENY KRNTENEDNKYTAASRNSHNLEFD GSDSSKNDTVCIHKDETDLLFTDQH NICLKLSGQFMKEGNTQIKEDLSL TFLEVAKAQEACHGNTSNKEQLTA TKTEQNIKDFETSDTFFQTASGKNIS VAKESFNKIVNFFDQKPEELHNFSL NSELHSDIRKNKMDILSYEETDIVK HKILKESVPVGTGNQLVTFQGQPER DEKIKEPTLLGFHTASGKKVKIAKE SLDKVKNLFDERARTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVP SLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKEQITELSTILEDSSGSQFEFTQF RKPSYILQKSTFEVPENQMILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFGRGFYSAHGTKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVSMMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFFE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDL FTDQHNICKLKSQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLSNELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDERASHQWAK TLKYREACKDLELACETIEITAAPK CKEMQNSLNNDKNLVSIVTVVPPKL LSDNLCRQTENLKTSSIFLKVKVH ENVEKETAKSPATCYTNQSPYSVIE NSALAFYTCSRKTSVSQTSLEAK KWLREGIFDGQPERINTADYVGNY LYENNSNSTIAENDKNHLSEKQDTY LSNSSMSNSYSYHSDEVYNDSGYLS KNKLDSGIEPVLKNVEDQKNTSFSK VISNVKDANAYPQTVNEDICVEELV TSSSPCKNKNAAIKLSISNSNFEVG PPAFRIASGKIVCVSHETIKKVKDIF TDSFSKVIKENNENKSKICQTKIMA GCYEALDDSEDILHNSLDNDECSTH SHKVFADIQSEEILQHNQNMSSGLEK VSKISPCDVLETSDICKSIGKLHK SVSSANTCGIFSTASGKSVQVSDAS LQNAHQVFSEIEDSTKQVFSKVLFK SNEHSDQLTRENTAIRTPHEHLISQK GFSYNVVNSSAFSGFSTASGKQVSI LESSLHKVKGVL EEFDLIRTEHSLH YSPTSRQNVSKILPRVDKRNPEHCV NSEMEKTCSEFKLSNNLNVEGGSS ENNHSIKVSPYLSQFQQDKQQLVLG TKVSLVENIHVLGKEQASPKNVKM EIGKTETFSQVVPKTNIEVCSTYSKD SENYFETEAVEIAKAFMEDDELTD KLPSHATHSLFTCPENEEMVLSNSRI GKRRGEPLILVGEPSIKRNLLNEFDR IENQEKSLKASKSTPDGTIKDRRLF VHHVSLEPITCVPFRTTKERQEIQNP NFTAPGQEFLSKSHLYEHLTLEKSSS NLAVSGHPFYQVSGNKNGKMRKLI TTGRPTKVFPFVKTKSHFHRVEQC VRNINLEGNRQKQNIIDGHGSSDDSK

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						NKINDNEIHQFNKNSNQAAAVTFT KCEEEPLDLITSLQNARDIQDMRIK KKQRQRVFPQPGSLYLAKTSTLPRI SLKAAVGGQVPSACSHKQLYTYGV SKHCKIKNSKNAESFQFHTEDYFX*
3048	8545	A	3307	1	12500	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPHVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNG/K/TVMS**MPHRLVR*TAA SNLKVQLKLNGLLAC*KMTVTKV LLVI*QMKMKWGLGAFILLMAQN* MFLCLKCKKL*NCLVILRILVRKLL QRYIQ*VYLQVNVMMILLFQCLR*KII MIKL*VKKIINAN*YYKIILK*LLALL LKKLLKITREILKMKITNILLPVEILI T*NLMAVIQVKMILFVFIKMKRTCY LLISTTYVLNYLASL*RRETLRLKKI CQI*LFWKLRKLKHKHVMVILQIKNS *LLLKRSKI*KILRLLIHFFRLQVGKI LVSPKSHLIK*ISLIRNQKNCITFP*I LNYILT*ERTKWTF*VMRKQT*LNT KY*KKVSQLVLEIN**PSRDNPVM KRSKNLLCWVFIQLAGKKLKLQRN LWTK*KTFLMKKSKVLVKSPVLAI NGQRP*STERPVKTLN*HVRPLRSQ LPQSVKKCRILSIMIKTLFLLRLWCH LSS*VIIYVDKLIKSKHQKVSF*KLK YMKM*KKKQKQVLQVLQISPLIQS LKIQP*LFTQVVVEKLL*VRLHYLK QKNGLEKEYLMVNQKE*ILQIM*EII CMKIIQTVL*LKMTKIISPKNKILI*V TVACLTAIPTILMRYIMIQDISQKINL ILVLSQY*RMLKIKKTLVFPK*YPM* KMQMHTHKL*MKIFALRNL*LALH PAKIKMQPLNCPYLIVILR*GHLHL G*PVVKSFVFHMKQLKK*KTYLQT VSVK*LRKTTRINQKFAKRKLWQV VTRHWMIQRIFFITL*IMMNVARIH RFLLTFRVKKFYINITKICLDWRKFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KYHLVMLVWKLQIYVNVV*GSFIS QSHLQILVGFLAQQVENLSRYQML HYKTQDKCFLK*KIVPSKSFPKYCL KVTNIQTSSQEKKILLYVLQNI*YPK KAFHIMW*IHLSDLVQQVESKFP F*KVPYTKLREC*RNLI*SELSIVFTI HLRLDKMYQKYFLVLIRETQSTV*T QKWKKPAVKNLNYQIT*MLKVVL QKIITLLKFLHISLNFNKTNSWY*E PKSHLLRTFMFWEKNRLHLKT*KW KLVKLKFLMFL*KQI*KFVLLTPKI QKTTLKQKQ*KLLKLLWKMMN*QI LNCQVMPHILFLHVPKMRKWFCQI QELEKEEESPLS*WENPQSKETY*M NLTG**KIKKNP*RLQKALQMAQ*K IEDCLCIMFL*SRLPVYPFAQLRNVK RYRIQILPHLVKNFCLNLICMNI*LW KNLQAI*QFQDIHFIKFLQEMKK*D T*LLQADQPKSLFHLLKLNRIFTLN SVLGILTWRTDKSKTLMMDALMI VKIRLMTMRFISLTKTTPIKQQL*LS QSVKKNL*I*LQVFRMPEIYRICELR RNKGNASFHSQAVCILPATTTQNSV ALKNAGLISTLKKKTNKFYAIHDE TSYKGKKIPKDQKSELINCSAQFEA NAFEAPLTFANADSGLLHSSVKRSC SQNDSEPTLSLTSSFGTILRKCSRN ETCNNNTVISQDL DYKEAKCNKEKL QLFITPEADSLSCLQEGQCENDPKS KKVSDIKEEVLAACHPVQHSKVE YSDTDFQSQSLLYDHENASTLILT PTSKDVLSNLVMISRGKESYKMSD KLKGNNYESDVELTKNIPMEKNQD VCALNENYKNVELLPPEKYMVRAS PSRKVQFNQNTNLRVIQKNQEETTS ISKITVNPDSSEELFSDNENNFVFQVA NERNNLALGNTKELHETDLTCVNE PIFKNSTMVLYGDTGDKQATQVSIK KDLVYVLAEEKNSVKQHIKMTLG QDLKSDISLNIDKIPEKNNDYMDKW AGLLGPISNHSFGGSFRTASNKEIKL SEHNIKKSKMFFKDIEEQYPTSLAC VEIVNTLALDNQKKLSKPOSINTVS AHLQSSVVVSDCKNSHITPQMLFSK QDFNSNHNLTSPQKAEITELSTILEE SGSQFEFTQFRKPSYILQKSTFEVPE NQMTILKTTSEECRDADLHVIMNAP SIGQVDSSKQFEGTVEIKRKFAGLL KND CNKSASGYLTDENEVGFRGFY SAHGTKLNVSTEALQKAVKLFS DIE NISEETSAEVHPISLSSSKCHDSVVS MFKIENHNDKTVSEKNNKCQLILQ NNIEMTTGTFVEEITENYKRNTENE DNKYTAASRNSHNLEFDGSDSSKN DTVCIHKDETDLLFTDQHNI CLKLS GQFMKEGNTQIKEDLSDLTFLEVAK AQEACHGNTSNKEQLTATKTEQNI KDFETSDTFFQTASGKNISVAKESF

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						NKIVNFFDQKPEELHNFSLNSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPCKKE MQNSLNNDKNLVSIE TVVPPKLLSD NLCRQTENLKTSKSIFLKVKVHENV EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDGKNHNSASN LSESSSRPSSLCVFS*TAVYVWRF* TLHKN*QKCRVFSVS/TLKIILVRK VYGLEKEYSWLMVDGSPMMER LEKKNFIGLCVTLQVWQSLFLEFGF IITIDGSYGNWQLWNVPFLRNLLID A*AQKGCFFN*NTDMIRKLIEAEDR L*KR*WKGMTQLQKHLFSVFLT*FH *AQIYLKLLAIKL VVQIPKKWPLL LQMGMMLLRPS*ILPS*LS*RMAD* QLVRRLLFFMEQNWWALLMPVHLL KPQNLLC*RFLTLVLGLLAGIPNLDS FLTDLFLCPYHRFSVMEEMLVVL M*LFKEHTLYSGWRRHLDYTYFA MKERKKRKQQNMWRPNKRD*KPY SLKFRRLKNMKTQQNHIYHHVH *QDSKFVLCKMVQSFMKQ*RMQQT QLTRVISVKSS*EP*IITGKC*MIRN KLRSSWKLGRPWNLLNKRNVYQ GMSQPWGSCVL*AIQKKKKIQLY*V FGVHHQIYILC*QKERDTEFIILQLQ NLKVNKLKELTYS*QRQKKLSINNYR FQMKFYFRFTSHGSPFTSANF*IQTF SHLVLRWT**DLSFLL*KKQDLPLSS ICQTNVTIYWQ*SFG*TLMRLLSLI C*LLQATSSGDQNPNAFLLYLEIF LCFLLVQKRATFKRHSTK*KILLRIL TYFAMKQKTSLCIYCMQMIPSGPPQ LKTVLQGRLLKSFLVQETSF*CLLL IVRYIIKVLVYHFVWPKGSLFPHLSQP R*LQSLVKGRKRLMTKRTAKREEP WIS*VDCLYLHLLVPFVHLFLRLHR RHFHQGVVAPNTKHP*RKKN*ILL R*LHLKNSMKFLFWKVIQ*LTKNLH **IPKLFCLVQEQKNNLYLSVNPLGL LPPVQKIISD*NDVVLHL*SKNRRVP RPVRKNVRKISRTQLQLKNIS
3049	8546	A	3308	1	9344	
3050	8547	A	3309	1	18345	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSIFYSNHDESLKKNDRIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVP SLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSHKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFS DNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKND CNKSASG YLT DENEVGRGFYSAHGTKLNV TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTTFVE EITDACRKDSVKMIQAKKFKQI*KK RSWLQHVTQYNIQKWNTVILTFNP RKVFYMMKMPALLF*LLLPRMFC QT*S*FLEAKNHTKCQTSSKVTIMN LMLN*PKIFPWKRIMYVL*MKIHK TLSCCHLKNT*E*HHLQERYNSTKT QI*E*SKKIKKKLLQFQK*LSIQTLLK NFSQTMRIJLSSK*LMKGILL*EILR

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						NFMKQT*LV*TNPFSTRTPWFYMET QVINKQPKCQLKKIWMFLQRRTKI V*SSI*K*L*VKI*NRTSP*I*IKYQKK IMIT*TNQDS*VQFQITVLEVASEQ LQIRKSSSLNITLRRACSSKILKNNI LLV*LVLKL*IPWH*IIKRN*ASLSQL ILYLHIYRVV*LFLIVKIVI*PLRCYFP SRILIQTI*HLAKRQKLQNFLY*KN QEVSLNLLSLENQATYCRRVHLKC LKTR*LS*RPLLRNAEMLIFMS**MP HRLVR*TAASNLKVQLKNGSLLA C*KMTVTKVLLVI*QMCKMWGLG AFILLMAQN*MFLKLCKKL*NCLV ILRILVRKLLQRYIQ*VYLQVNVML LFQCLR*KIIMIKL*VKKINAN*YYK IILK*LLALLKLLKITREILKMKIT NILLPVEILIT*NLMAVIQVKMILFVF IKMKRTCYLLISTTYVLNYLASL*R RETLRLKKICQI*LFWKLRKLKKHV MVILQIKNS*LLKRSKI*KILRLLIH FFRLQVGKILVSPKSHLIK*ISLIRN QKNCITFP*ILNYILT*ERTKWF*V MRKQT*LNTKY*KKVSQLVLEIN** PSRDNPVMKRSKNLLCWVFIQLA GKKLKLQRNLWTK*KTFLMKKSKV LVKSPVLAINGQRP*STERPVKTLN* HVRPLRSQLPQSVKKCRILSIMIKTL FLLRLWCHLSS*VIYVDKLIKSKHQ KVSF*KLKYMCKM*KKKQKVLQ VTQISPLIQSLKIQP*LFTQVVVEKLL *VRLHYLKQKNGLEKEYLMVNQKE *ILQIM*EIIKMKIQTVL*LKMTKII PKNKILI*VTVACLTAPTILMRYIMI QDISQKINLILVLSQY*RMLKIKKTL VFPK*YPM*KMQMHTHKL*MKIFA LRNL*LALHPAKIKMQPLNCPYLVI ILR*GHLHLG*PVVKSFFVHMKQLK K*KTYLQTVSVK*LRKTTRINQKFA KRKLWQVVTRHWMIQRIFFITL*IM MNVARIHIFLLTFRVKKFYNTKIC LDWRKFLKYHLVMLVWKLQIYVN VV*GSFISQSHLQILVGFLAQQVENL SRYQMLHYKTQDKCFLK*KIVPSKS FPKYCLKVTNIQTSSQEKILLYVL QNI*YPKKAFHIMW*IHLLSLDLKL QEKY*K*R*QIYCCQ*KFS*LRI*WQ *FK*K*YCLYS*R*NLAIY*SAQHM S*IIWPVYEGGKHS*RRFVRNFNFG SCSSRSMSW*YFK*RTVNCY*NGA KYKRF*DF*YIFSDCKWEKY*CRQR VI**NCKFL*SETRRIA*LFLKF*ITF* HKKEQNGHSLK*GNRHS*TQNLKE SVPVGTGNQLVTFQGGPERDEKIKE PTLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDELAETIEITAAPCKKE MQNSLNNDKNLVSIEIVPPKLLSD NLCRQTENLKTSKIFLKVKVHENV

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						EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDQPERINTADYVGNLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYND SGYLSKNK LD SGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFVEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNMMSGLEKVS KISPCDVSLTSDICKCSIGKLHKS VSSANTCGIFSTASGKSVQVSDASLQ NARQVFSEIEDSTKQVFSKVLFSKNEHS DQLTREENTAIRTPHEHLISQKGFSYN VVNSSAFSGFSTASGKQVSILESSLH KVKGVLEEFDLIRTEHSLHYSPTSR QNVSKILPRVDKRNPEHCVNSEME KTCSKEFKLSNNLNVEGGSSENNHS IKVSPYLSQFQQDKQQLVLGTVSL VENIHVLGKEQASPKNVKMEIGKTE TFSDVPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDELTD SKLPSH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEP SIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHVV SLEPITCVPFRRTTKERQEIQNPNTA PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR PTKVFVPPFKTKSHFHRVEQCVRNI NLEENRQKQNI DGHGSDDSKNIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTE DYFGKESLW TGKGIQLADGGWLIPSN DGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWKLAAMECAFPKEFANRCL SPERVLLQLKYRSTASGKQVSILESS LHKVKGVLEEFDLIRTEHSLHYSPT SRQNVSKILPRVDKRNPEHCVNSEM EKTCSKEFKLSNNLNVEGGSSENNHS SIKVSPYLSQFQQDKQQLVLGTVS LVENIHVLGKEQASPKNVKMEIGKT ETFS DVPVKTNIEVCSTYSKDSENY FETEAVEIAKAFMEDDELTD SKLPS HATHSLFTCPENEEMVLSNSRIGKR RGEPLILVGEP SIKRNLLNEFDRIEN QEKSLKASKSTPDGTIKDRRLFMHH VSLEPITCVPFRRTTKERQEIQNPNT APGQEFLSKSHLYEHLTLEKSSSNL AVSGHPFYQVSATRNEKMRHLITT GRPTKVFVPPFKTKSHFHRVEQCVR NINLEENRQKQNI DGHGSDDSKNIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QRQRVFPQPGSLYLAKTSTLPRISLK AAVGGQVPSACSHKQLYTYGVSKH CIKINSKNAESFQFHTEDYFGKESL WTGKGIQLADGGWLIPSNDGKAGK EEFYRALCDTPGVDPKLISRIWVYN HYRWIIWKLAAMECAFPKEFANRC LSPERVLLQLKYRYDTEIDRSRRSAI KKIMERDDTAAKTLVLCVSDIISLS ANISETSSNKTSSADTQKVAIHELTD GWYAVKAQLDPPLLAVLKNGRLT VGQKIILHGAELVGSPDACPTEAP ESLMLKISANSTRPARWYTKLGFFP DPRPFPLPLSSLFSDGGNVGCVDVII QRAYPIQWMEKTSSGLYIFRNEREE EKEAAKYVEAQKRLALFTKIQEE FEEHEENTTKPYLPSRALTRQQVRA LQDGAELYEA VKNAADPAYLEGYF SEEQLRALNNHRQMLNDKKQAQIQ LEIRKAMESAEQKEQGLSRDVTTV WKLRIVSYSKKEKDSVLSIWRPSSD LYSLLTEGKRYRIYHLATSKSKSKS ERANIQLAATKKTQYQQLPVSEIL FQIYQPREPLHFSKFLDPDFQPCSE VDLIGFVVS VVKKTGLAPFVYLSDE CYNLLAIKFWIDLNEDIKPHMLIAA SNLQWRPESKSGLLTLFAGDFS VFS ASPKEGHFQETFNKMKN TVENIDIL CNEAENKLMHILHANDPKWSTPTK DCTSGPYTAQIIPGTGNKLLMSSPN CEIYYQSPLSLCMAKRKSVSTPVSA QMTSKSCKGEKEIDDQKNCKKRA LDFLSRLPLPPVSPICTFVSPAQK AFQPPRSCGTKYETPIKKKELNSPQ MTPFKKFNEISLLESNSIADEELALI NTQALLSGSTGEKQFISVSESTRTAP TSSDYLR LKRRCTTSLIKEQESSQA STEECEKNKQDTITTKKYI
3051	8548	A	3310	1	7988	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESLH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKS VVCGSLFHTPKFVKGRQTP KHISESLGAEVDPMDSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTS GNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCR TKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVP SLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKDFLTSENSLPRISL PKSEKPLNEETV VNKRDDEEQHLESH TDCILAVKQAISGTS PVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYIAIHDETFYKGGKIP KDQKSELINCSAQFEANAFAEPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVS DIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFSDNENNFFVQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIEKNNNDYMNKWAGLLGPISNH SFGGSFRASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTT EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGTKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDLL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKELFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNL VSI ETVVPPKLLSDNLCRQTENLKTSKSI FLKVKVHENVETAKSPATCYTN QSPYSVIENSALAFYTSCS*KSQNIK KYLFES*ST*KCRKRNSKKSCNLLH KSVPLFSH*KFSLSLHKL*RKTSVS QTSLLLEAKKWLREGIFDGQPERINT ADYVGNYLYENNSNSTIAENDKNH LSEKQDTYLSNSSMSNSYSYHSDEV YNDSGYLSKNKLD SGIEPVLKNVED QKNTSFSKVISNVKDANAYPQTVN EDICVEELVTSSSPCKNKNAIKLSI SNSNNFEVGPPAFRIASGKIVCVSHE TIKKVKDIFTDSFSKVIKENNENKSK ICQTKIMAGCYEALDDSEDILHNSL DNDECSTHSHKVFADIQSEILQHN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QNMSSGLEKVSISKISPCDVSLTSDIC KCSIGKLHKSVSANTCGIFSTASGK SVQVSDASLQNAQVFSEIEDSTKQ VFSKVLFSKNEHSDQLTREENTAIR TPEHLISQKGFSSYNVNSSAFSGFST ASGKQVSILESSLHKVKGVLVEEDLI RTEHSLHYSPTSQRNVSKILPRVDK RNPEHCVNSEMEKTCSEFKLSNNL NVEGGSSENNHSIKVSPYLSQFQQD KQQLVLGTVKSLVENIHVLGKEQA SPKNVKMEIGKTETFSQVVPKTNIE VCSTYSKDSSENYFETEAVEIAKAFM EDDELTDKSLPSHATHSLFTCPENE EMVLSNSRIGKRRGEPLILVGESIK RNLLNEFDRIENQEKSILKASKSTPD GTIKDRRLFVHHVSLEPITCVPFRTT KERQEIQNPNTAPGQEFSLKSHLY EHLTLEKSSSNLAVSGHPFYQVSGN KNGKMRKLITGRPTKVFPFPKTK SHFHRVEQCVRNINLEGNRQKQID GHGSDDSKNKINDNEIHQFNKNS NQAAAVTFTKCEEEPLDLITSLQNA RDIQDMRIKKQRQVFPQPSGLYL AKTSTLPRISLKAAGVGGQVPSACSH KQLYTYGVSKHCIKINSKNAESFQF HTEDYFGKESLWTGKGIQLADGGW LIPSNDGKAGKEEFYRALCDVKAT
3052	8549	A	3311	1	14305	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETFYKGGKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSQDFQSQK SLLYDHENASTLILTPTSKDVLNVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDS LFSNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKSSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEGFRGFYSAHGKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDLL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNLVS ETVVPKLLSDNLCRQTENLKTSKSI FLKVKVHENVETAKSPATCYTN QSPYSVIENSALAFYTSCSRKTSVSQ TSLEAKKWLREGIFDGQPERINTA DYVGNYLYENNSNSTIAENDKNHL SEKQDTYLSNSSMSNSYSYHSDEVY NDSGYLSKNKLDGIEPVLKNVEDQ KNTSFSKVISNVKDANAYPQTVNE DICVEELVTSSSPCKNKNAAIKLSIS NSNNFEVGPPAFRIASGKIVCVSHET IKKVKDIFTDSFSKVIKENNENKSKI CQTKIMAGCYEALDDSEDILHNSLD NDECSTHSHKVFADIQSEELQHNQ NMSGLEKVSISPDCDVSLETSICKC SIGKLHKS SVSSANTCGIFSTASGKSV QVSDASLQNAQVFSEIEDSTKQVF SKVLFKSNEHSDQLTRENTAIRTP HLISQKGFSYNVNVSSAFSGFSTAS GKQVSILESSLHKVKGVL EEFDLIRT EHLHYSPTS RQNVSKILPRVDKRN PEHCVNSEMEKTCSKEFKLSNNLN VEGGSSENNHSIKVSPYLSQFQQDK QQLVLGTKVSLVENIHVLGKEQASP KNVKMEIGKTETFS DVPVKTNIEVC STYSKDS ENYFETEAVEIAKAFMED

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DELTDSKLPSHATHSLFTCPENEEM VLSNSRIGKRRGEPLILVGEPSIKRN LLNEFDRIENQEKSLKASKSTPDGT IKDRRLFMHHVSLEPITCVPFRTTKE RQEIQNPNTAPGQEFLSKSHLYEH LTLEKSSSNLAVSGHPFYQVSATRN EKMRHLITTGRPTKVFPVPPFKTKSH FHRVEQCVRNINLEENRQKQONIDGH GSDDSKNKINDNEIHQFNKNSNQ AAAVTFTKCEEEPLDLITSLQNARDI QDMRIKKKQQRQVFPQPGSLYLAK TSTLPRISLKAAVGGQVPSACSHKQ LYTYGVSKHCIKINSKNAESFQFH/T *RLF*W*GKFMDWKRNTVG*WWM AHTLQ*WKGWKRRIL*GSV*HSRC GSKAYF*NLGL*SL*MDHMETGSY GMCLS*GIC**MPKPRKGASSTKIQI *YGN**KQKITNILLPVEILIT*NLMA VIQVKMILFVFIKMKRTCYLLISTTY VLNYLASL*RRETLRLKKICQI*LFW KLRKLKKHVMVILQIKNS*LLKRS KI*KILRLLIHFFRLQVGKILVSPKSH LIKL*ISLIRNQKNCITFP*ILNYILT*E RTKWTF*VMRKQT*LNTKY*KKVS QLVLEIN**PSRDNPVNMKRSKNLL CWVFIQLAGKKLKLQRNLWTK*KT FLMKKSKVLVKSPVLAINQRP*ST ERPVKTLN*HVRPLRSQLPQSVKKC RILSIMIKTLFLLRLWCHLSS*VIYV DKLKISKHQKVSF*KLKYMKM*KK KQKQVLQLVTQISPLIQSLKIQP*LF TQVVVEKLL*VRLHYLKQKNGLEK EYLMVNQKE*ILQIM*EHCMIQIT VL*LKMTKIISPKNKILI*VTVACLT APTILMRYIMIQDISQKINLILVLSQ Y*RMLKIKKTLVFPK*YPM*KMQM HTHKL*MKIFALRNL*LALHPAKIK MQPLNCPYLIVILR*GHLHLG*PVV KSFVFMKQLKK*KTYLQTVSVK* LRKTTRINQKFAKRKLWQVVTRHW MIQRIFFITL*IMMNVARIHIFLLTF RVKKFYNTKICLDWRKFLKYHLV MLVWKLQIYVNVV*GSFISQSHLQI LVGFLAQQVENLSRYQMLHYKTQD KCFLK*KIVPSKSFPKYCLKVTNIQT SSQEKKILLYVLQNI*YPKKAFFIM W*IHL*SLDLVQQVESKFPF*KVPY TKLREC*RNLI*FRTEHSLHYSPTF*T KMYQKYFLVLIRETQSTV*TPEMEK TCSKEFKLSNNLNVEGGSSENNHSI KVSPYLSQFQQDKQQLVLGTVKVS VENIHVLGKEQASPKNVKMEIGKTE TFSDVPVKTNIEVCSTYSKDSSENYF ETEAVEIAKAFMEDDELTDKLP SHATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEPSIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKE RQEIQNPNTA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR PTKVFPVPPFKTKSHFHRVEQCVRNI NLEENRQKQNIIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEYFGKESLW TGKGIQLADGGWLIPSNDGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWKLAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRSAIK KIMERDDTAAKTLVLCVSDIISLSA NISETSSNKTSSADTQKVAIIELTDG WYAVKAQLDPPLLAVLKNGRLTV GQKIILHGAELVGSPDACTPLEAPES LMLKISANSTRPARWYTKLGFFPDP RPFPLPLSSLFSDGGNVGCVDVIIQR AYPIQWMEKTSSGLYIFRNEREEEEK EAAKYVEAQQRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRALQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVILSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSEILFQI YQPREPLHFSKFLDPDFQPSCEVDL IGFVVSVVKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASNL QWRPESKSGLLTLFAGDFS VFSASP KEGHFQETFNKMKNTVENIDILCNE AENKLMHILHANDPKWSTPTKDCT SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKKRRALDF LSRLPLPPVSPICTFVSPAQAQAFQ PPRSCGTKYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRAPTSSSE DYLRLKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI
3053	8550	A	3312	11089	17637	NHCHRFHLEWMPWCGCRSPSGPRH VNQKPEELHNFSLNSELHSDIRKNK MDILSYEETDIVKHKILKESVPVGT GNQLVTFQGQPERDEKIKEPTLLGF HTASGKKVKIAKESLDKVNLFDE KEQGTSEITSFSHQWAKTLKYREAC KDLELACETIEITAAPKCKEMQNSL NNDKNLVSIVTVPPKLLSDNLRCRQ TENLKTSKIFLKVKVHENVEKETA KSPATCYTNQSPYSVIENSALAFYTS CSRKTSVSQTSLLAEKKWLREGIFD GQPERINTADYVGNLYENNSNSTI AENDKNHLSEKQDTYLSNSSMSNS YSYHSDEVYNDSGYLSKNKLDSGIE PVLKNVEDQKNTSFSKVISNVKDA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVSDEILFQIY QPREPLHFSKFLDPDFQSPSCSEVDLI GFVVSVVKKTVRNEEASETVFPHD TTANVKSYSFNHDESLKKNDRIAS VTDSENTNQREAASHGFGKTSNGSF KVNSCKDHIGKSMPNVLEDEVYET VVDTSEEDSFSLCFSKCRTKNLQKV RTSKTRKKIFHEANADECEKSKNQV KEKYSFVSEVEPNDDPLDSNVAH QKPFESGSDKISKEVVP SLACEWSQ LTL SGLNGAQMEKIPLLHISSCDQNI SEKDLLDTENKRKKDFLTSENLPRI \SSLPNPEEPLNEETVVNKRDEEQHL DSHTDCILQ*KQAISGTFPVASSFQG IKKSIFRIRESPKETFNASFSGHMTDP NFKKETEASESGLEIHTVCSQKEDS LCPNLIDNGSWPATTTQNSVALKN AGLISTLKKKTNKFIYAIHDETSYKG KKIPKDQKSELINCSAQFEANAFEA PLTFANADSGLLHSSVKRSCSQNDS EEPTLSLTSSFGTILRKCSRNETCSN NTVISQDL DYKEAKCNKEKLQLFIT PEADSL SCLQEGQCENDPKSKKVSD IKEEV LAAACHPVQHSKVEYS DTF QSQKSLLYDHENASTLILTPTSKDV LSNL VMISRGKESYKMSDKLKGNN YESDVELTKNIPMEKNQDVCALNE NYKNVELLPPEKYM RVASPSRKVQ FNQNTNLRVIQKNQEETTSISKITVN PDSEELFSDNENNFVFQVANERNNL ALGNTKELHETDLTCVNEPIFKNST MVLYGDTGDKQATQVSIKKDLVY VLAENKNSVKQHIKMTLGQDLKS DISLNIDKIPEKNNDYMNKWAGLL GPISNHSFGGSFRTASNKEIKLSEHN IKKSKMFFKDIEEQYPTSLACVEIVN TLALDNQKKLSKPQSINTVSAHLQS SVVVS DCKNSHITPQMLFSKQDFNS NHNLTSPQKAEITELSTILEESGSQF EFTQFRKPSYILQKSTFEVPENQMTI LKT TSEECRADLHVIMNAPSIGQV DSSKQFEGTVEIKRK FAGLLKND CN KSASGYLTDENEVGFRGFYSAHGT KLVNSTEALQKAVKLFSDIENISEET SAEVHPISLSSSKCHDSVVS MFKIEN HNDKTVSEKNNKCQLILQNNIEMTT GTFVEEITENYKRNTENEDNKYTAA SRNSHNLEFDGSDSSKNDTVCIHKD ETDLLFTDQHNICLKLSGQFMKEGN TQIKEDLSDLTFLEVAKAQEACHGN TSNKEQLTATKTEQNIKDFETSDTFF QTASGKNISVAKESFNKIVNFFDQK PEELHNFSLNSELHSDIRKNKMDILS YEETDIVKHKILKESVPVGTGNQLV TFQGQPERDEKIKEPTLLGFHTASG KKVKIAKESLDKVKNLDFDEKEQGT SEITSFSHQWAKTLKYREACKDLEL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ACETIEITAAPKCKEMQNSLNNDKN LVSIETVVPKLLSDNLCRQTENLK TSKSIFLKVKVHENVEKETAKSPAT CYTNQSPYSVIENSALAFYTSCSRK TSVSQTSLLLEAKKWLREGIFDGQPE RINTADYVGNLYENNSNSTIAEND KNHLSEKQDTYLSNSSMSNSYSYHS DEVYND SGYLSKNKLD SGIEPVLKN VEDQKNTSFSKVISNVKDANAYPQ TVNEDICVEELVTSSSPCKNKNAAI KLSISNSNFEVGPFAFRIASGKIVC VSHETIKVKDIFTDSFSKVIKENNE NKS KICQTKIMAGCYEALDDSEDIL HNSLDNDECSTHSHKVFADIQSEEIL QHNQNMMSGLEKYSKISPCDVSLETS DICKCSIGKLHKS VSSANTCGIFSTA SGKSVQVSDASLQNAQVFSEIEDS TKQVFSKVLFKSNEHSDQLTREENT AIRTPHEHLISQKGFYNVNVSSAFSG FSTASGKQVSILESSLHKVKGVL EEF DLIRTEHSLHYSPTS RQNVSKILPRV DKRNPEHCVNSEMEKTCSEFKLS NNLNVEGGSSENNHSIKVSPYLSQF QQDKQQLVLGTKVSLVENIHVLGK EQASPKNVKMEIGKTETFS DVPVKT NIEVCSTYSKDSENYFETEAVEIAK AFMEDDEL TSKLPSHATHSLFTCP ENEEMVLSNSRIGKRRGEPLILVGEP SIKRNLNNEFDRIENQE KSLKASKS TPDGTIKDRRLFMHHVSLEPITCVPF RTTKERQEIQNPNTAPGQEF LSKS HLYEHLTLEKSSSNLAVSGHPFYQV SATRNEKMRHLITTGRPTKVFPVPPF KTKSHFHRVEQCVRNINLEENRQK QNIDGHGSDDSKNKINDNEIHQFNK NNSNQAAA VTFTKCEEPLDLITSL QNARDIQDMRIKKKQRQRVFPQPG SLYLAKTSTLPRISLKA AVGGQVPS ACSHKQLYTYGVSKHC IKINSKNAE SFQFHTE DYFGKESLWTGKGIQLAD GGWLIPSN DGKAGKEEFYRALCDT PGVDPKLISRIWVYNHYRWIIWKLA AMECAFPKEFANRCLSPERVLLQLK YRYDTEIDRSRRSAIKKIMERDDTA AKTLVLCVSDIISLSANIS ETSSNKTS SADTQKVAIIELTDGWYAVKAQLD PLAS
3054	8551	A	3313	1	207	CNLCLPDSSDSPASASQVAGKTGLC HHTGVVVFVFLVEMGFHHAGQAGLE LLT*VICVPQPPKALGLQV
3055	8552	A	3314	279	625	SLYVCMHVCMYVFILRRSFALVAQ ARVQWCGLGSLQPPPPGFKRFNSCL SLPTS*DYRRAPPHTNFFVFSAEME FHRVSQDGLYLLTSGDLHPRLASQS AGITGVSHRTRPFL
3056	8553	A	3315	1	418	GSIPPPGVYCVPYPLKHAPAPALP* TRQRGSPQSPGALRAK*HVLLETPO PPGPAPPGARTRTRPESE*SQPGRSP

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						VSRQSLTGADALEGPCLGLATKQPS WPHRCGTSGSSPGWLLARGFQETQ QDCIVPLNAQDIG
3057	8554	A	3316	1	354	GFIPPPGVVYCVPYPLKHAPAPALP* TRQRGSPQSPGALRAK*HVLLETPQ PPGPAPPGARTRTRPESGAWRWVR AGSSPPPPSPHPTPPCFFQVHQGLRS GSANEASLEDPQSRDRA
3058	8555	C	3317	299	365	MSCPECNLTGISSTKNKKLNQ*
3059	8556	A	3318	33	302	PSSWDYRHAPPRLTNF*FLVEMGF HYVG/QAGLELLSSGDPPALASQSA RITGMSR\RAWPK*HNVLRKFTNLS LGHIQNHGPRVGGQAKP
3060	8557	A	3319	3	409	SNFRSNFGYNIPLKHLADRVAMYV HAYTLYSAVRPFGC/SGYWGCAIGK ARQAAKTEIEKLQMKEMTCRDIVK EVAKIIVHDEVKDKAFELELSWV GELTNGRHEIVPKDIREEAKEYAKE SLKEEDESDDDNM
3061	8558	A	3320	1	255	
3062	8559	A	3321	1	395	FGYNIPLNHLPDRVAMYVHAYTLY SAVRPFGCSFMLGSYSVNDGAQLY MIDPSGVSYGYWGCAIGKARQAAK TEIEKLQMKEMTCRDIVKEVAKIIV HDEVKDKAFELELSWVGE\ESLKE EDESDDDNM
3063	8560	A	3322	515	560	
3064	8561	A	3323	3	661	KDGVVLGVRKISPS*TYEEGFQTKR LF*CLIGNVEMA\VAGLLADARSLA DIAREEASNFRSNFG\YTIPLKHLAD RVAMYVHAYTLYSAVRPFGCSFML GSYSVNDGAQLYMIDP\SGVSYGY WG\CAMRQAR\QLAKTELERLQLK KLPSGDIVKEVAKIIVHDEVKDK AFELELSW\VGDLTK*RHEILPK\D\ LRDEAEKYAKESLKEEDESDDDNV
3065	8562	A	3324	3	634	
3066	8563	A	3325	2	487	HIFGKAKEYANSQVVTKDQYAVIC LGGDAVPSASLHVSETMEKT*KK/H RMSHFVTCLTEGRRKCIKPVHYD RVKKITQRKKEIPVVFNLNRVPEALG KCTHADPEAAEGK/LSRAMHFILQS APDIRRELQKILEARPQTPAVDFGR RLLRFSITDRTQMGR
3067	8564	C	3326	373	727	MKPRLWEFSLHREGNTGTTGLDSL LWPPARTTKWAHLTKRNQAQPGY AGPASPTSHVLCAPAQAYLTHDVNS QVSLIKTSLQASSGSXXXXXXXXXX XXXXXXXXXXGAQAFFLGGGFF*
3068	8565	A	3327	2	536	VHLVPRQNACAIRLTEPCPPRLK*FS CLSLPSS/WDSQ/HAPPH/PGS/FCIFR RDGGSPMLS\GWFQTPDLRRSTRLSI PKCWDYRREPPHPVKIFLKLSSFSY WVFPVCALNLSLSLFVYTFLSNLS LLYSSHTGSKLQCYEMLHVETHIPK GEGVLSRVERRKVRLLSHTKPCQFS HESA

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3069	8566	A	3328	3	334	FLRQGL/NSVTQAGVQWGDGLGSLQ PPPPKLGSSHPSPSSCRHYRHTP/ RSG*FFVFL*RWGFAMLPRLV*TS G\PSDMPALASQGAGTTSMSSHHTWR PYLNF GKFP RKKN
3070	8567	A	3329	1	148	PKLKGLCLSFHEGKKRLSYF/CIMA* P*YPLDFGEQWPLHGSHAYSTIL*L DLFCKKEEE*DEIPYV*CFMLLWKS TTM*KKRLSYFLSWLNLNTHWISEN SGHCMVLMMLTVRSCS
3071	8568	A	3330	3	267	FFFFLDRFSLCGPGWSAV/VQS*LT VNS/TFLGPSNPPLSLWSSY/DVR/R MPANLS*FFRS*/SLAMLPRPVLSW PQAIFLRHAPKVLGVEV
3072	8569	A	3331	3	269	FETESHSVTRLECSG/TILAHCNTCL PGSSNSHASASQVAGIAGEHHHAQI IFIFLVETGFHHVQGAGLELLT*VIC LPRPPIVLGLQA
3073	8570	A	3332	1	299	FSLIKISMMLLMKMEK*NLQFIW/KP RRLQIAKARLNASSSSSSSSSSSSSS SSSVVWYWHKKRHIDHWNRLENS NINRHICSQILITKVP GANTKDHP
3074	8571	A	3333	3	261	RQDLSLCHPGWSA VVQS*LIHALTS* \VKQSTYLRHPTSWG*RCVPPCPAN FC\FFCRDRIL/TISPRLVSWAQVIELP QPPKVLGLQV
3075	8572	A	3334	3	290	VDFFFFFFSRRSNVLSHRLECSGTISS HGNLCLLGSSDSPASASQVARITGV HHHTQLIFIFLIETGFRHVDQAGLDL LT*VILPPQPPKMLGLQA
3076	8573	A	3335	3	358	
3077	8574	A	3336	76	386	VLPPPSSPALHSPAPPSTCPYLPGA/P PPLLPPCAGRSPAAAAPHCPAPCA PRH*GSR*LESPAPQGPQSRAARMP AWPLPPAPPTDPTAPPAPRSHWPAA PPT
3078	8575	A	3337	66	381	VLPPPSSPALHSPAPPSTCPYLP GAL PPLE/GPPSRPPRTFIGNPGGQGPGE VSPIVLRSPSQPH*PGNQGPCSSQP PGSPRSEHGC*HRCWALYGQKEKP APS
3079	8576	A	3338	1	303	KDRFSFCGPG*SAVTQLNLTADP*T PALK*SFHRSLLSRWDYRRAPPYLA N*KKFL*SRGLAMLPRLVFHSWPQ VILSPLSRARATAPSFPLFSSKDEPI
3080	8577	A	3339	2	212	RFSCLSLPSSWDMHHSPG*FFIFLVE TGFAHVQGAGLELPASNDPPASTS QSVVITAMSHRRLALVPIF
3081	8578	A	3340	2	273	RRSSTQPRLQCSGTIPAHCNLHPPS PSDYPAPASRVAGTTGARYHHAQPI SAFSSAETGFHHAGQDGLKLLT*AI HPPRPPKVP GPQA
3082	8579	A	3341	135	494	IKHRGMGLDFAVLPLQVKWPPDPG FLECIHFLQLKGTIPDLKERAPVTSR VEPGHAGHC/TSYGQVCHL*GRC/V EKRKGIACDCAFSMYDGLFCSNSNS RADWSHCTVSGTYQHTENSIMS

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3083	8580	C	3342	71	217	MPQPNFFVLLVDRGFHHVDQAGLD LLTSSDSPALASQSARITGVSHHA*
3084	8581	A	3343	1	106	
3085	8582	A	3344	2	1926	MAAAAVDSAMEVVPALAEAAPE VAGLSCLVNLPGEVLEYILCCGSLT AADIGRVSSTCRRLRELQSSGKVW KEQFRVRWPSLMKHYSPTDYVNW LEEYKVRQKAGLEARKIVASFSCR FSEHVPCNGFSDIENLEGPEIFFEDEL VCILNMEGRKALTWKYYAKKILYY LRQQKILNNLKAFLQPPDDYESYLE GAVYIDQYCNPLSDISLKDIQAQIDS IVELVCKTLRGINSRHPSLAFKAGES SMIMEIELQSQVLDAMNYVLYDQL KFKGNRMDYYNALNLYMHQVLR RTGIPISMSLLYLTARQLGVPLEPV NFP SHFLLRWCCGAEGATLADIFDYI YIDAFGKGKQLTVKECEYLIGQHVT AALYG\VVNVKKVLQRMVGNLLSL GKREGIDQSYQLLRDSL DLYLAM Y PDQVQLLLLQARVYFHLG\ILPEKS FCLVLKVL DILQHIQTL\DPGQHGA VG\YL\VQHTLEHIL\ERKKEEVGVE VKLRSDEK\HRD\CY\SFGFIMKA* RGMGY*LC*FYGW\DP\TW HGS GHE LDSRNMNV\HSLPHGHHPFY NVL VEDGSCRYAAQEN\LEYNAEP\QEI SH\PDVGRVYSQRFT\RTHYIP\NAEL \EIRYPEDLEFV\YETVQ\NIYKCKRK ENIE
3086	8583	A	3345	59	339	
3087	8584	A	3346	1	342	FCSCQPQAGVQRRDLSSQLPPLP\GF K*FSCSLSPSSWD\YRRPPP\RPGYFL YYLVEIGFCHICQAGLKLLRSGDPP AWASQSAGITGMSHHAQPHLLLLN CLLPFLGIPLHSPL
3088	8585	A	3347	1	294	ETESHSVT\RLCSGTILAHCNLHLP GSSNSPASASQIAGTIGARHHTWLIF VFFVEMGFHHVGTLELPGLK*SAC LKPLKVLG*QAGVQRHNLGSLQPPP PRFKQFSCSLSPNSWDHRCPTPHLA NFCIFCRDGFPPCWPSRTPWPQVI CLPQASQSAGITGVEPLQPQRSYP
3089	8586	A	3348	2	268	EAESHVA\RLCSDAISAHCNLR LP GLNSPASASRVAGIIGACHHDWLI FVFLVETGFCHVGQAGL/DNS*PQVI HPPRPPKVLGLQA
3090	8587	A	3349	3	444	FFFEIWSGSVA\RLCEGGTIFAHCN L RLLGSSHPPTSAS*VAGTKGTCHHV QLIAFFVDTGFFHHVARLVLS* TQ AICPPRPPKVLGSYASITAPGPTFFFL TIILGVQVDKRFYGNLTRKDIQKLG NYVWEGLELLSPQKFMLKP
3091	8588	A	3350	1	318	FFFFFLRQSFALAQAGM/QWHD LGS LQPPPPGFK*FSYLSLPSSWDYRYVP PRPASFEFLVEMGFHHVGQAGFELL TSSDPPASASQSAGIIGVS*RTQPGT NDFL

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3092	8589	A	3351	16	848	VGSGLVSAQQTGCGPGNPSPPGSVS GAMELRVEPAARGQGS LGDPPA\VL LPGAELPIPGSFFASQSCSPWVML QLTFPHF*LLLAPLPPVSPAPTGWDL VSQLOPVSSPRGRCPRSGPDLLPLH GQPFHSSSFSSSMQASGEVPQPCPS RSSGS/VKGGLQTVESGPGALKC EALAWLRG*GLLGHSGFAGSVPEV TPGSPHVLNP\GRGLPCAGYCLHPA AL*GMVFGLPPLPGSSLV*PTIWLLT LKSPTS*GIP*HRKPWFVSVMHKVG WKV
3093	8590	A	3352	1	293	VLRQGLSLSTQDRMQWHYDSSLQP *TPGLK*SSASQVAATTGTCHHTWL TFLFVF/DFWRWSL/NCIAQAGLE/PP GFK*/CPKHWDYRHEPGMPGWVFLI S
3094	8591	C	3353	127	345	MFDFELELFXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXLI AQGECLYVWKINSQHSVFLLKKL CF*
3095	8592	A	3354	2	215	AHCNLC L PGSSDSPASASRVGTG VHRTQLIFVFLEEMGFCHIGQAGL ELLT*VICLPRPPKVLVLR
3096	8593	A	3355	164	311	QRSQGIWVWRFIRRF*II
3097	8594	A	3356	1	381	YINVIIHFVHINCWRECQKVQLT*K\ SF*QFLKNLNIHLSYDLAIPVLGICPR EMKAYVHIKTCK*MLIAAFHIAQN WNQ/P/RCPSTGEWYKQTVIFYTMQ HYS AIKNNE*LIHKTTWKNLKEARA SGV
3098	8595	A	3357	2	764	RTLLHLFAGGCGGTGVAIFTCPLEVI ETRLQSSRLALRTDYYPHVHLGTIS GAGMARPTSATPGLFHGLKSILEKE GPKSLFRGSRPNLVGVAPSRAVYFA CYSKAKEQFNGIFAPNSNIVHIFSAG SA/GVRGSKQMNTLQCARYVYQTE/ GIRGFYRGLTASYAGISETIICFAIYE SLKKYLKEAPLASSANGTEKNSTSF FGLMAAA/GSF*GLSSCIAY/PHEVIR TRLREETSTSFQCTARLVFREESYL PL
3099	8596	A	3358	155	875	DQHPVTPGLFQVLKAVYFACYSKA KEQFNGIFVPNSNIGHIFPAGSAAFIP NPLMD\PIWMVKTRMQLEQKVRS KQMNTLQCARYVY/HDRKAFGGFY RGLTASYAGISETIICFAIYESLKKY LKEGPLAFFGKWD*GKIPQVFLDL WPAAALSKGL\ASCMAYSHTEVH* GRRL\REKGHPSTKSFCPERRALGVP GEEGYPCLFIEGLFAPSFIRQIP\NTA\ IVLGYLWRLIVYLLGRP
3100	8597	A	3359	1	281	FFFAPETESYSVARLECSGTILVHCT LCLPGSSDSPASASQVAGTTGACHH TWLILVILVEIGFHHVQGAGLG/IS*L QVIRPPWAPKVLGIIG
3101	8598	A	3360	135	218	TLQFTSLISYSFCQSWGSKVPLSLPP

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						P*/PANF/*FLVETGFLQVGQVGLKL LISSDPPTSASQSAGITDVSHCAGPE F
3102	8599	A	3361	198	390	
3103	8600	C	3362	5	316	MPAKLFLMVEFSGVACSSAKXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX YYRLLFSPCHSF*
3104	8601	C	3363	186	323	MPWLEHTAHFPDKAWITRMALLRN GIVPYDSLPLWITLGRWPNGGT*
3105	8602	A	3364	2	3096	TPRLQSNTRALYQYCPPIINYPQLE NELFCNIYYLKQLCDTLRFPDWPIK DPVKLLKDTLDAWKKEVEKKPPM MSIDDAYEVNLNPQGQGPHEDESKIR KAYFRLAQKYHPDKNPEGRDMFEK VNKAYEFLCTKSAKIVDGPDPENIIL ILKTQSILFNRHKEDLQPYKYAGYP MLIRTITMETSDDLLFSKESPLLPAA TELAFTVNCSALNAEELRRENGLE VLQEAFSRCVAVLTRSSKPSDMSVQ VCGYISKCYSVAAQFEECREKITEM PSIIKDLRCRVLYFGKSIPRVAALGVE CVSSFAVDFWLQTHLFQAGILWYL LGFLFNVDYTLSESGIQKSEETNQQ EVANSLAKLSVHALSRLGGYLAEE QATPENPTIRKSLAGMLTPYVARKL AVASVTEILKMLNSNTESPYLIWNN STRAEGLEFLESQQENMIKKGDCDK TYGSEFVYSDHAK*LIVR*IFVRVYN EVPTFQLEDPKAFAASLLDYIGSQA QYLHTFMAITHAAKVESEHQHGDRL PRVEMAFEALRNVIKYNPGSESECI GHCRCIFSLLRVHGAGQVQV/AL* EVVNIVTSNQDCVNNAESMVLSSL LALLHSLPSSRSAFWETLYALDIR VQKLIKEAMAKGALNHLLDMFCNS THPQVRAQTAELFAKMTADKLIGP KVRITLMKFLPSVFMAMDARDNPE AAVHIFEGTHENPELIWNDNSRDK VSTTVREMMLEHFKNQDNPAN WKLPEDFAVVFGEAEGELAVGGVF LRIFIAQPAWVLRKPREFLIALLEKL TELLEKNNPHGETLETLTMTATVCLF SAQPQLADQVPPLGHLPKVIQAMN HRNNAIPKSAIRVIHALSENELCVRA MASLETIGPLMNGMKKRADTVGLA CEAINRMFQKEQSELVAQALKADL VPYLLKLLEGIGLENLADSPAAT*GS ELVKALQGG*LEVLQYGENRVNEIL C/RFLSVWECLSKIQEHDLFIS*/ESH TAGYLTGPGVAGYLTAGTSTSVMS NLPPPVDHEAGDLGYQT
3106	8603	A	3365	1	358	NRLNATPIKIPTAFFAEMDKLNPKFL KLNS*NLRYNARDST*PKQY**RKR TWINKNNAGGLILPYCILLQRNNNQ DIG*KNVLKIM**WHRDRHDQ*NR NQSPEINP*YIGKLFSTVL

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3107	8604	A	3366	2	40	LPRLKQFS\CLSLPSSWDYKR\RP PANF/SVFLVETEFYHVGQAGLELFT SSDLPTLASQIAGITGVSHCAWPE*S AS
3108	8605	A	3367	1	223	IIVKKWKQPKCPPTDEWINKMWDI QAIEYNLAI*/DKVVIHATTCMKLEN IMLSERSQLQRATYCNDAIYIKNPE
3109	8606	A	3368	307	332	TTYHFFF*TESHAAQAGAHWRDLS SLRPPPPGFKPFSCLSWDYRRTPPH PAN\FLAFLADTGLHHAGQAGLKLL TSNDPPTPASQSAGTTGVSHRAQPF FSELPITIFFSL
3110	8607	A	3369	3	411	QTLPSATVSPEQAGAFPLALHSAQE SLGPAQTVPGSTGPPQAPSGPGPPG EPG*ERLCASHKAFISHKQSH*SPQ* PFQGRFDAFPQYKQQTRPGHT/GQK GLRGPRTQTLSTSQPTACSENSQG SQSPKRTLS
3111	8608	A	3370	3	166	EESCSVVQGGVQWCDLS*LQTLPP\ GSSNFCASASRVAGITGAHHHAQL KKKMLF
3112	8609	A	3371	4	312	FLR*SFTLIVQAGVQWRYLGLSLQPP PPGFKRLSCLSLPSSWDYRHVPP/*P GYFFVFLVKMGCLHVGQAGPKLLT SGDPAASASQSAGITGPHRTWLRS FLI
3113	8610	A	3372	3	282	FFFETGSNSVAQAGVQWCNHSSLR PRPSG\SSDPPNSSSQVAWTTGVHH TQLLFKFFCKDEVSLCFDWSQTV* RVEHIRDEYETTQHCLYPSN
3114	8611	A	3373	1	164	ETEFRSVAQAGVQWRDLGSLQPPPS GFK*SSCV/SLPSTWDYRYMPPCPA TLLNT
3115	8612	A	3374	1	114	ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS
3116	8613	A	3375	363	1246	DTEQIYCIQEPEYGGKKYCTKQSRS YVSWTTHFSSSFIDQSLLSESMA*KS TAPHSSDF*DFLT*KT*NLFFFLRRSL ALSPQAGVQWRDLGSLQAPPPGFTP FSC\ASPSSW\DYRHLPPCPANFFVF FLVETVSIFVFTVLAGMVISI*PQ/CD PPTLASQSAGITRLSHRAR\LCFVF* KKRNAREGGRLLTIKADFLIFFSFF FEMESCSVSKAGVEWHGLSSL*ALP HRFTPFSCLSLLSSWDYRRPPQLA NF\CIFSRDEVSPC*PGWSGSPDLVIH LPWPPKVLGLHA
3117	8614	A	3376	3	324	DRISLCCPGWSAIVQSQLTAA\SPLG LKQSFYISLPSS*GHLAPLHPANIF GFPL*KWGLPMLPMLVLNSWAQVI LPKCWGLQASATVPGLFINFYDYIM DQSSFN
3118	8615	A	3377	3	673	RWSHSVQAGVQWRDLSSRQPPPP GSRDSPASAS*VAGTTGTTHHAQFF FFFFFLRRS/LSSV/SQDGVQWHDH SLQPVPPGFKQFSCLSLPSSWDYRC AAPRPANFFVF**RRVFSTLARLVSI

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						S*PCDLPTLASQTAGITGVSHCTQLA KFCIFS*DGVCHVGQAGAVLILCLF LHSKINMFSPLHCTPASTVYSHLPQ RPTRKRLYIRWRWERTWPANAEL
3119	8616	A	3378	2	323	RRSFTLVAAQAGVRWHILGSLQPLPP GFKRFSCLSLPSGWDYRLMPPCPAN F*FLVEMRFHHVGQAGPERLTSGD LPA*ASQSAGITGVATATPSQYKLCSL IIMKLN
3120	8617	A	3379	1	311	DFFF*ETASHSVTQAGVQWCDPSSL QPPPPVFKQSSCLSLPSSWDYRHVP PCSVDT/CISILLIPFLRSGE*SPLLS WSSCDLGQGTAPLGFWFPMGKARP V
3121	8618	A	3380	3	404	PCLANFF/VFFVETGTHYAA*CGLRL LGSSALPV*TS*SAGIIGMSHCTC/LQ ITLLKTESHSVAQAEVQWHDLGSL QPLTPRFKRFSCLSLPSRWYRCAS PRLANFCTFKFLYFLVETGVSPCWP GWSGTPDLR
3122	8619	A	3381	739	1003	NLYLNY/CFF*IETGSHSVTQSGMQ WHNLASLQRLPLRLKQTSLSLLSS WDCRHMPNLA/NF/CVLRDKISPF CPGWSQTPGLKQCIEF
3123	8620	A	3383	1	299	ETESGSLPRLECSGTISAHCNLRLL GSSNSPVAS*VAGTGACSHAQLIF VFSVESGFRHVGQAGLNF*PQVIHP PRPRKVLGLLPVSHHTRPISFFL
3124	8621	A	3384	12	336	SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSRLTFSSHSLNMELVQD LTASAPMYSSTRDPP/CLGLPKCW DYKREPPRPAH
3125	8622	A	3385	2	318	FLSSHFLTQSL/DSVAQAGVQWHN LGSLQAPPPGFTPFSCSLPSSWDYR RPPRPANFFVFLVKTGFTVLARM VSL*PHDPPASASQSAGITGVSHW CPANN
3126	8623	A	3386	1	325	ASTAQAGVQWPAAQLQTPPPGFTF FSCSLPSSWDYRRPPSPANFLYF* *RRGFTMLARMVSIS*PCDPPASSQ SAGITGLSHRAPVIRILRRAGRNT IGGLD
3127	8624	A	3387	3	530	RQSL/DSVAQAGVQWRNLGSLQVL PPGFMPFSCSLPSSWDYRRPPRPA /NFFVFLVETGFTRGSS*PRDPPAS ASQSAGITGVSHRTRPKDCYS*RCS YCKVLTRLCFRKLTTGEEAPMP/PF* RQS*CLTSVTLSSAWRSICYDRLVDI QFKILFMKTKLPLFFSQNELYFIIL
3128	8625	A	3388	3732	4979	NFVFLYLRELSSQAASLTSHPLSNFF FKRQGLAMLPRLECS/GLFTGAVIA HYSLLQLLGSSNPASANQVAGTTGA CYHAQSIF*S*NFFIFLSSVS*NLCLN QNAGFYLLFFYF*Y*MCRYASSTFLT NELCGKKK*TLSIEIKSIFFKHHVLY WLFGLVFLNLLLILPVLNEHRKIL

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						E*GRKVYQDILPGFGCKF*RMVFLIF VHIL*APRYPSQ*GKLIPCI*LLYL*W LSPSPSTVSLAFHDKFVNLHFYIDMS LFHGQACSIKMIFLKDVNCA*LIGYI LFCFFFFFFFFLRCGV\SVAQAGVQ WRNLGSL\QAPPPRFMPFS\CLSLPS SWDYRRLPPRPANFFFFFLDF**RPL VFL/SFTVLARMGL\IS*PRDLPTSAS QSAGITG\VSHHVQLPYFVLNKFV LGSNSGF
3129	8626	A	3389	1	585	AFFFFLRQGLALV/THAGVQGQDYS SLQPLPPGLKAILLPQPECWDYRC MSPCLA/N/FFVFFVAMGFRMLPTL/ VLELLGSSDPPTLAS*SAGITGVSHC TWPLFI*VWSFGKV*ELS*HRFCISSF IHI*KFWKRWG\SLCSPGWS*TAGL KRSS*LGLPKYRDYRHEPPCPAFFTF LLECYDLHILLICSHFYLR
3130	8627	A	3390	3	459	QPGVQWHDLSMQPPPRFKCFSC SLL/SS*DYRCPAPMPQPNFCIFI*RY GFT\MLASLVLD*L*VIRPPWVSQS AGITGVSHHTWARDRADF*MGVW ASPIARVPRGQQVRSCQPL*GS/WDP ET*HNGHFHFWIKQSEPPIFKGRR*N P
3131	8628	A	3391	1	258	FFFKTDSCSVA\RLYESGAISAHCNL RLPGSSDSPALAPQITGTTGMC/RS* FFIFLVETGFHHIGQAGLKLLTLWIH CPPKMLGLQA
3132	8629	A	3392	3	316	VAQAGVQWWYLSSLQPPPPGFTSC LSPQCSWDYRHAPPCSANF*FLVET GFHHDGQAGLELLTSSDPPALASQS AGITGVHPPAPNSSCLHTDKRVHT WHKPS
3133	8630	B	3393	49	279	SSSDSDDEEKKHEKLKKALNAEEA RLLHVKETMQIDERKRPNYSMYET REPTTEEMEAYRMKRQRPDDPMAS FLGQ*
3134	8631	A	3394	2	357	
3135	8632	A	3395	1	1765	MSATVVDAVNAAPLSGSKEMSLEE PKKMTREDWRKKKELEEQRKLG NAPAEVDEEGKDINPHIPQYISSVPW YIDPSKRPTLKHQRQPQEKQKQFSS GEWYKRGVKENSIITKYRKACEN CGAMTHKKKDCFERPRRVGAKFTG TNIAPDEHVQPQLMFDYDGKRDRW NGYNPEEHMKIVEEYAKVDLAKRT LKAQKLQEELASGKLVEQANSKPKH QWGEEEPNSQTEKDHNSEDEDEDK YADDIDMPGQNFDSKRRITVRNLRI REDIAKYLRNLDPNSAYYDPKTRA MRENPYANAGKNPDEVSYAGDNF VRYTGDTSISMAQTQLFAWEAYDKG SEVHLQADPTKLELLYKSFVKKE DFKEQQKESILEKYGGQEHLDA PPELLLAQTEDYVEYSRHGTVIKQ QERAVACSKYEEDVKIHNHTHIWGS YWKERRGMKCCSHFSKYSYCTGEAG

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						KEIVNSEECIINEITGEESVKKPQTL MELHQEKLKEKKRRKMKKKKHR KSSSDSDDEEKKHEKLKKALNA*E A\RLHVKETMQ\DERKRPYNSMY *TSRP\IEEEMEA\YRMKRQRPDDPM ASFLGQ
3136	8633	C	3396	106	426	MFLKEPVXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXRLXXXXG*
3137	8634	A	3397	25	435	TKYWLLFFLILILPFFFWRRSRSVT QAGGQWHDLSLQPPPPGFKQFSC LSLPSSWDYRRAPLHLANFYIFSRD/ MDFTMLARLVNSRSQ/CDPLASAS QSAGISGKSQHTRPVLVLLKTYTNS H/SF*VKGLGWEFIL
3138	8635	A	3398	3	320	KTESHSVTQAGAQQDLSSVQSP PGFKRFSCSLSPSNWDYRRVPLHPA NFL*/FLVETGFHHAG*VGLELLTSG DPPTLASQNAGITGVSHCARPIVIFL YLITSR
3139	8636	B	3399	70	199	XMQVTGFGRGQNHNVQGSTPTDAS PRRRDVCTAQTQDSKLVNS*
3140	8637	A	3400	198	397	TKNRNTLSRFLLEAPRVFGPPSP/RP PKP/ASGP*PPIACPAGTHIPCGPYPC CHVGGGWPAQPLAALG
3141	8638	C	3401	164	313	MTLHFQELKSLKFYLNXXXXXXXXXX XGGRFKGSLGGPKFTRACNVKAFS L*
3142	8639	C	3402	165	361	MVKFCANNQGKTKLIFMFFHKESHI IIGRPRAQREKKEKEEGNPNECLLD VSLRTGFSGLPGRV*
3143	8640	C	3403	146	389	MTPISLKGRCRQLGDGKRCSLEDLA LIEGCPHAGRPPPRKSTLEPAFGSPR CQDPVSAMCMTRSPANLDSAERQ APGLGR*
3144	8641	C	3404	157	404	MLSLTSSPLNQGVVSFVHAILKY QGCKPHFIKKLSRXXXXXXXXXXXXX XXKXXXXXXXXXXXXXXXXXXXXXP PAPSFLWGEG*
3145	8642	C	3405	73	252	MHTPLLAWPGMAWCYRQPLSTPRL ILNYVKPRKMIFRTFAYIRLYLCTYF AVFHRRKWP*
3146	8643	A	3406	2	617	IYIFLKALNFCREVPISPPPKVRVLF KDSQVTSFPVPAL*KGGQGLGYKT APYKEKTNSLQARVNLGPSRGPLK RPPSSSSSPNPALLFIQTRVKLVNG KRPEATCLGRKASYSVRFSAAWDP\ PAGCAQPPTVSPDTPKQVSRTKAR N*TKNRNTLSRFPS*KLPRVSGPTQV PNPPKPRSRGD*QRTFPFPVPDGNPV LN
3147	8644	C	3407	129	281	MSSHARVNLGPSKDPLKRPPXXXXX XTQRQLFKTFINRCLQFVDFFEKIKL *
3148	8645	A	3408	1	303	QAGVHWRNLG\SLQPPPPPTLRRFS

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						CLSLPSSWDYRHPPSHPANFFFFLL LVEARFHHVGGGLELLTSSDPSTS ALQIAGITGVSHRAEPAPFFK*CFG
3149	8646	A	3409	3	1039	QQPFVNPALPPGYSTGLPYTGM SAFQYGPMTFVPPASAK*HGVNLS PTPPFQQPVGYGQHGYSTGYDDL QGTAAGDYSKGGYAGSSQGTKQV CRFWGLGKGVSVSSSTGLPDMTG SVYNKTQTFDKQGFHAGTPPPFSLP SVLGSTGPLASGAGPWLCTPTIPTH LASPPAAPLTAAAPPSAGCTEWLG SAQPAQLPAAQVSSLQTCRLQSL GQLNPGERGGAGAKAYPGQERTTR ARIWEPKCPFSKNSPTCVSHALCGE SASPDWATVCNVFMYVFNVIEVW GGVGGWRQMLARSAPPHSKPPSPN CSKISTPNPHLPFRSFLHSLATAQWA H
3150	8647	A	3410	2	344	LRQSVSLLPRTQAGVQWPNLGLSQ PPPPRFQRFSCLSLLSSWDYRHAPPC PTKFVFLVETGFTMLARLVIS*PH DLPALASQS/AGITGVSHCAQHGV YIRCFRELA\SYSIL*SLQ\WPHV*SL AYSIL
3151	8648	A	3411	52	174	
3152	8649	A	3412	2	692	RPP/QADPPRCWPR/PLGLGGCVPW GAGRLRRGHGPEPDSPPRRSPRGP ASPQR*PPRPDPWPPRQASPCRPT D*SRTAGRTTDPQEEAVGGQGPSR GG*APSNSSEPPLYGSGPLDSAFSLG TAFRKTLRIDLTSQSRPPHRSLSLYS GKGLAPGELADALNFIYPTDFGL HCTIGDVATGPWRCNQIKRRKHCQ LGKSKLIYFFFPPTPSAKNFFSRY RHHS
3153	8650	A	3413	3	367	MLNYPLDFHPSFFVGGFFFEMESRS\ VARLEVPGVISHCHVCLPGSVSDS PASASQVAGTTGVCH*AQLIFVFLV ETGFHHFDQDGLDLTS*SVHLCPS KCWDYVIHPPQPPKVLGLQA
3154	8651	A	3414	1	595	MGIHHVQGASLELLTSGDLPASASQ GRGVRLYYNEGRSSQSASVTALFLS SLPTVTSAMAGTRPPSARSHQTLQA CRAQKTKTRMSSI*GTGAKHQASSP GKAPLSTSPYFWKPSLQTPCSGSR SLWASLPSPLAALFLCFWQDAT*RS STTRSSLPSWPSRSTRALRLSTS*PE CAPSA*ASSKAGERSTGDRL
3155	8652	A	3415	259	941	PVSWSLNSCRFFFF*QDQLPSVV/Q AGSGQ*RNLDLQPLASRFK*FSSS RL\SSW\DYRHMATMARLIFLVE MGFTMLARLVNFLTSSDPPTSAPF KWLGLQGKPNTRAVGFN**LGY SIILYHSNSPGTDLVFILFIYLFYFL RQEQNSAAQARVQ*WHNLGSLQSP PPGV\H*FLCLSLPSSWDYRCAPPHQ ANFFIFSRDGVSPCWPGWS*TPDLR
3156	8653	A	3416	165	289	ISGLSGLYHIDRLIVCNCKQKPTYS

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						*NPGLSW*TDFKCLI
3157	8654	A	3417	3	796	PGPRAPPIRCSPLRSAPRRPST*SAA AWPASAAAGFCPCFYSA PPSSTSSR WPAAAGCSLATTAKTSSRVVEMLP RRAAAAGSYEGRAVRA/VMEYAW GAAAA/DHALSVASSILVILFHPLLL RPLCWTPECLSS*EVIGLLALAAV FQIISLGNLPREVHPDLHPSCQAPLS LTSITGAYGFGVGQPRIILTRLCLLL LAASPTTEDGPSGAMPSPGTSTHLP NLGMKCGRKSLPAEMGLPEGRKLF LPGGLWNPIFWPVFHHY
3158	8655	A	3418	2	603	GFFFFKIVLIQDLFPSTPLPSSVHSGD YGDGQDPGSGTRNTFRFCSPSPFPS COLPRPEAHTHANTRNPPSPHLLSF PHQSSEP*EGVKSLEEA*KWGEMA ITP*PTPLWR*LWRTPNSFPLSGQPF STPARPSVPSPIQPKTKHVQQHPPAS T*KTGSVPTSLTPSTGVLGEWPPEDP AKGLMPEGKEEQKAFGP
3159	8656	B	3419	34	375	MLLGRLTSQLLRAVPWASLPRKGA QLELEEMLVPRKMSVSPLESWLTA RCFLPRLDTGTAGTVAPPQSYQCPP SQIGEGAEQGDGADVADAPQIQCKN VLKIRRRKMNHKKYRKL*
3160	8657	A	3420	2	361	YSTSPAGQVGR LSPSQGGPAGAGG DAG/TPGRCPSAPWRAGSRPAASCP DWIPG/PAGHVAPPQSYQCPPSQIGE GPGGTPETQADQVRERPEAHLAEG GAKGSPRRAGRPPRSTCGANESG
3161	8658	A	3421	1	417	RITAATGGKGGARLICPAGR/CLGV CQPSGASFSPAFSQMPSSPCSAPSPI WLGHHW*DCGGAT/CPCGPGIQSG QEAAGREP/GSPGG*RTSSWGPASPP APAGPPCEGERPPYLGRPAMCCKG ARRPGCPALQRRRAKAGGR
3162	8659	A	3422	31	756	GRRALRQAGPGSSREGPGARQRDS RGGEPEGAGLPVLGPF GASERDTA RVGGLGASGRELCWKQSPPCGLGW RREKGSEGRGGTRRPSGPPTTEG AAA*PE/PGTCVPAPLGP/GPPPTDH APGAPDFPAVEGRSLGRRPPALAQ S/P/GSAGQPGLRSPFTH/QPAGPGR GLSPSQGGPAGAGGDAGQEDVRQ PPGELGSRPARFLPQTGLPGPAGTC GLHRNPTQCPPSPDRGKGPKQGG
3163	8660	A	3423	69	258	PRTNRCATNHTPANF*FFVETGLH VAQAGLELLGSSSPALAPKQLVTG ASHHTRPQ*NFLQ
3164	8661	A	3424	8	292	QSFLFLKTRYLLRHP/GWNTVAQ*Q LTVVTSRLN*SFHLSLPSSWAI AVR MPPCPANFLFF/TRDRVSLC*PRLVS NTWVQMILLPQPPEMLGLQA
3165	8662	A	3425	123	357	WGKRPGQGGRNPWGPPLPGGK/PP KKGFLGPFTGRFQGSSPGL*KGPFL KGGP/QF*KPKPGSQNRVFKPKIWE TPLGN

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3166	8663	A	3426	2	311	FHSCYPGWSAMVRSQLTATSASQF K*FSCLS/LPSSWDYKCAPHPANFL FLVEMRFHHVLVRLVLNS*TQVIHL PRPPKVLGITGVRLGAQPCTFFFFYC SSV
3167	8664	A	3427	7	534	TSDFIYKALKLQQEVPAKSHLVQN YRFFFFFFLWWSLAPVAQTGVQWH DLSSLQPPPGFKRFFCLSLPSSWDY RCPPRPANF*FLVETGFHHVDQAG LKHLTSDDPASASPSAGITGVHPRP GQENQDLPGLCVDQLYTENSRRFFSK NYYQTPNFTSRKRDCLKISVFFFA
3168	8665	A	3428	368	688	LTVEFLNLLNLSLVCFIHQTN*IICY FNT/SSSHQNA*YI*EPHVPS*GQRGK ASRQRG*TPPRSGTAASWPRVEK*R EARPQNPAQQTYYVRESPTDASPSS PKMAA
3169	8666	A	3429	1	90	FFVFLSHQRNLCLRRYSRDMAAIHK SKFFL\WPGRVAYAYNPSTLGRRGG QIT*AQEFKCS*AAIHKSKFFL
3170	8667	A	3430	259	331	RNE*LLTRFSPLSLSH*VLGVSMF
3171	8668	A	3431	1	639	LGKFHTFQMSPGGGVGLLSL*SYRN SCLAG/GGCDHMSVHVCIRARGVK VRSKNSNHPTETRK\VLGMRSLT RESSISDSMWLARKQTLHTPVMMQ TPHLTPTI*EEPQRIARPE\DTFMSV/Y YPMQTEHHQTPLDYNRRGTSLLD DEEPIVEDVMMMSSEGRIEDLNEGM DFDTMDIDLPPSKNRIRTE\LKAD FFDPA\ASIMDESVLGVSMF
3172	8669	A	3432	1	354	LETSPLMFTMLDRDMSG/TMGFNEF KELWAVLNGWRQHLSSFDTRSGT VDPQELQKALTMTGFRLSPQAVNSI AKRYSTNGKITFDDYIACCVKLRL TDSFRRRDTAQQFIQCVMSV
3173	8670	A	3433	1	788	MAYPGHPGAGGGYYPGGSPVVKEE NLIRQNDVYVFPVSQYGGAPGGPA FPGQTQESL\YGYFAA\VAGQDGOID ADELQRCLTQSG\IAG\GYKPFNL\ET CRLMVSM\DRDMSGTMGFSIEF\K ELLGLLLEWAGRIQHFI\STDREW EQ*DPQELPEGP*QTMGF*V*VPPGC *ISFAKRYSTNGK\ITFDDYIACCVQ T*GVFTDSFSKTGILAQGGCLLNFI WIDFHFCVHGVFKSLGSCMNVIN DSNWSSPLLVLFAFG
3174	8671	A	3434	6222	7046	RTVTTFLSKDSHGVIYCAQGGKIPDH QNPQCNRKQHPVSTILMLDKASFC QLRK RKHNLSVNCINRNPMSLKN TSWHSSLSVTQRHQQQSKLHFQSGI LLH*PSQNIL/SNI*KCINYC*HCSSV LLSYLFIETESYSVAQAGVQWHDLG LLQLLPLRFKQFSCFSLPSSWDYRS APSCPANFCILVEMGFCHVGQAGL KLLASSDPPALASQSAGITGVSHYT QPCSPFLKSTGLFSCVLSNPYHKG RIYLGRMCFLNSTWHLVKSTLFCPL FI

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3175	8672	A	3435	3	287	SRSVAQAGVRWRDLSSLQPPPPRFK QFSLNFPSSWDYRCAPPRPANFV*I LAEMRFRHVGVGQVLELLTSGDPPA SASQSAGITDTSHCAWPFTF
3176	8673	C	3436	88	303	MTFLESSAVPPHWTGQDGRVCWTG WIPQCQAGSAPEVLECLSTQQVKSL QTLGGAAVSHKTNICLPFTKLW*
3177	8674	C	3437	354	416	MKESPGGELPQTGKKPVFLF*
3178	8675	A	3438	274	460	TLKNLRSAASTLGNPASPAHSSILS CPMRGHCRTL*KCHDWSFRAKMPS PFPQVGIYPPPN
3179	8676	A	3439	480	613	LSFRAKMPSFPFQVGIYPPPN*GPIC LLCFSFLCECVFYRNHLD
3180	8677	A	3440	1	864	YPTTPYQHHPISPPPIPTHNHQKP PTPSHRPQPTQRYTYHHNHTALPI APTRQSNPPHNTHHHTPS/TPRTNSS PPH\HHTLPQRIPPYPPT*HTPQAHS HPAG*RASSQPRRAPSPASRPSPTDP ALRANPLSRSYGSGLPFTFYLHCSN MPKACSPWRPAADMCTARPRFRPF KPDFQGPARRHRTTPETRRFRHGPI SRGEP\PGQPCPSQRKENSTPEFPPA SSGIGRVTDTGRLAAAPSPPLRIRGS EPDSPFESAEGHRRPSRPFRTALAQ SLRNE
3181	8678	A	3441	23	266	EMESHSVTRLECSGAISAHCTLRLP GSSDSPASAS*EAGITGMCTT/ARLIF GFHHVGGAGLKLL/NIVILLPRPPKV LGLQA
3182	8679	A	3442	840	887	
3183	8680	A	3443	127	593	DKATKLTFRSYAAVILKIHVLTW VILFRRKIIRDETLKLLDLISLVGKG QCYRVVFFWFFFFFEMKSHSVTR LECSGAISAHCNLCLPGSSDSPASAS LVAGVTGM*HHTQPIFVFLVATGFH HVGQGWSRTPDIRVIRPPWPPKVLG LQA
3184	8681	A	3444	2	514	FFFFLQSL/DSVAHTGGQ/WGGG/ LQPPPPRFEGFLGLKLLGS*HYK/PP RMANFIFSRDGVFAMLARLVNSS ASSDLPGLASHSAGITGVSHHARPI FSYKEHQSY\GLRACPAPV*PHLSYL QPQPQYFQIRSHTEAPGST/WNFGE DTIQPSTFSFYLT*KIIPILYRVKK
3185	8682	A	3445	2	147	FFFCRD/RSLTMLPRLVLYSWAQVIL PSWPPKMLG*QAQATVPSPPKSIN
3186	8683	A	3446	2	328	TITYRGAKIRITSDSSSETMQAREE* SEIF*VLK/ESSSPH*PKILYSGKLSFK SKGEIK/YF*GKQN/LKEFVSSRPVL QGMLKVVLQREGKLYRSETQTYKK KEKASEKE
3187	8684	A	3447	1	357	GDRVLLCCPG*SADHSSLQS*PSGL KRYFCLGLLSNWKHRCMPPCPANF FNFYFCRDK/SLPMLPRLVSNSWAQ GIFLSQPPVSVGDYRCGAYHALTLFI YGRMGVFAMLAQAGPQTPL
3188	8685	A	3448	2	84	GLTLLPRLVSNSWPQEILLPW/PPKV

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						LKL*AQAGLKLLASGNPPALAPKVL KL
3189	8686	A	3449	1	439	
3190	8687	A	3450	1	552	GNEFSILKSPGSSVFRNGNWPPIGER IPDVAALSMGFSVKEDLSWPGLA ^{AV} GNLFHRPRGYPSWVM\VKSGGTKL ALTPQAVVISYPLENRVYVMVGKAN SVFEDLSVTLRQLRNRLFQENS ^{VLS} SLPLNSLSRNNEVDLLFLSELQVLH DISSLLSRHKHLAKDHSPDLYSLEL AGLDEIGKRY
3191	8688	A	3451	3	1111	ILKSP\GSSVFRNG\NWPPIPRE\RDPP DVAA\LSHGLPL*KKDLSWPGLA ^{VG} NLFHRPRATVMVNVNGVNKLDLP P\GSGIS\YPLENAVPFSLDSVANS\IH SLF\SEETPVVLQLAPSEERVY ^{M/VK} GRANSVFEDLS\VTLRHSRNRLVFK KTLFLSFTPPQILLSRNNEVDLLFLS ELQV\LDISSLSPRKHL\ARDHSPD LYFTGSWAGL\DEIGKALLGEDSEQ FRDASKILVD\ALQKFAD ^{DHVPVFM} VGNPVVELVHCPSHLNTSPPLGKTR DLPLRPKQAQEPQQVPYNLA\YKYN FEYS\VFNMVWLWIM\ALALA\VIIT SYNIWNMDP\GYDSIIYRMTNQKISE WIECYLWPRIRKRGFGNWLFC
3192	8689	A	3452	3	371	MLPLARCSSSCLAPLSTYQTQVK ^{TQ} VHTETCI*MFIAALFII ^{VRR} *KQPKCP SENK\WNKIWHIHTMK*YSATKKN KVLTYATI*MNTENMLSQRSY*QKT T*YLFLLMYMKIQNREMYRYKVD
3193	8690	A	3453	2	318	ETESRSVAQAGVQ*RNLS ^{SLQ} /PLPP GFK*FFSLSLRSSWDYRCMHDA*LI FLFLVETGFCHASQAGLELLTSSDPP ASASQSAKITSMSHHALPLFSNKVT FWDSW
3194	8691	A	3454	33	504	GLHNFLTYKATHISAVWYAVRVEN RSTEQNRVQK*TYMYVVKDAR*VN GNRILF*YC/WNN*IITWRKMNLNL DLTLHRKVYLKWVIDLNVKAKTVS PLGQNITESLHNFGVGKYFLDT*SI/ MPHKFFFNKLDIIRIKIFCS*KDAINK MKKWPGVVAH
3195	8692	A	3455	16	1011	WPVRAQAGQRPVLHTQVASL ^{FAGV} PCVL ^{SHPKKGLLVPPFPSSKKGHLG} KPHCPLPSAGRGAAGLGPLAQ ^{QPV} PAPASPMAPCKPKGLPPLPMG ^{VEPE} ILATMPVLTSHPP/SPEPMQSGN ^{MPP} S/PPSLCAFVPRWSHPPVPGW ^{ARS} CP/ALPAAPPSL*HWTRMQPP ^{FCVPL} RVPWVPSSGARGMKESGLDG ^{QGF} GPTPSASPWGPWFDIRLPGCK ^{QGIL} AFKVTGPPTGFPDFEGKRFK ^{KENKP} PG*LESKAPDTVK*NPPSTNPP ^{PAPA} FLTWDCGAYRGPAGFL ^{LVCQPSLLS} LILKNIDDTLKCVERFEKLT ^{ASKQP} KATVVLARRS
3196	8693	A	3456	1	348	PQQLRCFSFWRKDTKVDWLLN ^{RG}

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						ARWLEKKTRLHRGPWARPRLMRA QREEALRREGGNPPPRGPGGEEAPL LRSSSGRPAR/HQT*QKSGASPSDPR SASR*ALRREGGNPPPRGPGGEEAP LLRSSSGRPARLRPSRSPERHPPTLA PPPARPSCPALPRLSMSAG
3197	8694	A	3457	2	247	PGCTILAHCNLCLSGSSDSPASAS*V TGNNRHAQPCPLI*RTGFCHVG/R MNMLVFNSLTSSDPLEVST*GPQPP KVLGLQA
3198	8695	A	3458	1	515	GLGSLGPAAVPTCPPRSPPP/GSPE GALQCGTLPAGTATPDGHVGVAVP FPPTVAPTRRSRSPSPQSC*WGLQH QLCPGSMEEMHTPHGLALPGASHIV PPTLCAPGGSEGARGI*PPA*AGYAL SLPTQFQTLILHPSCCRPGVP/PINLA AQLPPQVPHAPHAWQLPSAPK
3199	8696	A	3459	2	223	IYISPKALKFCREVGPIPPK\KGSF PKIPR*QIFPPRC*KTGKGQGIKRP IRGKVLRCCKPGLNLGPPRVL
3200	8697	A	3460	2362	2696	
3201	8698	A	3461	1586	2325	SPQRSGAARARPAPHRALLGRVPA RDAGSGRRTRSSRTRCGGCARRWS SISRRRRSSETSAGSWRRLSKPSGPG RWRHCARNTGRRCPWWQISVVP RPSSRP/WLAALAEALKDSGEKPGK GASRPEDLQLIGRLQTRLKEREDIK QLTKKKVEDVPSRVVSVPNLASA KNFLSGDLSSRINAPPITSPSLDPSP SCGRITYKPNQSTDAKTATRTPDGET AQAKEVQQKQGSPPHGFQWFTKYFSF
3202	8699	A	3462	125	489	YYLFFFFFFLRLQSLTLVAQAGGQW RNLSSLQPLPPGFKRFPCLSLSSWD YKCPPP/RPG*FFVFLVETGFHHVAQ AGLELLTLGDPPTSISQSAGITGVSH QARPD*ETLEFQGGDRVNL
3203	8700	A	3463	1503	1511	LFPVPFACPSLNCPSPPPIGVHLPIG*I QRLETPP*EEGRWIPRRTCGPARPGP PPGAPSVTLPPRTVHFHGHAKGIHFR KP/RHPG*CVFILTLDCVHLH*KIND FIDTNFAMKSGYPNRIVRISFLIHT
3204	8701	A	3464	54	593	RTALPAQHVASTWPGRPSRLLLRG GPGAPRSMQTGDSVGRGASKEPN*\ PHSGLPKHPLARSPPQRPSHRAMGQ GSPMPAGPT*TCAQALPPSQDGLD LGNRAGWGCSPECLSKAPGGEGPA QAHPGPNPHTYRKQWCWKLSPGH ALAPSPPRREVALNLNLYSFIVPRDSP RPCIISL
3205	8702	A	3465	2	324	FFFFFLKWSLA/SFAQAGVQWCDLG SLQALPPGFTPFCLSLSSWDYRRP PPHLA/NFFVFLVDMGFTVLARMV SIS*PHDPPALASQSAGITGVSHACP AYNVFKDDG
3206	8703	A	3466	142	413	AQEFKTSLGNAKPCLYKKYKKM SWDYRRPSRPANFSCFLVETGFCH VAPAGLELLGSSNSPT*ASQSAGITG

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						VSHHTRPQIFLLPLSN
3207	8704	A	3467	241	523	NISGSFCMPILTAPLFTVAKRWKQY VPISG*MINKMWYIHTVEYYASKR KIR*/PAAATWMNLEDMMMLSEVSQS LEDKYSMLPFM*SIYVKYLEQSNA
3208	8705	A	3468	137	382	NSAVHQKFISIPNTSLPHSLAILKPQI NSLEEET*PFWCKKSSPVPKMRGER NDDNFHKVLLNVTNVDPQGLRSP KWFCWG
3209	8706	A	3469	2	363	FFFDTESYSVAQAGVQWHDLCSLQ PPPAGFKOFFCLSLPSSQDYRHLP WLANF*FLVETGFHHVGQAGLKL TSSDLPASGSQSAGITGMSQRTLQQ LSLKTTELNRNFCVPYCIINA
3210	8707	A	3470	135	466	GIDTILTLNQ*SLKTRQ*FTLIIF/IFF FFLRWSL/DSVAQAGVQWRDLGSL QAPPRGFTPFSCSLPSSWDYRRPLP RPANFFYF**RRGFTMLARMVISIS*P RDLPAEFL
3211	8708	B	3471	27	21189	MKVSAARLAVILIATALCAPASASP YSSDTPCCFAYIARPLPRAHIKEYF YTSKGCSNPVVFVTRKNRQVCAN PEKKWVREYINLEMSMICSGHHV YPNLPTDSFGLDQFRGNYLHSRDY KNPEAFKGRVLVIGLGNSGSDIAV ELSRLATQVHDVKVLGNKPKVHIIST RSASWVMSRVWDDGYPWDMMYV TRFASFLRNVLPFSISDWLYVQKMN TWFKHENYGLMPLNGSLRKEPVFN DELPSRILCGTSLIKPSVKEFTETSAV FEDGTMFEAIDSVIFATGYDYSYPFL DETIMKSRNNEVTFLKGIFFPLMEK PTLAVIGLVQSLGAAIPTADLQAW WAAKVFANSCTLPTTNEMMDDTD EKMGGKCLKCPYQFRLMGPGKWDG ARNAILTQWNRTVKPTRTRVVSEV QRPHPFYNLLKMLSFPLLLLAVTLT FY*
3212	8709	A	3472	9	339	ITLSLLSFFNLRPSFALLAQAGVHW RDLDLQPPPLRFK*FSYLKSP*RSW DYGHAPPRPANSVLLVETGSLHVSQ GGLILPTSGDPPASASQSAGITGVN CARPPSLFS
3213	8710	A	3473	1	50	
3214	8711	A	3474	1	1256	MAAAAAQGGGGGEPRRTEGVGPG VPGEVEMVKGQPFVGPRTYQLQY IGEGAYGMVSSAYDHVRKTRVAIK KISPFHQTYCQRTLRENQILLRFRH ENVIGIRDILRASTLEAMRDVYVVQ DLMETDLCKLREKPSKLSNDHILLT FLLPDSLAPSSYIH\SANVLHLRS* SPPTWLIQHHLADLKVCGFGLAGIC RSWRHDHTGFLT EYVATRWYRAP EIMLNSKGYTKSIDIWSVG\CILGAE MLSTRAIFP\GKHYLDQLNHILGILG\ SPSQEDLNCIINMKARNYLQSLPSK TKVAWAKLFPKSDFKAL\DLLDRM L\TFNPNKRITVEEALAH\YLEQYY

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						DPTDEPVGEGSPSPFGMELDDLPE RLKELIFQETARFQPGSAGRPPSPR QTSLHPGGWTCPPARPLSRRDC
3215	8712	A	3475	877	1463	LPFTAWP*E/QLQQA VHAGLPQQAK ILFDGGSEIGKILPAFQSGNLSQQLH **IGQRAGRGGRLRIGROGGFSFHQ* DGQQIALH/QGPERVAASGPRWF APAGENPV*WWFRNRQNPLIALRSL PAFQSGNLSQQLH**IGQRAGRGG RIGROGGFSFHQ*DGQQIALHRLA LRELQQA VHAGLPQQAKILFDGGSE IGKIPV*GLLRWPPLPRDVQWDSAP LLRARWGL*GER*PREVPAALQGE* PQALLPGGGEPGWQPAEPHPAGGV HRAGPPGGGCWARAGGHQKHL RPAAGVPPDRGCLLQLGQIPH*AGE QVQAGPGTGQPAGEQAQRGLSGNA GPHQVPAEGDTGHLCD
3216	8713	A	3476	29	1076	EQRDPQDIFSQRKSSAFPPSPEIEILS GGKSLSLQLHTPSPG/QQGETPRGG QQSQH/PCQPGGGVPRYACAGGV PVERTGAQGWVHPALRRARYPDA GVQSHMKPAGDWGPGSNKPAGTD ADAVSGRR*LPKTLPSLGLGKKSPP GVPGHPEYPE/HGGSEALLHEFLLP VSRLH/HGPLYPQMSNGLHHYFVP DGDYEENDDPEKCQL/PLQGE*PQA LLPGGGEPGWKPAEPHPAGGSSPC WAARWEDAGRVLGGHQQKHLR RRGRELWQVPAAGVPPDRGCLLQL GQIPH*AGEQVQAGPGTGQPAGEQ AQRGLSGNAGPHQGPAGEGDTGHL GAQGLIRAAGPHH
3217	8714	A	3477	3	591	ERNYLFFLRWSLTLSSRLRGQWRN LG*MQPPPP\GFKA\FSCSLPSSWD YRRMPPCANFCILVEIGFHCLAKL VLNSRPHDPPTSASQSAGITGVSHR AQT*KGIHLNELCTALAKEGRAWS GR*RAGAATPAP/PAPFTL*PGCIPES WSPMPPPHLPLTALCKATHAGTK HPLTKTVSSCGAVLQPTPQRKD
3218	8715	A	3478	1	235	RDHPGQH/GETPSLRKIEILAGHGVR HL*SQLLGRRLRQENCLNSGGRCSE PRSCHPTLAWAIEQGSVSRKEGHF RLA
3219	8716	A	3479	2	928	RPPRPGTERALPSRLRSRPRVRTETP SPSSSGPPPSRNTGMAPLRR*RV*R GTVPRSG*KGR*PCSRRRRSVPSGR TPALRGTRAPSDQKGKARPPEP APSRPCGSRFCRASRSRTSPRPPTP ARESGNPGRSP\DGGEKAAAQGS*K ESAACSNRAWS*WAA\SPPWITVTR QKRRGTLDPQPNQEDKPGARTLKS EPGKQAKVPERGQEPVKQADFVRS KSFLITPVKPAVDRKQGAFLNFKEG LQGISLSHQNLAAQSALMMEKEL HQLKRASYASTDQPSWMELARKKS QAWSDMPQIIK

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3220	8717	A	3480	1	435	EKINKIRWLPQQNAAHFLGTNDK AIKLWKISERDKKAEGYNLKDEDG RLRDPFRITALRVPILKPMDLMVEA SPRRIFANAHTYHINSISVNSDHETP NIVDIKPANMEELTEVITAAEFHPPH QCNVVFYSSSKGTIRLCDMR
3221	8718	A	3481	204	397	VPILKPMGSYG*EASPRIRIFANAHT YHINSISVNSDHETYL SADDLRNL WHLEITDRSFNIV
3222	8719	A	3482	1	1462	PLRSWLPRLPDSQADIISTVEFNYS GDLAT/GDKGGRVVIFQREQEVLQ PRRALP*SVSSFLSTSCREVWQGCE FSLPFRERIK/GRPHSRGEYNVYS/TA FQSHGTGGFDYLSLEIEEKINKIRW LPQQNAAHFLSTNDKTIKLWKISE RDKRAEGYNLKDEDGRLRDPFRIT ALRVPILKPMDLMVEASPRRIFANA HTYHINSISVNSDHETYL SAR*PGGI NLWHLGNHR*EAFNIVDIKPANME ELTEVITAAEFHPPH QCNVVFYSS SKGTIRLCDMR\SSALCDRHS/KSFFE EPEDPK/SSRSFFS\EIHSIS\DVKF\SH SG\RYM\MTRGLPVRWKVWGPSTW EEAGPVGGPTRVHEYL\RTKL\CSL\ YENDCIFADKFECCWNG\SDSAIMT GSYNNFFRMFDRDTRRDVTL\EASR ESSKPRASLKPRKVCTGGKRRKDEI SVDSLDFN\KKILHTA\WHPVGQCYL PWLATN\NLYIFQDKIN
3223	8720	A	3483	603	659	MCGFFFVFFFWRRSL/DSVTQAGVQ WRDLGSLQPLPPGFKRFSCSLSPSS WDYRRPPCLANFLFLVEMGF/TTV LARLVSNS*PRDLPTSASPSAGITGV S*HASSRL
3224	8721	A	3484	84	202	
3225	8722	A	3485	3	577	ILGFPPFVRWGSHTVAQAGVQWCD HGSLQPRSPGVK*SSHLSLLGSWNH RHATTTTPG*FCFFSRIRSHCVAQAGL *LLTSNHPPALASQTVGITGVSHWT WPNTGFSVLTATNKNLKFHYAISK CLVRAKLSSRLKIEERNKALSAPV VSVSIFDRVLRLLGYSASDWQPEFV ETAVSNFVIYGIFRGQ
3226	8723	A	3486	3	248	SLYIEIPGGALPEGSKDSFAVLLEFA EEQLRADHVFICFHKNFSFLGFEIV RPGHPLVPKRPD ACFMAYTFERESS GEEEE
3227	8724	C	3487	185	340	MDNFCSSLCDFCHQKNLRLVXXX XXXGGRFKGPLEGPKFTRACNELV FSL*
3228	8725	A	3488	1	546	NDRLN*TRELTSHERRRFRPSSRLT DAQ\INWRQVLSAGSLY\IEIPGRR AAEGGARN SFAVLLEFAEGVQLRAD HVL\ICFHKNREGQKPPLL\RTFSFFG LED FEDRGNPLVPKETPDACFHGLT TFERE\SSG\EEEEVGARLRGLGQFP RPGAHLVPKPGWGKEPVDSPHLAL GLSPML

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3229	8726	A	3489	1	526	FFFLERDPCSVTQAGMQWHDLGSL QPPPPGFKWFSCLSFPSSWDYRCPP HPANFCIFSRD/MGFTILARLVSNS*P HDPPTSASQSAGTTGVSHSAWPVC/ LFEIEFHS\VAQAGVQWRDLGSLQP LPPEFK*FSCLSLPSSRDHRHLPPLPA KFHIFSRDRVSPCWPGWS*TPDLR
3230	8727	A	3490	276	735	FFFFFFLRQSFSLSVQAGVQWHNLG SLQPPPPGFRQFSCLSLPSSWDYRHP PPCPANFCIFNRELIIVYLIKTF/IHV GQAGLELLTSGDPPALASQSAGIPG MSHCAQSTH*FLLAQQLFCSIYPSFH AQQVIPRIVTHKRETGSQTLYSIV
3231	8728	A	3491	2	344	FIFIF/NFLRWSL/DSVAQAGAQWRD LGSLQGPPPGFTPVSCSLPSSWDY RCLPPRANFFAFLVETGFTVLARM VSI*PRDPPASAYQSAGITGVTTAP GLLF*INICLAAFYFV
3232	8729	A	3492	109	559	QFLHRLVHDSGEVWMKLV**NTL LAKMVSISWPRDLPASASQSAGITG LIGALVLSVGIYAEVER/HEI*NP*KC LPGSSHPPHPPGRRHVHGLLHWCA GVPP*QPGKH
3233	8730	A	3493	1	593	ETESRSIVQAGVQGRELGSLQTLPP GFTPFSCPSL\SWDYRHPPQHSANFL AFLVETGFTVLARIVSIS*PHDPPAS ASQSAGITGVSHHARPQTGRLLFL FFFFETESCSVTQIGVCSGHDLGSL QLRPPGITPFSCSLPSSWDYRRPRL RPANFFFFVFFSRDGVSLC*PGWSRS PDLVICPPRPPKVLGLQA
3234	8731	A	3494	3	484	RFFFFFFLRRSFT/SVAQAGV*WHDL GSLQPPPPWFR*YLCGLPLNSWDYR RGPPRLVNL CIF/M*R*SFTVLARLV SNSWPQ/CDLPP/SASQGAGNTGVS HARPDEIFYQC*Y*ETEMVRRST TQDRAGSTTVLKLGLQLPEREIVN LALGALVYRNITPN
3235	8732	A	3495	104	288	GEVICGRRRSEVSRCNLVDLEPKGP WGHWQGG*GDRRAGGT*GE/GHL RKKAI*GLQVQGRPRTEGPLGA/PG KGD*PTTEGPRGDARNCDACPRPR ARPVLVW
3236	8733	A	3496	3	641	RPPFFFFFFFRRSL/NSVTQAR LQWHYVLGSLQAPPPGFTLFSCLSLP SSWDHRRPP/RMPG*LFFAFLVETGF QRVSQGWVSIS*PQ/CDPPASGLSKC WGLQGVSHLRPSHLSFLAFFFSET GS\FSVAQAGLQWA\NHSSLQAPSP GFTPFCHSLPSSWDCHRPPRANF /CCIFSRDGVSPC*SGWSRSPVLVIRP PRPPTVLGSQG
3237	8734	A	3497	1	296	VSRRFKQSIPP*AS*GWDHRCVPPAS LANFFFLLEMG\FPMLPRLVLNSWA QVILPSQPSQSAVITGMSHCACLYW LLKTKQIKIKQTGMSKVIKLFPL
3238	8735	A	3498	1	347	KKTGRRKRNMIDYEKKKNKEQEER

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						RKKRKKRKSSSSSSSPEEKKEEKKK KREEEENRKKEEEEE*DK/KEED RRKHESRRRLRAVGDEVINKVCQE LKRTIPVGRDYRPLDPSS
3239	8736	A	3499	2	286	PQPCSLAPNPPRMPPGSF/TPCSPPR SNITL*KQRPPSPPPSPEPPRIAQQRV AQNLTSPRPAAAKPPGWLSTNLSK ALPETPTVAQSPVLFTHF
3240	8737	A	3500	3	954	RPRAGAAGGGGGGSRPSGAHPSRS AC/GCPAGTRPGRAPPAASARPSRS KRGGEERVLEKEEEEDDR*R*R*RR SMCQRRSEVAPSSDRPGRCAPPSP TASGDLRVPRRGSRSPPGTAPGPG *RAGASPGQRHPPGCSWPQ*TRKG EQVFFSFPASVATGPDSPSPVPLPPG KPALPGADGTPFGCPPGRKEKPFDP RSSWNVMGFRSNILLEA*FPEQATA FPRAGN*WQIFAAHAHRCASPACP S\PRASPENLRAPHQGASARPL*GM MDPDGFL/ALSAQPHPCPKPIAPISP KIPQSPGSWTGDTLSPH
3241	8738	C	3501	68	199	MPIIPALWEAQAGGLLRPGVCDQPG QYSKTSSLINKLKNPPSL*
3242	8739	A	3502	11	520	IRVDDFVAHRSRCCVAFPSSTPRSR RRPKRRRRRRRENDPAASSLPAPHL CSVSQSAAGARLVLRPRACGAQAQ RP*LASGLRTSALRRRGHPRAELRS GPQRRQASE/PSPRGVAGARWRR EDG/RPSKRSRMAQREAQQTSPQR GNRPKTSEKCPPEEKAVCRTPG
3243	8740	A	3504	78	595	NQNRLKEAGWRLKLADETSSSSHQ QVCGTHHVSACYS/GSPYS*KHPD SPSPATSRKQNLSTQSCISPMWPCSQ RSICQFGHGGTESQGILLGLLRKAI GSPGKRSAPVQPNWEGNG*EAAW ASSSSPCKVTAPLAPSELPFSKFL RNKKAQRKISHLLEVTVGHLLC
3244	8741	A	3505	2	267	ADLSAEAL*TRREWDDIFKVLKTSS/ LGQPKILYPSKLSLINEASSSSSSSS SS/REFTTRLVL*EMLKGILHMEAQ QYLPS*KHTKV
3245	8742	A	3506	1	323	IAGEVNTPRSVTDRSS*Q/IIQEGIVQ LNSAIH/QTGCTNINRILPLTTAEYTF FSHLYRTFT/KIAHILGHMTHLNKG KRIEIIQSMLSDHNGIQPEISNRKIAG KSPNT
3246	8743	A	3507	3	814	SSGLAGTPFPSEGA VCRSQPG*GSG \SPPLPVGPACWYLP CGP*DQRCPPG SLGPSAEPGS*NLSCPRPMCSPAGT SCPAPV/PDSVTPVLRARGTACLPSP TFPAWSVPRFQPGAAPSSADLVHFFH AASGPSASLSSSLSTKAPSLPLGACL PAGGVT*LFGPPSG/RLWRPP*GLTG GGLVWAAGVHWACLWPGQASGG SIRHVCVAVGVQGAPAQKEGGAGL GKGLGSFACGRPHLPAYFACGRPH LPAYFVLDLPFAKVLNRINI

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3247	8744	C	3508	112	252	MFRSMYNXXXXXXXXXXXXXXXXXX XXXXLGMXXXXXXXXXXXXXGLG F*
3248	8745	A	3509	448	715	FFIISIKIIEFFFFETESCSSVTQTRVQ WFDLGS\LOPPPPGFKQFSCLSLSIS WHYTHVPPHLANYRIFSRDGV*PC WPGWSQTHDLE
3249	8746	A	3510	55	295	SQYAYTKEMESIVNNLPKKKTPGL HSFTGEFYQTFKNEMIL/YIL*FLPEI* SRG/IYPSSSSSSSL*LPKLDKDIHRK EN
3250	8747	A	3511	2	853	DLMCKKMKHLWFLLLVAAPRCV LSQLSSSSSSSSSSSSSSSSSSSSSS DSVRHNSYYWGWVRQPSGKELEW IGSLYFTGTTHYSPSLKSRVTISADT SENQFSLTLTSVTAADTAVYYCARP RNIVGSSSSSSSSSSSSSSSPSTKGPS GFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPA/V LQSSGLYSLSSVGTVPSSSFHGPRT Y\CNCKSQSPATTKVDKGELSPK\A CDKNSTHAPPGPQHLETPWGGPVS LFFFPKKT
3251	8748	A	3512	3	2310	QLLTMDWTWNILFLVAAATGAHSQ VQLVQSGAEVKKPGASVKVSKAS GYTFTNGLAWVRQAPGQGLEWM GWTIASNGKTNYAQKFQGRVTMTT DTSTNTAYMELRSLRSDDTAVYYC AREKDNATGAWFAYWGQGTLT VSSGES*AWYPGIQICSMLEL*ISAF WGRPGLTLAGGREGAKVTQVAPA RCTPNAHEPRHWTLHGPRIDKNR GASAPWAQLCPTPRSHGTTSLAAS KGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGK TYTCNVDPKPSNTKVDKR/VW*EA STGREGVCWKPGSALLPGRTPAVQ PPRAARHAPSVSSPGGL*PPHSCSG RGSSGFFHQAPGRHRLDAPTPGPAH KGAGAGLRPAKSHIREDPAPDLSP QRPNSPLPQLGHLSSQIPVTPNLLS AEPKSCDKTHTCPPCPGKPAQASPS SSRRDRCPRVACIQGQAPAGC*HVV LHLFLAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKF NWWYVDGVEVHNAKTKPREEQYNS TYRVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGGTRGV RGPHGQRPARTLCPESDRCTNLCP YR\QPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMEALHNHY TQKSLSLSLGK
3252	8749	A	3513	1	1677	AEVQLVESGGGLVQPGGSLRLSCA ASGFSFSKAYMNWVRQAPGKGLE WVGRIKTKKDAAGTTDYAAPVKGRF

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						TISRDNSKNTLYLQLNSLRAEDTAV YYCAKDEFSSTRKNFLTGQSKTFAA YYGMDVWGQGTLVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVL QYSGLYSLSSVTVPSSSLGTQ\TYT CNVNHKPSNTKVDKTVELKTPLGD THTCPPCPTP*LALGGPSVFLFPPKP KDTLMISRTPR\VTCVVVDVDPKRT PEGQVPTWYVDGL\EVHKCQDKSR GKEQYNSY\YRVV\SVLTVVHQDW \LNGK\EYK\ICRVSHKSPQAPIEETH LPKPKGSPQNPQVYTLPPSRDELTK NQVSLTCLVKGFYPADIAVELESN GQPGNNFK\TPPVLDSDGSFFLYSK LTVDKSRWQQG\NVFSCSVMHE\A LHNPYTQKSLSLSPGKMIPTADKPP LPGSLAGRTKDAWHGTPVYILPRAP KHGNAKPTPWPWAKKKKKKKKKK KGGRSRVSLEGPKLRTQLS
3253	8750	A	3514	1	164	TRVNENQIESKAAYALFYKRQDVA RRLSPAGS/SGAPASPACSSPPSSEF MDVN
3254	8751	A	3515	1	712	EILIIHLKRFSYTKFSREKLDLVEFP IRSGARERMAGGRQKGEVYQY*P SPHPQ\DLDFSEFVIQPNESNPELY KYDLIAVSNHYGGMRDGHCMCQA VGGACPGSGGQGGDQDLPSE*LGM *ASGEGSSVVGK*TRSEIWTLSEEA RKGRRG*LSFPFR\TFACNKDSGQ WHYFDDNSVSPVNENQIESKAAYV LFYQRQDVARRLSPAGSSGAPASP ACSSPPSSEFMDVN
3255	8752	A	3516	3	3090	IPLLQLLLRRLWRRHGRWTEPREPQ HEELPGLDSQWRQIENGESGRERPL RAGESWFLVEKHWYKQWEAYVQG GDQDSSTFGCINNATLFQDEINWR LKEGLVEGEDYVLLPARAWHYLVS WYGLEHGQPPIERKVIELPNQKVE VYPVELLLVRHNDLGKSHTVQFSH TDSIGLVLRARERFLVEPQEDTRL WAKNSEGSLDRLYDTHITVLDAAL ETGQLIIMETRKKDGTWPSAQLHV MNNNMSEEDDFKGGPGICGLTNL GNTCFMNSALQCLSNVPQLTEYFL NNCYLEELNFRNPLGMKGIEAEAY ADLVKQAWSGHRSIVPHVFNKV GHFASQFLGYQQHDSQELLSFLLDG LHEDLNRVKKKEYVELCDAAGRPD QEVAAQEAWQNHKRRNDSVVDTFH GLFKSTLVCPDCGNVSVTFDPFCYL SVPLPISHKRVLEVFFIPMDPRRKPE QHRLVVPKKGKISDLCVALSKHTGI SPERMMVADVFSHRFYKLYQLEEP LSSILDRDDIFVYEVSGRIEIEGSRE DIVVPVYLRRTPARDYNNSYYGL MLFGHPLLVSVPDRFTWEGLYNV LMYRLSRYVTKPNSDDEDDGDEKE

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						DDEEDKDDVPGPSTGGSLRDPEPEQ AGPSSGVTNRCPFLLDNCLGTSQWP PRRRRKQLVQLQTVNSNGHNRLH HSPCTKSNAKPVHCYSTWKP\EMK K\RYIDE*EGEGLREGNAFRRGYV* RKAPVRLQECIELFTTVEPPPFGGK\ EREKPWYCP\SCCKQHQLAT\KKL\AD LWMLPEILIIHLKTFFPYTQVLPEKK LEHPSWKFPYPGTLD\FS*/EFVIQAH QNEVEIRELYK\YDLI\AVS\NH\YGG MRDGTLTQHLACNKDSGQWHLLLI DNSVFPLFN*GIQIRVPRAAYVL\FY QRQ/DTLARLLSPCRAHLAPSVLP CLHAPSPQLVSSCDVILRALGPAPPE KKKKKALSALSLLVSAPLLLFVLGA PARHCRLSRGYCSPVPLNRSPLGKN RSCLLAVRAPPCVCPSSSDPPF
3256	8753	A	3518	1	271	PLPPGFK*FSYLRLPSSWDYRCPPPH PTNF*FLVAMWFCVHGQAGFELLT SGDPPTSASQSAGITGVSHRSRPVD FLNYLLRKSYPFT
3257	8754	A	3519	3	633	FFFI*DRVSLIAQAGVQWRNCGSLQ PPPTGFKQFSCLSLWRSWHYCRH HAQLIFVFLVKTGF\TMSVKADLEL LTSGDPTASASQSAGITGVNHQCPA SKQF*FHCKSW/CLF*MQSLSF\FLG GGQSRVSGQAGVQWHDLSLQPLS PGLKQFSSLSLPSSWDYRGVPLRLA NFCIFSRDGVSLCWPGWS*TPDLKA NPTRLGLPKGWGL
3258	8755	A	3520	2	430	CLKNMVGAGEVDEDELEVETKEECE KYGKVGKCVIFEIPGAPDDEAVRIF LEFERVESAIKG*WYS*ILKNKKVEF TALIFTSKAYCLIKVKPLSYRIPALF CLLFAFQRLTLN\GRYFGGR\VVKA CFYNLDKFRVLDLAEQV
3259	8756	A	3521	3	1076	HEERQRQRELERQKEIEEREK\RRK DRHEASGFARRPD\PDSEDEDYER\ ERRKRSMGGAAIAPPTSLVEKDKE PRDFPYEEDSRPRSQSSK\AAIPPPVY VEQDRP\RSPT\GP\SNSFLANMG VAHKIMQK\YGLPGGPRVLGKHEQ GLSTALSVEKT\NKRGGKIIVGDATE KDASKKSDSNP\LTEILKCPTKVLL RNMVGAGEVDEDELEVET\REECEK\ YGKVGKCVIFEIPGCPLMMEASTG YFLEI*EELNSAIKAVVALN\GRYFW CTGW*KAMFLQIWAKFRVLDLARN QVWIFKEPRARVISGDPLNELQAVE KKEKGPQPPWLFAYPRLLEGLLRY MLIDPFFYFVVF
3260	8757	A	3522	1381	1787	LEYVAHPLHQLLILNNFYSLNEKY LVFFFLNMYMTFKCNLLFRLPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3261	8758	A	3523	1147	1553	LEYVAHPLHQLLILNNFYSLNEKY

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						LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3262	8759	A	3524	1456	1862	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3263	8760	A	3525	889	1295	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3264	8761	A	3526	743	1149	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3265	8762	A	3527	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTSDSPT LASQSAGITGVNHHAWLFFFC/SD TVSLCYPGWSRVA*SRITATSA/PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLRYPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGFTVLARRVLIS* PRDLPASASQSAGITGVSHHT/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYILFIYFHRDEGSLCCPGWS* TPELK
3266	8763	A	3528	1966	2372	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH
3267	8764	A	3529	10304	11097	FAFSPK*HSLRCPCI*FSSGLLHEVL *LLPLCWP*THGWDPGSREANKSPK LHAIRCWWLEENLWLSSNSQSLQ TVKN*ESHIN*SCRSNLI/HH*FWNQ VK*K*LLNISGNCFLLRWSL/DSVA QAGVYWRDLGSLQPPPGFKRFSCSL SLPSSWDYWHLPCLAKFCIFSRDG/ GFTIWARLVLS*SCDLPASGSQSA GITGVSHHTWLQVITYFLKEMRSCY FSQVGWPQTPGLKQCSHLKLLSSW DYRHMSPHLAISGS
3268	8765	A	3530	87	411	ARLVQNTVAQLKEVQYKLFGLF FE*/QSHSVAQAGYSAVIIAHCNLSL

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						LGSSDPFFSAS*VAGTTGMCQHA W LIFDR*WR*GLAMLPRLEM*IFLISH LRLIWSAWS
3269	8766	A	3531	31	403	THLNGLQIRGSPLFFF/FELESSVA\ RLQCSGVISSHCNLRPLGSSNSPASA S*IGITGAHHNPG*FF/VFFSRGRFH HVGQAGLELLTSSDPPRPSTLPQSG WGFTRHGAIA PQWGQVPFHRS
3270	8767	A	3532	7	1047	
3271	8768	A	3533	3	53	
3272	8769	A	3534	7	960	
3273	8770	A	3535	1538	2287	WWSSSKLRLIYYYSLFFFFFFFFFG M*SYSVTQARVQWHHLGSLQPLPP GFKQFSCSLPSSWDYRHPHLANF LYF**RWGFTMLARLISNS*PQ/CDL PASASQSAGTTGLSHCAQ/LLFAFLT DNSVLIETALT*LQSCAS*KLN*IPL ESSDFYTFFFETESHVS/TQAGVQCR NLGSLQPPPPRFKQFSCSLPSSWDY KCTLPRPANFCIFTRQGFTMLARIVS PGSLGLMISLPRPPKVLGLQV
3274	8771	A	3536	3	263	LGVGDRVSLCHPVWSASSL*SQTPG LK*SSHLSLPSRWDNRHAPPCLA/SL KNFCRDRGLTMLPRLVSNWAQAI LPPQLPEVLGLQV
3275	8772	A	3537	33	295	AGMQWCSLGS LQPPPPVLRSSHLS LPSSWEYSHTCNFCIFCRDGFVLP RLLG*SNRPASSS*NTGITGVSHRAQ PSLFLSYFFF
3276	8773	A	3538	3	33	
3277	8774	A	3539	1	375	
3278	8775	A	3540	3	340	HEVVAA*YY\G*PSIAQEVAGTLAE LDVTLQLEDKFLQNKVFLTGP HIS LADLVAITELMHPAGAGCHVF*GLP TLATWRQLVEASPGEDLFQEVHEVI LKATDFPPADHTI
3279	8776	A	3541	30	284	YSVSTPLRDSNPNNHLSLGHCPASS QTEPQAPQALGQPATKLLPHPQPP /MPQPSSKP*VSATSLCTSPPLPLCP AGGSSGTT
3280	8777	C	3542	127	435	MAASXNPEVLDITEETLHSRFLEGV RNVASVCLQIGYPTXASVPHSIINGY KRVLALSVETDYTFPLAEKVKAFLA DPSAFVAAAXLGCCHHSCSXCCCS P S*
3281	8778	A	3543	3	417	
3282	8779	A	3544	2	881	RGKLCAYGRPPMMRRSIEGN/LENN PASEELLPH*RGHLGFCFTREDLT EIRDMLLA\NKVPTAARCWCQLPP CEVTVP\QNTGLGPEKTSFFPGL* VSPTKNLPGGTH*K S*SYVQL\KTKG DKMGSQTKAKAAEKMMLKNLPPSPF GAGQPKQGV\RKNGKHPTNPESA*I STRGKLCHSRFLGGCPANVAKCLS CKIGYPTVASSTPII\NGYKRVGP CLWTPDYTFPLAEKVKAFLADPSC LCVLLPPVGAATTACFALLQPPA

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						KVEAKEESESEDEDMGFGALFD
3283	8780	A	3545	2	311	DGVSLLLSPRLQWHNLGLLQPPPP* FKGFSCSLPGSWDYRHV/PPCLAN FVFLVETGFRHVGQTGLELLTSGDP PASASQRAGITGVSHRTWQKMYFL SQKYF
3284	8781	A	3546	1	290	KTTTTFF*DRVLFCCPG*SAVAQ\SW LTAALTSWAQGSS*DHRLKP/HMLS FFYFCRQGLTMLPKVVLNSWAQAI LPPQPPM*PGLQACTYAWSRLAL
3285	8782	A	3547	229	486	IKIKINQAWVCACLSLPSSWDYRHG PPHPANF\FVFFLVETGFTMRARLA SNS*PCDPPTSASQSAGITGVSHRAG CSEAFRSQV
3286	8783	A	3548	2	431	ARGSIYQNDTTI*NMYLDNRASECT VRELVKQK/R*MEKPTIIFGDFNNPV SLIEGSSK*KISGTMENLKNANTANFT* LIFIKCSAQQHQAHSFPV/PHRTF/S KIDHFLWCKRGLNCKMKIQQNVV CDHTALNKKPMPERSLEK
3287	8784	A	3549	2	194	VDDFFFFLWWSI/NSVTQAGVQWRN LGSLQALPLGFMPFSCSLSPSSWDY RCPPPAHPANFFLHF**RRGFTVLAR MVSIS*SHDPPASDSQSAGITGLSHR AR/LKGHYDF*EMAC/HLICKRGRQ VP*LFFFFFFEMEYHSVTQAGVQWR NLGSLQALPLGFMPFSCSLSPSSWD YRCPPPAHPANFFLHF
3288	8785	A	3550	2	489	ARGTQALMMMT/GTACHASPH*GG RLTS*PGAICFTHGDMAA*WREESC LLVT/WDLVMSEGLGMRYAFIGPLE TMHLNAEGML\SYCDRYSEGKIHV VQTFGPIPEFSRA\TAEKVNQDMCM KVP**PGSTLAAR\RHWRDE\CLMR LAQV*RSSSCSPQLNFLC
3289	8786	B	3551	13	441	MEGVEEKKKEVPAVPETLKKKRRN FAELKIKRLRKKFAQKMLRKARRK LIYEKAKHYHKEYRQMYRTEIRMA RMARKAGNFYVPAEPKLAFFVIRXR GINGVSPKVRKVLQLLRLRQIFNGT FVKLNKASINMLRDCRAIYCMG*
3290	8787	A	3552	1	775	RRVPA\VPETLKKKRRNFAELKIKR L\RKKFAQQML\RKA\RKLIEKAK H\YHKEYRQMYRT*NFEWARMGK KKLANF\YVPAEPQIWR\FVIRIRGIN GVSPKGSERFFQLRLRQIFNGNLL *KLNQGFRFNMAEDF*SPYIAMGGT PNLKVSKMN*SYKRGLWAKSNKK R\I\A\TDNAL\IARSLGKIRHILAW DLIHEIYTV\GKRFK\EANNFLWPFK LSFSTKVEMKKKTTHFVEGGDAGN R\EDQINRLIRRMN
3291	8788	A	3553	1	356	SHHVQLLEFFVEMGSPCVSQAVAL* LLGSSDPPVLASENVGIK/GPPHPA* S*F*IIACVFVYIYFLEMGSCSFAQA GVLWYNHSSLQR*TPGL*QISLLSPL SSWDYRHVPPCLVIYF

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3292	8789	A	3554	3	352	HEGFTMLVRLVSNS*HRDPQASASQ SAGITGVSHHANP/CFFLTESNWVA QAGVQWRVLS*LQPPPA*FKGFSC SILSSLS/WGYRCLPP/HPANFFFF*K GFFFWFPSWNAMGKKWFN
3293	8790	C	3555	55	201	MPKNYPRLWWQHVCNPQPTWEAE VGELLEPQEA EVAVSQDHATALQP G*
3294	8791	A	3556	3	212	QEFFFFFFEM*SRCVTRLEGSGAISA HCKLCLPGSCHSPASASQDSIFNTQ HLNVGRNSTSKSKPIDYF
3295	8792	A	3557	2	265	EKESRSVTRLECRGAISAH*NLHLP GSSHPPSASHVAGTTGACTT/AQLI FFVFLVETGIHHVGQDGLNHL/NLVI RLPQPPKVLGLQA
3296	8793	A	3558	354	675	HFISYFPDGAELTSSIRVPFFYSNVLF FF/CRQESRCHQAGVQWHDLGS LQP PPPFGKRFSCLSL*SS*DYRQAPPRP ANFCIFNRGPVSPCWPGWSQSPDFV LVPNS
3297	8794	A	3559	1	1203	
3298	8795	A	3560	2	634	VNTEKLTAFVNTLNGKNGTGSHLV TVPPGPS*ADALISSPILAGESGAML GLGASDFEFGVDPSADPELALALRV SMEYQRQRQEEYARRAAAASAAE AGIATTGTEGERDSDDALLKMT\SQ QE\FGRT\GLPDL\SSMTEEEQIAYA MQMSLQ\AEFGQAESADIDASSA MDTS*PAKEEDDYDVMQDPEFLQS VLENLPGVDPNNEAI
3299	8796	A	3561	506	930	IRTTQIGLCLSQVYFIVFDLHAQYEH KATNITPTLSKIISIRPRRFIPVT*L LNMFAFSSPMVPVLSQRIGTI*FLF RFFNT*IFSDGLTNRLTCSR FANCKV NPVIGSISKYVLCSSSFGFNPSIGSET SGLAYRK
3300	8797	A	3563	3	271	FFLET*SCSVG\RLCSGVILAHCKL RFPGSSDSPASASGVVGTGAHHHT RLFCIFSRDGFHHVGQDGLDLL/NL VIHPPWPPKVLRLQA
3301	8798	A	3564	1	218	ETGSPSVTRLECSSIQSAHCNLDLP GSSDPPVS\APQVAGTTGTCHNTQLI FVFFVEMGFCHLSQAVLQLLG*TIH PLWPPKVLGL*AQVILLSQTPQVAG TTGTCHNTQLIFVFFVEMGFCHLSQ AVLQLLG
3302	8799	A	3565	1	294	ASTFFFFFFGDRVSLFLPRLEYNGAIS AHRNLC/LPGFSSDSPASAS*VAQD YRHAPPHLANFVFLVETGFLHVGQ AGLKLPELSVIHPPWPPKVLGLQA
3303	8800	A	3566	3	292	FFETKFSSVTQAGVQWHNLGSLQPP PPAFKRFSCLSLPSSWDYRHLPPRPA NF*FLVEMGFHHVDHADLELPTSS DPPTLASQSAGIIGVSHRARP
3304	8801	A	3567	3	389	
3305	8802	A	3568	1	672	
3306	8803	A	3569	1	2018	MSDNGVRTGAPSTDQRTGMSVRAE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WRRGEFLVTGRRPLVGGGAGEEGE LGGDARSSRDPELQSYAAFVAVVT RIWLPAPRCPALGGLASGPGKAEQF SRSLYLPDHLGEGNGLLGKSLEPY RSACMSAAGLKITGSKETKRLLLLI SIDWSRDLMNLCIYFRVYCQEKQEE RRELPRITGPPPEAAVVAFEWLKTS TLTGLHPQLPLSLPQPECALPYLVR AFSRGDYMGRIQEVGWVTAGLVIW AGTCYIYKFTKGRAQSVRTLARN GSTVKMETVVGVQSQT LAINEAEIK TKPQVEIGAETGARS GPRAEVETKA TAIAIHRANSQAKAMVGAEPETQSE SKVVAGTLVMTEAVTLTEVKAKAR EVAMKEAVTQTD AEAGKIVKKEAV TQTKAKAWALVAKTEAKREAMTQ TKAETHILAEKETEINRVMVTQSET LAVPREVAKMGATNKTGIVDETKT RALEETVSVAKTQSEARPGATVDA RGNPNGMSREVAGVDMKSCAQSQ AVTKIQGDDMPGTGVEDMGNCKT MSRAESGADTRASAQPQIFAKTQTE AIPGAKIDAGGNTNAMCKVGAGAD VRACIQPQTVAKKQAEVTS GARVD GRGNTNVISKAITGADMRAAAQPQ AVASTHAEAMSDAKVKNRGNPNA MTKAGAKANLRANSQVEALPDAR DKSRGNPNVMAKVGDGTDMLSCT QPQLVASVQADTLSDGKIKV RGNV NTMPKEGAGVDMKAQGMASQSGE ALPNTRGKARGKAKAKCKTGPGM DMKTCTQPQAGVKTPAEALLDSRV DGRGNPNATSKAGTKADQRVCGQP LVVANPQGEALPGAKNKVKGNPHT VLKVGAGEGTTDSAQPEAVVSFQG EALLGTKNKVKGNPNVVLKAEVGE GAMGTAQLQIMASSKGEALLDSKN KVKGNSNAVSKAGAGTDTTGSVQP QIVANSQGEVLP GAKNKIRGNPTTV PNSGVGPYTTDSARLQAVANSQGE VLP GAKNKVKANLNAVSKAEAGM GATGSVQPQAVANSHCETLPGAKN KVRGNWNAVSKAGAGMDTRGSAQ PQAVANSQGEVLP GAKNKVKGNPN VVSKAGAREDTVGSTQPQVLASSQ RETLPGARNKVKGNSNVVSKAGAR EDTMGSAQPQVVANSQRETLPGAR NKVKGNSNAISKA EAGAGIMGSVQ VQVVASFQGEVLP GAKNKVRGNSN AVPKAEAGADTVGSAQPQAVANSQ SETLLGARNKVKGNTIAVPKAGTG AGTRHSAQPQIVAGSQGETLPGARD KSMSTSEAEATAEDEAYAKPEAEA MPTSESEGGSGTQACRKTQPNIHDI YWNGIGVEDWIAAERWIKFRFQTM DGDWENSVSWADDENEASIGSWSG ASDKAGIIRSWAVACDETSVKSWA GARAENVVGIGTWARAGEQASGGL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WAGGQTSEGTWAGDKASGGAWT GAENQASGGSWALAGNQAIGELW AAGQASDGSWPGGQASGVSWVGE EAIGGSWTGAENQASEGSWAGAGA GNMSSVSYWAGVVDQAGGGSWA GTSDQSGGGGSKPRFEDQASGEGSW AGAGGQASGGGSM LGPEDQSSGRSW ADTADQASGG SRLGHVDQSSGGA WAGTLDQSGGGGSKPRFENQTTEEG SWAGAGGQAGGGGSKVGPEDQSSG RSWANS GDQISGGFLVGIVDQANG GSWTGAGHPASVGP KPIFEDQVSGR GSWADAREQVVGD SRLGLRDQSSG DSWAGTGDQASGWFCVCPGSQTN GGSWG GASGQDVGGSRPGPTNQSS AGSWDSPGSQVSGSCWTGAGAVD QAGGCSKPGFEDQAIGGGFWPGAG DQTGGGSRPGSEDQSSGIGSWGVA GGQVLGGARPGPADQSSGGSWAGT GNQSSGRSWIGPGDQAVDCSKPEFE DQACGGGSWAGAGSQASGESWAG SRPGNEAIGGSRMGSEDQATGGSW ARSEDQASGRFQVSFEVEANEGFW FGPGAEAVIGSWCWTEEKADIVSRP DDKDEATTASRSGAGEEAMICSRIE AENKAKSRLGAGEEAGVESWTLAR NVGEDELSRESSPDIEEISLRS LFWA ESENSNTFRSKSGKDASFESGAGDN TSIKDKFEAAGGVDIGSWFCAGNEN TSEDKSAPKAKAKKSSES RGIYPYM VPGAGMGSWD GAMIWSETKFAHQ SEASFPVEDESRKQTRTGEKTRPWS CRCKHEANMDPRDLEKLCMIEMT EDPSVHEIANNALYNSADYSYSHEV VRNVGGISVIESLLNPNPYSVRQKA LNALNNISVAAENHRKV KTYLNQV CEDTVTYPLNSNVQLAGLR LIRHLT ITSEYQHMVTNYISEFLRL LTVGSGE TKDHVLG*EQRQSQC HD*SRGQ GK LEGQFPG
3307	8804	A	3570	1	611	YAALGADVTRVSLPTPRCPALGAL ASGPGESGPTLLQDCGAKCPG/GPQ PRGENREKEETTRIGPGVMESKEKR AVNSLSMENANQENEEKEQVANK GEPLALPLDAGEYCVPRGKS*GGSA FRAAHP\EYRWDM MHRPW RTHRPR DEEKRIMEKDWGGGETADGKKLE GEKPVGVISLRGESGTDPPSPMTHH D*VFALLPLNP
3308	8805	A	3571	1	379	EMESHSV\TRLECS/GTILVHCNLCL LGSSDSPASAFQVAGITGVHYNA*V IFVFLVETGFCYVGQAGLEFLTSTD PPASGFQNCWNYRDEKPHPAETVS KTTTTKNYICVSTINYKKKNLGLSNI L
3309	8806	A	3572	6	222	DRVSRSA AQAGV/QWC/NLSSLQPL PPRFK*FSCLSLPSTWDYRHTPPRPA NFCIFSRDRVSPCWAGWSQSLDLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3310	8807	A	3573	1	445	
3311	8808	A	3574	1	3212	DSINNLAELNKFALRKQLEQDVL SYQNLRTLEEQISEIRREESFSL YSDQTSYLSICLEENNRFQVEHFSQ EELKKKVSDLIQLVKELYTDNQHL KKTIFDLSCMGFQGNFPDRLASTE QTEIMKDLKGGCKNGYLRHTESKI SDCDGAHAPGCLEEGAFINLLAPLF NEKATLLESRPDLLKVVRELLGQ LFLTEQEVSGEHLDGKTEKTPKQKG ELVHFVQTNFSKPHDELKLSCEAQ LVKAGEVPKVGLKDasVQTVATEG DLLRFKHEATREAWEEKPINTALSA EHRPENLHGVPGWQAALLSLPGITN REAKKSRLPILIKPSRSLGNMYRLPA TQEVVTQLQSQILELQGELKEFKTC NKQLHQKLILAEAVMEGRPTPKT LLNAQPPVGAAYQDSPGEQKGIKTT SSVWRDKEMDSQQRSYEIDSEICP PDDLASLPCKENPEDVLSPTSVAT YLSSKSQPSAKVSMGTDQSESINT SNETEYLKQKIHDLETELEGYQNFIF QLQKHSQCSEAITVLCGTEGAQDG LSKPKNGSDGEEMTFSSLHQVRYV KHVKILGPLAPEMIDSRVLENLKQQ LEEQEYKLQKEQNLNMQLFSEIHNL QNKFRDLSPPRYDSLVSQARELSL QRQKIDGHGICVISRQHMTMIKA FEELLQASDVDCVAEGFQEQNLN CAELLEKLEKLFLNGKSVGVEMNT QNELMERIEEDNLTYQHLLPESPEPS ASHALSDYETSEKSFFSRDQKQDNE TEKTSVMVNSFSQDLLMEHIQEIRT LRKRLEESIKTNEKLRKQLERQGSE FVQGSTSIFASGSELHSSLTSEIHFLR KQNQALNAMLIKGSRDKQKENDKL RESLSRKTVSLEHLQREYASVKEEN ERLQKECSEKERHNQQLIQEVRC GQELSRVQEELKLRQQLSNDKL LQSLRVELKAYEKLDEEHRRLEAS GEGWKGQDPFRDLHSLMEIQALR LQLERSIETSSTLQSR/LKEQLARGA EKAQEGALTLAVQAVSIPEVPLQPD KHDGDKYPMESDNSFDLFDSSQAV TPKSVSETPPLSGNDTDSLSCDSGSS ATSTPCVSRLVTGHHLWASKNGRH VLGLIEDYEALLKQISQGGQRLAEM DIQTQEAPSSTSQELG\TKGPHPA LSKFVSSVSTAKLTAAEAYR/RGLK LLWRVSLPEDGQLPLHCEQIWRNE RQRVPKLHKKLFEQEKKFAKTP*RF LQLSK\RQEKVIFDQ/LVVTHKILRK ARGNLELRPGGAHSRTCSPSR/PGS ALATRKEHRNQHSAEQASRNSWQ GGQRRHRKEPSLWLSKPCPSLRCPF SLTNTMTVNIPWKVIIHLICLIPPRQ
3312	8809	A	3575	1	1362	SGNIKVLERFLYIDTKFSQNRQCKA LPMASAYQSNLPHNYTMTVHNN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QLAQALRVYSQHAIGAVLYKYSMQ VHEDCYKFWNSG\MQLCEERSLTD QHCVHKFHSLPKSGEKPEADRNPPV LYHNSRARSTGACNCGRKQAPRDD PFDIKAANYDFYQ\FWEEKCCGKIG SVYSISQYLEPSTPGSWLLA*KWNP/ RPAPPDSADKLKEKEPQTQGESTS LSLALSLGQSTDSLGTYPADPQ/DRR R*SRSSWSSRSSEN/SRRDQTSIDRH/ LTVEYLPGLHNSNCPKGLLPTFSSW VFVKLPG*SYNFHTRFR/NQQGFIP GNKLSYALGTLSSRARSWR*RLR HKLLACSK*SYSWKEKCGCNGKRK TAR*H\TRAFVGFYEDSRGRFMC SGALTK**K*WGSGA/IRDSAFKSP*I VDMPLY\NRHPLKVEGLKTLITLQL MRLFVVVPDASFA
3313	8810	A	3576	1	673	EGGW MEDYDYVHLQKKEEFEMTH IELLDKGSITRQGMSQL*LEQLKLFV RLEQEVSRPIDHLAIWTPAQPLAP GRSGG\LGPSDRQLLLFYLEQCEAN LTTLTNAVDAFFTA\ATNQPPKILV GASKVLL\SAHKL VFIGDTLSRQA K\AADVR\SQVTHYSNLL\CDLL\QGI VATTK\AAALQYPIAFPGPKDMV/E KRVKELGHSTQ\QFPPRS*GQLGSPP EGW
3314	8811	A	3577	3	531	FFLLQSL/DSAGQARVQWCDLGSQ LPFRFMRVSCSLSSWDYRHLPP RLAMIFVFLVE\QGFTVLARLFSNS* PQ/CDPPTSASQSAGITGMSHHA\RL FLFETGSGSIAQGGVQ*CNLGSLOP LPPRLKPSSHLSS*DYRRVPTCP SNFCIFGRDGVSPCCPDWSGTPGLK
3315	8812	A	3578	1	223	GSGGIHRLPLSSRPEQPIVWLWAPG CFSHLSRLQVTV*/GEIKQRCRELHH SLAQHPRHQAGNHISHPILHLKIL
3316	8813	A	3579	3	341	FFETESCSVSQAGVQWRDLGSLQA LPPGFTPFSCSLSPSSWDYRHLPPHP ANF/SVFLVETGFHRVSHDGLDLT RDPPTSASQSAGITGVSHRARPIVAI FMFCEYPLFSSH
3317	8814	C	3580	168	347	MTYGLLLFLGNNPHLNLYXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXSTIV*
3318	8815	A	3581	852	1216	GFLINGNTDFFFETESRSVAQGGV QWRDLGSLQPLPPGFKRFSCSLPSS WDYRHLPPQYPS*IFVFLVETGCSSY STIL**RPAHVQAGLELLTPGDPPAS TSQNAGITGLSHRTWSAI
3319	8816	A	3582	2	238	
3320	8817	A	3583	680	891	
3321	8818	A	3584	697	979	IFGV SQGYKILWKMNSLPGVSFES KRSF*QK*LQILSS*FAKKIFYWHEN NRCKWRPNIPKCIYSITSQKLFYPS LLFFLLPTFLGVGGAR
3322	8819	A	3585	2	518	GRGYQNPGRQCTSDRLSEHVSEGES

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						PPDSQEDSFQGRQKSKDKAATPRK DGPKRSLVLSKSVPGYKPKVIPNAIC GICLKGRESNKERKG*IHFIHCSQCE NSG\HPSCLDMTNGACFYD*DLTPW QCMECKTCHICG\NPHHEEEMMFC\ DMCDRGYHTFCGGPGSNPTRPLNL
3323	8820	A	3586	1	165	SLEDRVLLCHPGTAYCSLELLGSISP PALTLTSEAS\LPGRDYREIPGSPCQL FL
3324	8821	A	3587	1	249	LVDRVLLCHPGTA/VLQP*TPGINQS SCLSLPSS*D\YRYVPPCLVYCFIFLA EMGLTVLPRLISNSWPQAILPSQPPK VLGLQT
3325	8822	A	3588	3	282	NSWDYRHPLSCLANFCIFSRDGGFT ILTKLVLNS*PRDPAASASQSVGITG VSTHGLASWN\FNKLKNSYTQVD*L GSQEWPLKVCLAKPRTAS
3326	8823	A	3589	1	714	
3327	8824	A	3590	1	726	MAEGETESPGPKKCGPYISSVTSQS VNLMIKGVVLFFIGVFLALVLNLLQI QRNVTLFPPDVIAIFSSAWVPPC CGTASAVIGLLYPCIDRHLGEPHKF K\REWSSVMRCVAVFVGINHASAK VDFDNNIQLSLTLAALSIGLWWTFD RSRSGFGLGVGMLFLATVVTHL*V YNGVYQYTSPDFLY\RSWLP\CIFF AGGITMGNIGR\QLAMYECKVIAEK I/LIRNEEGKK\YLLYRKAR
3328	8825	A	3591	469	537	PGLARRAMASGRSHGWP*IPPLRST FQGGRTLDAAFRINCHGKTYLFKG SQHWRFEEDGVLDPDYPRNISDGF GIPDNVDAGLALPAHIYSGRERVYF FKGKQYWEYQFQHQPNIIEEREGSS LSAVFEHFAMMQRDSWEDIFELLF WGKTSAGTRQPQFINLDWHGEPWQ ADAAMAGRIYISG
3329	8826	A	3592	193	384	
3330	8827	A	3593	96	1635	ARSPAMAPLRPLLILALLAWVALA DQESCKGRCTEGFNVDKCKQRDEL CS\YYQSCCTDYAECKPQVTRGDV FTMPEDYTVYERLGEKNNATVH EQVGGPSLTSDLQAQSKG\NPEQTP VLKPEEEAPAEVGAASKPEGIDSRPE TLHPG\RPQPPAEELCSGKPFDAFT DLKNGSLFAFRGQYCYELDEKAVR PG\YPKL\RDVWGIEGP\DAAFTRI NLFRGRPYLFKG*\QYW\RAFEDGV\ LGPWIYPRNISWTAFDGHSPGQTW D\AALGLPCPLAYSGRERVYFFQRG KQYW/ESYQFPGTSPVQEECEGSSL\ SAVF\EHFAMM\QRDSWEDIF\ELLF \WGAERSGWVTR\QPQFHLAGEWH GVPG\QVD\AAMG\GRILHLQGMAT RPLLWPKKK\RFRR\NRN\KGYRS\Q R\AHSRGR*PETPRRP\SRAMWLSF VLPSEESNLGA\NNY\DDYRMD\WL VA\ATCEPIQECFFFSFGDKYYRVNL RTRRVDTVDPPYPRSIAQYWLGC

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						APGHL
3331	8828	A	3594	44	166	
3332	8829	A	3595	3	1173	SSAPEAAKKPTPCHRCRGLVDKFN QGMVDTAKKNFGGNTAWECKTL SKYESSEIRLLEILEGLCESSDFECNQ MLEAQEEHLEAWWLQKSEYPDLF EWFCVKTLKVCCVPGTYGPDCLA CQGSQRP\CSGNGHCS\GDGSRQG DGSCRCMHGYQGPLCIDCMDRL QLRSRNETHS\CTAVRTGLSDSYPP CCLSLGCWRGVGHAWIRGRNTHQ PGYSSRVWIAAFSPACDESKTCSG LTNRDCGECEVGWV\TRAPCVDV EKCAAQTPPCSAAQFCKNANGSYT CE\ECDS\CVGCTGEGPGNCKQCIS GYAREHGO\CADVERVPH*PEKTL EEKTKTCYNTPG\SYVCVCPDGFE T/RRCLCAAGRRLKPQKGESPTQLP LP
3333	8830	C	3596	1	300	MRSFGQLTLCPRNGTVTGKWRGSH VVGLLTTLNFGDGPDRNKTRTFQA TVLGSQMGLKGGAGSVWLQAAGL GLLPASLLWPSLLCHCYVLPPAGV PLV*
3334	8831	A	3597	359	1229	MPQPPTLGQEMTGPSQPWTGKGGL PGP*QLRAKAQEVDSHLGRKKIKQ QNRSKSC
3335	8832	A	3598	2	311	VRWNSAAPLVTSRGAPASARPRGQ ALPGGSAPSAPHGQLPGRAQPAPVS GPPPTSGLCHFDPAAPWP\GLGLG MLPPHPQDWPAQP*HPPGLGLFFEIF SAS
3336	8833	A	3599	1	426	
3337	8834	A	3600	18	738	
3338	8835	A	3601	65	425	RLPQPPGAAVGGSTRPCPSWKAVR VDLVVAPVSQFPFALLGWTGSKLF QRELRRFSRKEKGLWLNHGLFD/R GAGKQQWQDS*VTEVLLLLQKTF QAASEEDIFRHLGLEYLPEQRNA
3339	8836	A	3602	3	233	FFFFFKTLQIPLLSPPPPGPCRVQSL LPNPFPEKGA\PPFQTDERGQDFRLD PPLGSPSPRV*SLNCYVPVPPKEK
3340	8837	A	3603	7	510	THAPAPSPRAQAP*PLFIHCP*APRV TPPPPPQPVKCVVPAEVI/SPPPPGPCR VQSLIPLTRFPEKGAYLLSRQMKRG QDFKAGIQPLGLSLPQPGSTGRGRV TAGD
3341	8838	C	3604	846	989	MKSYNGMREMGDQASRRKLIKWN TDSKFLDMENGEQKKITPRPGVKI*
3342	8839	A	3605	3	232	KSLLREGLESAMLVLKSLLPFSYFV SSMSSGNWSALHNHGLPEDTGTAS PYNRCS*RGDRHLGKRSSTRGTTLG PN
3343	8840	A	3606	303	400	
3344	8841	A	3607	3	404	LRQRLTVTQAGVQ*HRLSSLQPLPP RLKRFSCSLPSSWDYRRVPPHMA NFLY/FLVETGFHHVGQAGLKLLISS

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						DLPALASQSAGTTGMRHRAQPKSF QLEQKWKTEPHKLIYVVTNLKRM YKLKTYHIPYYF
3345	8842	A	3608	2838	3122	FFFFFFETKSCSVARLECSGTISAHC NLHLPGSSDSPASAS*AAGITGACH HTRLVFLYF**RRGFHHVSQAGLEL LT*VIHPPQPPKVLGLQA
3346	8843	A	3609	1	325	RLFFFFFFETVSHSVTRLECT*AILAHC NLCFPRSSNSLASASQVAEITGACY YTQLIFVFSVETGFHHVQGAGLELL T*VIHPPPPPKVLGLQVSATVPGLI GTFSL
3347	8844	A	3610	3	398	GSLQPPPPRLK*FSCLSISSWDYKR LPPCPANFCIF\TELGFHQVGQAGLE LLTSGDPPASTSQTVGITGISHHAWP PEILSKGTMGKQMVNMLLLASSCR EMGHSAPAHLGQCLPMILPKDLAVI IINPV
3348	8845	A	3611	3	311	AQTGMQW\DLCSVKPPPPRFERFSC LSLLSC*DYKRTPTCPANFC/DFVVE TEFHVGQAGLELLTSSDLPASASE NPQITGMNYCIWPEWYYYIHSLTNT IHK
3349	8846	A	3612	310	415	SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRRL/DSVAQAGVQWRDLGS LQRPPPGFTPFSCSLPSSWDYRRPP PRLANFFVFSVETGF\VSARMVSIS *PRDPPASASQSAGDTGVSQAPV
3350	8847	A	3613	1	114	ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS
3351	8848	A	3614	335	477	TPASLKIPVE**NTLLAKMVSIS*PR DLPASASQSAGITGVSHRARC
3352	8849	A	3615	135	804	GIDTILTLNQN*SLKTRQ*FTLIH/IFF FFLRWSLALSPRPDCGLQWRDLGSL QAPLPGF\TPFSCSLPSSWDYRCPPP RPANFFCNFFFSRDGGFTVLARMVS IS*PQ/CDPPTLASQRAGMTGLSHCT RLFFF*WMESPSVTQAGIQWHDLGS LQPMPPQFR*FSWLSLPSSQDYRCM PPCQANFCIFSRDEVSPC*PGWSGS PDLVIHLPWPPKVLGLHA
3353	8850	A	3616	3	285	HEIIVLRVRVSPCCPGWSA\TVD*SW FIAASYS*VKRLSCLSLRLIWGCRQ VPPWLSFKLFWRQGLAVLPKLVS SWPKMTLLPQLRLGLQE
3354	8851	A	3617	3	575	PSLRHASHEAGWQCPLHGQPLPGY TELRTLPQ*GDGYGRPGVSAASQR R/GLAGQCVEGRDWVEGKAG*CSG GHGEGKGPLD*GALLPGPQNR\S GAGDPC*AVESVGCQ*PGECHFQR DPPGSGAAPGAPPAVP*LHRQPD AAGGTAGPSLPHLPPPLGLRVERS KPGGAAEEQGHPHLEHGP GD
3355	8852	A	3618	3	379	FFETESCSFTQAGVQWHDLGTL*SP PPGFK*FSLSLSSWDYRRPPRTA/ NYIYIVFLVETGFYVVGQAGQKLLT

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						SCNLPALVSQSARITGVSHCAQLCN FLLTVKHFKPLTLRLEARTPQSFL
3356	8853	A	3622	1	214	ETESRSV/SQAGVQWRDLGSL*PPPP PGFQRFSCSLSPSSWDYRRAPPLPH NFCIFSRDGVSPCWPGWSQIS
3357	8854	A	3623	2	309	WCVFFETETHSAAQAGVQWCNLS LQPPPGVKQFSCSLSPSSWDYRCA SPCLASFICFSRA*GFTMLTCLLELT SGNPPTSASQSAGIQGVSHHTWPSI F
3358	8855	A	3624	1	294	FFFFFFLRQGLTLARLECSGMISAH CSLDLPG\SGDPPTSAS*VAGTTGTC HHAWLIFLFLVETGFHHVAQAGTLS KHRNHIQPVQVRATCSKDGO
3359	8856	A	3625	23	282	ASTGKPLSPQVQSES/CLALQLP*RS WN*TRVMSTTPWPNFFGIFVEMGF RHIGQAGLELLTSSNPILASQSAGI TGLSHRVQPTSS
3360	8857	A	3626	37	289	QWHDLGSLQPLPPGF\RLSCLSLTS SWDCR/QPALRPANFFCIFK*RWGF TVLAQDGLDLLTSSDLPASAS*SAGI TGVSHRAWA
3361	8858	A	3627	70	362	KLHFKAIEGISSLGEQMKPSMWML LCPQIKIKLTLPIQIKQAKTCRQIPKV QGSQ*KNVGPSSFPVPW/EHGSGMI EAPWALNPYLGLGPVQILETQK
3362	8859	A	3628	60	303	KLKNHHHHHHQQQQQKQQQQQKK QMDPRVSFSFFKKKKSSTPKPSQ*FP *SSRNS/HPR*ISESDLRPTAIPIGL KMKLPL
3363	8860	C	3629	193	285	MLLVSYPRNSNRCQIQYHEAFCPIIF LRVL*
3364	8861	A	3630	159	483	DPTSFGHGYLVFPTPCFKGFYFF*DR VSFCCSGML/IGSLQAQPSGFKPKPS SHLRLSSEDCRHTPPRLANLFFYFF L*RWDLTMLPRLVSNS*AQVILPSW PPIMLG
3365	8862	A	3631	6	244	DRVLLVTQAGVQWHDLGSLKPPPP GFK*VSCLSLPSSWNYRRLPPRPAN F*FLVETGFLHVCQAGLKLPTSGDP PASA
3366	8863	A	3632	2	262	NDLGSLK\PPPPGFK*VSCLSLP/RVS WNYRRLPPRPSLIFVFLVETGFL/HV CQAGLKLPTSGDPPPSASQSTWITG VNHRARPQIGF
3367	8864	A	3633	1	1149	
3368	8865	A	3634	280	602	TDFFFFFFLRWSFTLVAQAGV*LHD PE*LQPPPPGFKRFSCSLSPSSWDYR HPPWPANF*FLVETGFHHVGGQAG LELLTSGDPPASASQSVGITGVSHR ARPELNF
3369	8866	A	3635	3	679	SLHQSGRSNPTCCFPSSKGTGTNGH PTPSQSPPGTRDGPLFFPHSASTPP PTGASQPLTGTGRPPSPVEPVSHAC ASL*FSEGLRSEHPAVACGKTLQSP TGSKEACSGEQGNCVLAIEIVVLGT QDPSAH*GGAGARGGGALWVTEG

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						VKGPGPVSGQCRKSQPHACGEIPCR APPTMGTSGLPLGLPKLCPHFHCSR ASPAPSNSPFCFWSPTSGGPNPFPC
3370	8867	A	3636	1	334	EMESRSVAQAGVQWHDGLSLQPLP PGFKRFSCSLPSSWDYMRAP/PRP G*FFVFLVEMGFHLVGQAGLKLLTS /S/DLPTSASQSAGITGMSHRTRPNSL LVIQSGRFNTKITR
3371	8868	A	3637	2	309	FFFFETRFRFVAQAGV*WHAYGSPQ PRPPGPKPSSQLSLPS*DYRHTLLCL ANF\DFLVETGFYHVAQTGLELLSV RDPPALASQSAGIAGVSHRARPGCI F
3372	8869	A	3640	19	458	KHLFYSSNLYFRSTFRHTRRRSPCEP SLALR/WCVLEPGSSRV**RLHPNTV GFQDASAKPRERTTSFHAFANF*K QYIFQC*LPPLTWLEIFSPFSRETKST KRCRLQDPGPSHFWRVVLGCLLWG QDRAPSWAPLQMQLCHCLYL
3373	8870	A	3641	1	322	FLRRSLALVTQARVQWHDPGSLQP SPSGFKRFSCSLPSTRDYRHPPRL ANFF/VFFLYL**GFATLAWLVNLSH L/CDPPASASQSARTTGASHHAQPP VSFFKTRI
3374	8871	A	3642	333	438	
3375	8872	A	3643	391	492	
3376	8873	A	3644	598	699	
3377	8874	C	3645	176	319	MCSAQPAFSVDIIKSRHLGILGFYK PRILCQKHMRLRLHSHFQNFQR*
3378	8875	A	3646	2	50	QLLGTGTMHHYA*LIF
3379	8876	A	3647	3147	3308	FFKKNLCASAHYY/TWCVPLPFFFF LRQGL/NSIGQAGVQWCNHSSLQPC PPQDLE
3380	8877	A	3648	1554	3041	GTRERRAPDPCAGKCRNHVAGGRL KLSLHLSLPSSWDHRHAPL/PHD*FF KYLRR/RSPCVTQAGLKLLGSSDPPI LASQSIGITDMSHCT/WPSSPTPCHF LRDSFAPSPRPGMQ*CDHSSL*PQTL GLKQFSHQPPFYFFVQMG\FAMLPK LVLNWPQ/DNPSALAPQSAGIVGM SCCAQPPCFNINSHS*IQE
3381	8878	A	3649	280	444	
3382	8879	C	3650	135	377	MAGSWGAGQVQWLMSVIPILWEA KMGGSLRSLRPAWVTQGDVSN RLFHSSASVLWLQATLGTIPKSLEYI TLAFRAK*
3383	8880	A	3651	1791	6596	CPKDTQILIFQKNNFSIRRFTQHLAD FLKEFCLTFKKKGRSLL*FCCFVYI IF*KKFVCFCSLHWCVPLPFFFFLR Q/RHSIGQAGVQWCNHSSLQPCPP RLK\HPCTSASQVAGTTGMHHYA*L IF*IFETGSPCVTQAGLK/PPGLK*SS HLGLPEYWDYRHEPLHLPSSPTPCH FLRDSFAPSPRPGMQ*CDHSSL*PQT LGLKQFSHQPPFYFFVQMGSCYVA QAGLK/PPGLKQSFCLGPPKCWDCG HELLCPASMF*YQHPHMYTLKTTV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TFSTQNYIRYSLNCRKIKTIPKSDCR VDFFLQNT
3384	8881	A	3652	3	332	ETESHVAQDGVQWRHLSSLQPPLL GFK*FSCSLSPSSWDYSCPSPT/P*LI CFFFFFLIEPGFHHFGLAGLELQTSG DLPASAFQDAGITGMSH*TRPELLS LDHTPFT
3385	8882	A	3653	3	272	FETESH/VSPRLECSGVIFAHCSFCL PGSSDSPASAS*VSGMIGTRNHAQLI FVFLVEVRFHVQGAGLELLA*VI HPPQPPKVLGLHV
3386	8883	A	3654	1	272	ETGSRSTRLCSCGAITAHCSLDLPG RSNPPTSAS*/RIAGASGECRHTQL/I* KFIFFVNTGCRYVVQAGLKLLASGA KQSSCLGLSKCWD
3387	8884	A	3655	249	906	RIHFPRVSGPSQSNPKFAVASRGFFS LSLSSAQPDPLPPPLGEALALSLHPV PRRSTETVAGDSSELQLGLRSPQQP LAGLAFLARLFLFPPP*RCKSKPN* NDRRRSSVDSQIHLVGRESAHLPLAG LRVCVSLPLLARCFGQVLQGVPG WIPSPGGS/AGVSGRRREERHMGVV VMRVRVEARVSS*ESKI/SRALR*ST HLGLPKCWDYRREPPCPAH
3388	8885	A	3656	1	514	FFFFSRSL/NSVIQAGAQRDLGSLQ P/LLPPGLKQFCSLLSSWDYRCPP PRLANFYIF/M*RRGFTILARLVLS* TQ/CDPPTSASQSAGITGVSHPTQ/LL FSF/CLKESGSSLMVSATLRFHK*RH SGPSRAALSSSP*LEPRKLKFGTASL QNKWAMQQTRQHWAGRGSKPM
3389	8886	A	3657	2	307	FFFFFFETESYSVTQAGVQWHDGLL LQPLPPGLKQFSSLSLPE*L/DVTGSP PPCPVNFCTFGKGLGFTMVGQAGS GTSCLKVICPPGLPKVLGITGCEPRR L
3390	8887	A	3658	79	91	NTFW*RRGFTVLARMVLIS*PHDLM TC/PASASQSARITGMSHCARLVLYF SRDGVSLCWPGWSQTADLR*STCL GLPKCWDYRYEPPCPASLHHFLIYA TSIIKYL
3391	8888	A	3659	162	493	DGSSPPVAQAGVQWRDLGSLQAPP PGFTPFCSLSRSWDYRRPPRPA NF/SCIFIVETGFHRVSQDGLDLTS* S/VPASASQSAGITGVSHRARPRSCIS FDSTVTLAQ
3392	8889	A	3660	3	251	GGALRLHQVPPALPLRGAVSGAAA VQMSDCTPCCEVHLLQD*VPAGE ARVQWHDGLSLQPPPPRFKRFSCLI LPSSWDYRH
3393	8890	A	3661	3	251	GGALRLHQVPPALPLRGAVSGAAA VQMSDCTPCCEVHLLQD*VPAGE ARVQWHDGLSLQPPPPRFKRFSCLI LPSSWDYRH
3394	8891	A	3662	17	287	KYHRIQCPNSGCEAVYSSVSGLKA HLGSCTLGNFVAGKYKCLLCQKEF VSESGVKYHINSVHAEVRLL*SCGP

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						DM*ATREVDVPIVMD
3395	8892	A	3663	3	567	DRKLKYTRPGLPTFSQEV LHKWKT DIKKYHRIQCPNQGC EAVYSSV SGL KAHLG SCTLGNFVAGKYKCLLCQK EFVSESGVKYHINSVHAEDW FVVN PTTTKSFEKLMKIKQPAARRRKA EA AAQEQKVSKKGGSSLGIELPETEPS LRVGKDQRRNNE\DW*QPPCKEP/ GAGASASTVPESKAPKD
3396	8893	A	3664	1	184	SSRDILLCTDIASRG LDSTGVELVVN YDFPPTLQD\ELAARRRRSLPGLASS VKEPLPQAT
3397	8894	A	3665	2	1748	HEARTKGNMALSAA RLRLFFPVN SVCFLAP\RRGL\TVRSPDE\LPVVR IPVASTSGKLEQRQ\SRRLNPEGR C LVRPGPLLVSARRPELN\PARLTLG RWERAPLASQGWKSRRARRDHFS\I ERAQQEAPAVRKLSSKGSFADLGA WKPRVLHALQEAAPEVVQ\PTTVQ SSTIPSLLRGRHVVC AAETGSGKTL S YLLPLLQRLLGQPSLD\SLPIAPRGL VLVPSRELAQQVRAVAQPLGRSLG LLVRDLEGGHGMRRIRLQLSRQPSA DVLVATPGALWKALKSR LISLEQLS FLVLDEADTLLDES FLELV DYILEK KDLAVFLYHLRLEAEVEV VEMLGP HGQPCPQHNSDISAYTYERTLMME QRSQMLRQMRLTKTERERE AQLVK DRHSALRLESLSDEEDES AVGAD KIQMTWTRDKYMTETWDP SHAPD NFRELVHIKPDQSNVRRMHTAVKL NEVIVTRSHDARLVLLNMPGPPRNS WCTTSSRTEKRQWNC PAVRTEKNA QTRQTIIAETKTQKKDTEPRIEADL AVQYDNHYTNTKYCLCQMLREQL ESPQGRLLHAAQSSREIW
3398	8895	A	3666	1	1704	MALTRPVRLFSLVTR LLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRLNLRPV LVRPGPLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQQEAPAVRKLSS KGSFADLGLEPRVLHALQEAAPEV VQPTTVQSSTIPSLLRGRHVVC AA TGSGKTL SYLLPLLQRLLG\HPSLDS LPIAPRGLVLVPSREFF\QHLRAVA QPLGRSLG LLVRDL\EGGHGMRRIR LQLSRQPSADVLVATPGALWKAL KSRLISL\EELSFLVLDEG\DTLLG*K ASWELVDYIL\EKSH\AEGPADLED PFNPKAQLVLVGATFPE\GVGQLLN KVASPDVTTITSSKLHCIMPHVKQ TFLRLKGADKVAEL\VHILAKHR\SR AEKGLGPSGTGFVFCNSSSTVNWL GYILDDHKIQHLRLQGQMPALMRV GIF\QSFQKSSRDILL\CTDIASRG LD STGV\ELVVNY\DFPPTLARLTFHRA GESGPVWGAEGPG\TVISFVTHPW DVNPWFKKD*SLAARPK EEVL PGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AIPR*KKPFAPQSNPDFEQNLIK M
3399	8896	A	3667	2	222	RWSLTLFQAGMQWPNLSSLPQPPP RFKQF*CLSLPSSWDYWYTPPRLAN FCIFSRDGVSPCWSGWSRTPDLR
3400	8897	A	3668	1	29	
3401	8898	A	3669	2	206	VTQAGVQWLALSSLPPLPG/LK*F YCLSLPSSWEYRHTPPHPTKFCIFFL VEGVSPYWP GWSQTPGLR
3402	8899	A	3670	3	139	TSHMWWCRHVVSATREAEVGEPL EPRQSRLQ*AMTAP\CTPAWATK
3403	8900	A	3671	86	384	
3404	8901	A	3672	3	746	RQEEGLPPVVD AID DASVEEDLAVA VAGGRLEEV SFLQYPARRRRALLR ASGVRRIDREKRELQALRQSREDC GCHCDRICDPETCSCSLAGIKCQMD HTAFPCGCCREGCENPMGRVEFNQ ARVQTHFIHTLTRLQLEQAESEF/QG AGGPCPGQPTQPW*GGPGPYFPTGQ APHEQ*AGRQQLQQRHD\YSSTASS SASGTSEAPDCPTHPLPGPGFQPG VDDDSLARILSFSDSDFGEEEEED
3405	8902	A	3673	72	332	LPALETPRAQSKCSPPPQSWVSRDY RCVPTHALANF*IFGEMGS/LLCCPR LISNS\WPQGILPPPPKVLGLQGSYS AKITTGFFLK
3406	8903	A	3674	33	396	RVWYLHRVTGRPASCLREVPGGDS LETASLREIWRSRRCRAT/ECSQQL NHRLARQREHEARLRQQREQNSRY FTDV*HL\RSKQAEWSSKTTYQRSM HAYHREKMKEEKRRSLWARLEKL M
3407	8904	A	3675	217	935	QRQREKEDQIRQQWEQNSRYFRMS DICSSKQAEWSSKTSYQORMHAYQ REKMKEEKRRSLEARREKLRLQMQ EEQDLLARELEELR/REHELAKKN PGAAREAEISQRAEETDC*TTFVR TLEKEQPETSRDGAGPSPEACRLL GNAE/MKKKKQQAESAEGNKRYE NEYERARREALERMKAEEERRQLE DKLQAEALLQMEELKLKEVEVGT SPSQP*PPPQLLVSMRWALERLP
3408	8905	A	3676	1	382	EMEPCFVS*TGV*WHDLSSLPPLP KFKRFSLKIPEASWDYRRT/PMP/V LTGFHHVDQAGFELLTSSDPPTSAS QSVGITGMGDHTWPTLHTLTKPCE VDENAVMRELKLTGQGPLRKWQF EHLNPA
3409	8906	A	3677	1	2456	MPTYPKLEKTDQSTSYTKFNDLSPD SSRERYTSLEIKSVCYTALPEQGQK QLQLWYNVCVKTQCKTTQECSLKWI FTMNETSDREDGLPKGHVTDSEN DEPLNLNASDSESEELHRQKDSSE SEERAEPASDSENEEDVNQHGSSE SEETRKLP GSDSENEELLNGHASDS ENEDVGKHPASDSEIEELQKSPASD SETEDALKPQISDSESEEP RHQASD SENEPPKPRMSDSESEELPKPVSD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SESEPPRHQASDSENEELPKPRISD SESEDPPRHQASDSENEELPKPRISD SESEDPPRNQASDSENEELPKPRVS DSESEGPQKGPASDSETEDASRHKQ KPESDDDDSDRENKGEDTEMQNDSF HSDSHMDRKKFHSSDSEEEHKKQ KMDSDEDEKEGEEKVAKRKA LSDSEDEEKASAKSRVSDADDS DSDAVSDKSGK\KRRTIASDSEEEA GKELSDKKNEEKDLFGSDSESGNEE ENLIAD\NLENLVMKRK*NLQVLT KIWEEKGETQVKEAEDSDSDDNK RGKHMDFLSDFEMMLQRKKSMSG KRRNRDGGTFISDADDVVSAMIV KMNEAAEDLKETFIDSGVMSAIKE WLSPLPDRSLPALKIREGVLKILQE LPSVSQETLKHSGIGRAVVMYLYKH PKESRSNKDMAGKLINEWSRPIFGL TSNYKGMTREEREQRDLEQMPQRR RMNS/DLVVRHPERDLEKVLGTGEEK ALRPGDPGFVPRARVPMPNNDYV VRPKWNVEMESSRPGILKKGLSRLE KHKRRFAEQRLSKVHRAVKFSIEG NRMPL
3410	8907	A	3678	1	564	TLKQVGLTEHVMYLYNDPKESRSN KDMAGKLINEWSRPIFGLTSNYKG MTREEREQRDLEQMPQRRRN/DST GGQTPRRDLEKVLGTGKEKALRPGD SLNLV/PRARVPMPNNDYGVPRPK MKCGNGVIQVSGDPPQKGIQSDWI NQMRKFHRY*GKKADLAHAVENP AIEGNKMPIGDPCPGMCPPIILL
3411	8908	A	3679	63	361	
3412	8909	A	3680	151	384	
3413	8910	B	3681	385	479	MAGAFRRRFASEVRAQGLESLEH GLRCAGSLRGGQSLPTTMWSPVKV GFE*
3414	8911	A	3682	3	698	VFFFFFFSGCTRGPLFESDFHRAPHRC GQGLAAP*AAGAPQPRAPGETRGPE PAPHWRSASGDKPPGQAAPPALVP GEGPSWSDPRGHRCSQATLPRVL AGPLQP*LS*LSL*DPPELRS*LPL* LRL**SLEPP*PLLDSNRFP*PRSP PPLENPRPRPRPRKKPRPPAEPPRY PTESVSDDLPAWSTRISVHLQTS WPSWASLASSMFFKVTKPNSRELW SS
3415	8912	A	3683	138	550	FCCCFTSSEHSLAYGSCSPRRTEVL CAQQNPSETQAAPLAS\YMWK*PC NSRLKGPGLGEGWPES\RM TSGV TVPGGTSPGTRAGGSPCPGGLSPEA LRQ*GAGSGPRVSPGA/PGCGAPAA YGAASPCPQRCGAL
3416	8913	A	3684	2	555	FFFFFFLGAHVALYSNPTFTGLHIVV GKDWP*P*P*AAGAPQPRAPGETRGPE PAPHWRSASGDKPPGASGCLQLLF QGEVPPGDS*PQRSSLALRPPFPRVL GPGPFQPAKAKQRYRPPQGSQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						APP/GPPRKQPQPLRKVSG*SGGCDLRLRHRPACPGRVCTLAQLEPATRMGWSYVGQCGL
3417	8914	B	3685	95	371	MASDEGKLFVGGLSFDTNEQSLEQVFSKYGQISEVVVKDRETQSRGFGFVTFENIDDAKDAMMAMNGKSV DGRQIRVDQAGKSSDNPIPW*
3418	8915	A	3686	314	1055	SKCFHLHQVWKQKGEEYRVGTGYGWSWISKTHVYRFVFKLHGNTNVN YRKSLEGTKNNMDENMDES DKRCSRSPKKIKIEPDSEKDEVKGS DAAKGADQNEMDISKITEKKDQDV KELLDSDSDKPCRKTNGSRR*HENRVTCKLSGEFSSRCGQC**GFSSKD*LQKENKIIQTRWTS*KEN*TVYTGRKTA TRKNQVGGWN*GYRKD\STNSSKN LSESPVITKAKEGCQSDSDETRTEPKCK
3419	8916	A	3687	11	345	DSLTVASQSGVQWHNLISLQPLPPGVK*LFCLSLPSS*DYRRAPHPANFSF LVEMGFYHVGQAGLELLISSDLTSL ASQSAGITSVSHWAWPENVYLN LQ QTEKSLMVSG
3420	8917	A	3688	1	521	NPTKSCMLEG*NPHVHCKREGAQA ITGMPI*KATKYLKYFLLQKLCVPF QS/YESGVGRCTQDRHWGWTHHQ WPRKGTEICLQVQSYAELKGIDVDS LVIEHIQ/V/NKAPIMYHLTYRTHGQ MNP/YHKLPCHIOMMLSEKKHLVP KAEKEDARKKKIPQKKHKLKRQTN SAKRKCK
3421	8918	A	3689	1	281	ETGSHSDAQAGVQWHDLGPMQPLP PGFKRFSHLSLLSSWDYRHAP/PRPG LFL*RWGFHQVGQVDLELLNSSDP ASTSQSAGITSASHRAWPN
3422	8919	A	3690	3	314	HAEHEITELTATFTKFDNRDGNRILDE KEQEKMRQDLEER\LTRVLQLET VLERVVAQIDALSSKLEMLEKKGVSLSLFTSFNIRAFKSLFSHYSSVTPIN YL
3423	8920	A	3691	61	400	LVTGIWSATCLWVLLLLLFEKGCPS VQRLQCS\NVITACCSNL\RGSDN PPTSASRVPGDHRCCHYTWANFLIF LWEMRSHCVGFRLGLGTPVLKLQT ILQPQPPKVLGLQA
3424	8921	A	3692	33	436	REQEL/CKGKQKDGTSFGEYGGWY KACKVDSPTVTTTLKNLGALYRRQ GKFEAAETLEEAAMRSRKQGLDNV HKQRVAEVLNDPENMEKRRSRESL NVDVVKYESGPDGGGEGVSGRASFCGKRQQQWPGRHR
3425	8922	A	3693	37	355	NSEYGGWYKACKVDSPTVTTTLK NLGALYRRQKGFEAAETLEEAAMR SRKQGLDNVHKQRVAEVLNDPEN MEKRRSRESLNVDVVKYESGPDGG EEDGTGSLKRS
3426	8923	A	3694	229	2000	QRERARPSGARMYDTMSTMVYIK

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						EDKLEKLTQDEIISKTKQVIQGLEAL KNEHNSILQSLLETCLKKKDDSN LVEEKSNMIRKSLEMLELGLSEAQV MMALSNHLNAVESEKQKLRAQVR RLCQENQWLRDELANTQQLQKSE QSV AQLEEEKKHLEFMNQLKKYDD DISPSEDKDTDSTKEPLDDLFPNDED DPGQGIQQQHSSAAAAAQGGYEI PARLRTLHNLVIQYASQGRYEVAVP LCKQALEDELEKTSBGHDHPDVATML NILALVYRDQNKYKDAANLLNDAL AIREKTLGKDHPAVAATLNNLAVL YGKRGKYKEAEPLCKRALEIREKV LGKDHPDVAKQLNNLALLCQNGG KYEEVEYYYQRFLEIFQTKLGPDDP NVGKTKNNLASCYLKQGGKFKQAET LYKEILTRAHEREFGSVDDEANKPI WMHAEERECKGQKDGTSFGY GGWYK\ACTVDSPTVTTTLNLGAL YRRQGFEEAETLEEAAMRSRKQG LDNVHKQ\RAEVLN*PLRTLEKPQ EPVESL\NVDVVKYESGPDG\GEEV SMSVEWNGGVSGRASFCGKRQQQ QWPGRHR
3427	8924	A	3695	1	314	KVDSPTVTTTLKNLGALYRRQGGK EAAETLEEAAMRSRKQGLDNFTKQ RLPEVLNDP\ENMEKRRSRESLND VVKYESGPDGGEEVSMSVKWNGM RKMMLGAG
3428	8925	A	3696	2	450	VNKAGGLIYQLDSYAP\RAEAEKTF SYPLDLLKLHDERVLVAFGQRDGI RVGHAVLAINGMDVNGRYTADGK EVLEYLGNPANYPVSIRFGRPRLTS NEKLMLASMFHSL\KFVVLADP\RQ AGIDSLLRKIYEIYSDFALKNPFFSL EMP
3429	8926	A	3697	2	823	FGTRGKAAMAIFS\YVVVNKAGGLI YQLDSYAPRAEAEKTF\SYPLDLLK LHDERVLVAFGQRDGI\RVGHAVLA INGMDVNGRYTADGKEVLEYLGNP ANYPVSIRFGRPRL\TSNEKLMLAS MFHSLFAIG\SQLSPE\QGSSG\GCL TDPFQFH\CSRTLTGIKF\VVADPRA QAGIDSLLRKDFMEILLQTLPLKNPI PIPLEMP\IRCEPL*PQNPEA*SLEVA EKAG\TFGPRVHRLNPVMGPPQNPE SSLQQEYCLLTLPVEIPAALVSAP
3430	8927	A	3698	165	354	ENFGGKITNFAKLFGYILPYSHYFW CLEKNRNR/SLTLLPRLVSNSWAQA FLLWPPKVLRLQA
3431	8928	A	3699	3	166	SETGFCHVAQAGLELLVSRSPASV SQS\TGISHQARPSISYFYDHSAPITH TDH
3432	8929	A	3700	1	421	ETKSHSVTKTEVEWRDPSSLQPLSP GFKQFSCRS\PNASWDYR/PSPANFV FLVETGFYLVGQAGLELLTSNDPPA SASQSAGITGVSHCAQPRITNSLTTA SFIQPRKHSEFPVMTCPSSNATESK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VGGRGPHGAIARLM
3433	8930	A	3701	2	205	APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQFHLPRPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ
3434	8931	A	3702	2	205	APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQFHLPRPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ
3435	8932	C	3703	282	445	MISAHCNLLPPEAGELLEPGGRRFS EPLHSSLMTEQDSVSKINKNKTSIS NPE*
3436	8933	A	3704	170	607	WPSG*FQR*SMRLKYYKIHLNVSRR PQLAPGKELYFSF*LLFYFYFYFIHIII FEMESHSVTRLECSGTISAHCNHL PGSSDSPASASPVAGTLIDACHHTW \LIFYNF*VEMGFHHVQGAGLKLTT *VTHPPRPSKVLGLQA
3437	8934	A	3705	3	231	FETESLFPRLECSGTISAHCNLRSLG SSNFWLIFCILVEMGFHHVGQTSLE LLTSSHPTSAFQSARITGVSHRTW
3438	8935	A	3706	4	144	
3439	8936	A	3707	333	416	FTGLPCLFSPQNNVSLQSCIDLKFN NN
3440	8937	A	3708	1	1219	MAAVPELLQQQEEDRSKLRSVSVD LNVDPQLQIDIPDALSERDKVKFTV HTKTTLPFQSPEFSVTRQHEDFVW LHDTLIETTDYAGLIIPPAPTKPDFD GPREKMQKLGEGECSMTKEEFAK MKQELEAEYLAVFKKTVSSHEVFL QRLSSHPVLSKDRNFHVFLDYDQDL SVRRKNTKEMFGGFFKSUVKSADE VLFTGVKEVDFFEQEKNFILNYN RIKDSCVKADKMTRSHKNVADDYI HTAACLHSLALEEPTVIKYLKVA ELFEKLRKVEGRVSSDEDLKLTLL RYYMLNIEAAKDLLYRRTQS/ALI DYENSNKALDKARLKSVDVKLAEA HQQECCQKFEQLSESAKEELINFK \RKRVA\AFRKNLIEMSELEIKHARN NVSLQSCIDLFEE
3441	8938	A	3709	527	724	TMKIGLGFSLVSINIFSPVELINFKR KRVA\AFRKNLIEMSELEIKHARN NVSLQSCIDLKNN
3442	8939	A	3710	1	1220	QEGGSAGSAGSGADGTGLRQSLAG HVGRPGRGQWGQRSGDLPGHRPP PARSEHRCVAEG/NLSLYVFGGYNP DYDESGGPDNEDYPLFRELWRYHF ATGVWHQMGTDGYMPRELASMS LVLHGNLLVFGDTGIPFGESNGND VHVCNVKYKRWALLSCRKPKPSRI YGQAMAHNGSLYVFGGTTGYIYST DLHKLDLNLTREWTQLKPNLSCDL PEERYRHEIAHDGQRIYILGDGTSW TAYSLNKIHA\YNLET\NAWEEIATK PHEKIGFPAARRCHSCVQIKNDVFIC GGYNGEVILGDIWKLNLQTFQWVK LPATMPEPVYFHCAAVTTA\GCMYI HG\GVVNIH\ENKRTG\SLFKI\WLVV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PSLLELAWEKLLGAFNLANL\RTQLLH\LGFTQGLIERLK
3443	8940	A	3711	2	266	FLMESRSVTRLECSSTITAHCNLCPLVSSDSA VSASQVAGTTGMRHHAQLIFVFLVETGFHHVQDGLHLL/NIVIHLPRPPKVLGLQA
3444	8941	A	3712	1	453	FKRAMDLVQEEFLQRLDFSQHSWLPARALVEEALAQRFOVDPSGEIVELAKGACPWKEHLYHLESGLSPPVAIFVVIYTDQ/RWTVANIAGCPLPEPWRGLRDEALDQVSGIPGCIFVHASGFIGHRTREGALSMARATLAQRSFLPQIS
3445	8942	A	3713	20	891	RWNSRYDHHQRSFTETMSSLSPGK PWQTKLSSAGLIYLFHGAQVLAQL LGTSEEDSMVGTLYDKMYENFVEEVDAVDNGISQWAEGERYALTTTL SARVARLNPTWNHPDQDTEAGFKRAMDLVQKEVSCRD*IFYQHSWLP ARGLGGKSHLPQRIPRWNPSPGK\IVE LAKRCHVPWKEHLLPPGNLGLSPS KWPFIFFVIYTD/SRL/EQWRIQCVAQ/VSPTHSQSRAALPEPWRGLRGTRP WT*FSGIPGCIFVHASGFI/SAVNATREGALSMARATLAQRLIPTNLLV
3446	8943	A	3714	176	450	
3447	8944	A	3715	1	472	
3448	8945	A	3716	418	1354	AAARRATCLGCRSCSGATARRASS WRTAPRVHSAWKL\DGRRLASGS FDKTASRLLA WRRTRFGQKKTIIGG HGG*C/VTSFCWHPSNPEPICYGV/Y GDKTIRIWECEYKNALPLVNIKGE NINICWSPDWQTIAVGNKDDVVTFI *CQDTPFQSRRAVQVPRSTKSPWNH DHNMFLLTNGNGCINILSYPELKA\ VQSINAHPN\NICNQV*PHGESTLP QASCKMLLVSLWDVG*VSVCFGAF SRLDWAC*EPFSFSDGKMLASASE DHFIDIAEVETGDKLWEVQCESPT\ SQVAWAPQKASAGHLPR
3449	8946	A	3717	1	296	LWDV/EELVCVGAFLRDWP/VRTSV SAHDGKMLASASEDHFIDIAEVKTG DKLWEVQCESPTFTVAWHPKRPLL AFACDDQKTANMTSSREAGTVKPV GAS
3450	8947	A	3718	2	276	RSTFALVAPAGVQWHDNRSLOPLL PRFKQLSCLSLSSWDYRCPPPSPA NF/SLFLVETGFRHAGQAGLQLLTS GDLPTSASKSAGITGMGLQ
3451	8948	A	3719	3	613	GLRALRRGQGLPGL*CCSRPQPSPR AQGHPSMGGPMQRTVTPRGMA SV GPQSYGGGMRPPPNLAGPGLPAM NMGPVGRGPWASPSGNSIPYSSSSP GSYTGPPGGGGPPGTPIMPSPGDST NSSENMYTIMNPIGQAGRANFPLG PGPEGPMAAMSAMEPHHVNGSLGS GDMDGLPKSSPGAVAGLSNAPGTP

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						RDDGEMAA
3452	8949	B	3720	134	471	MYAKGGKGSAPSDSQAREKLALY VYEYLLHIGAQKSAQTFLEIRWEK NIMPSPGDSTNSENMYTIMNPIGQ GAGRANFPLGPGPEGPMAAMSAME PHHVNGSLGSGDMDG*
3453	8950	B	3721	223	692	MEPSPRAQGHPSMGGXMQRVTPPR GMASVGPQSYGGGMRPPPNLSLGP GLPAMNMGPVGRGPWASPSGNSIP YSSSSPGSYTGPPGGGGPPGTPI MPS PGDSTNSENMYTIMNPIGQAGRA NFPLGPGPEGPMAAMSAMEPHHVN GSLGSGDMDG*
3454	8951	B	3722	228	292	XLARDDHERVMGRQPRASLRA*
3455	8952	A	3723	1	1753	MYAKGGKGSAPSDSQARENLSAF QAATELTSLDRLALYVYEYLLHIGA QKSAQTFLEIRWEKNITLGEPPGFL HSWWWYGLGCCGVFWDLYCAAP DRREACEHSGEAKAFQDYETPERP AHRHGNAGRAGSSSGMIDVGGSSD PQILRPPTTPVCSLTNASSLSHGAGHL QRGGGTPQSAAAAPSPVMGSMAPG DTMAAGSMAAGFFQGPSPSPH NPNAPMMGPHGQPFMSPRFPGGPR PTLRD\GSQPPAGPPWVSPSSPG\A MEPSPRAQGHPEHGRPNARGVTPP RG/MGPAWGPWAYGGGMRPPPNLSL TRPRACLPMNMGPRKFVGPWAQPP VEYSIP\YSSSSPGSYTG\PPGGGGPP GTP\IMPSPGDS\TNSENMYTIMNPI GQGADRANFPLGPGPEGPMAAYG \GMEPHHVNGSLGSGDMDG\LPREF PQAPVAGLSNAPGVTPRDDGEMAA AGTFHAPSSQSE\NYS\GMTMSRV NWAAAPGALCGPRLPRRCLRAK GLKVTPSGTLDLANQGLPMLGGP TRKTLTILLKTQGPREFFSVWTLPA ICILVPERKALWGGPSSPGRQGGGA H
3456	8953	A	3725	65	210	ATRAGLIFDDSEHDVWQDASSFRL IFIVDGWHPELTPQQRSLPAI
3457	8954	A	3726	2548	3800	NSLILLFFFFRQRLTLECSGVISAH HNLHLPSSSNS/P/ASAS*VAGITGM HRHAWPICIFLVETGFRHVQGAGLE LLTSGDPPAPTSQSM*ATTSGLILL SKILFPFHSTKVFK*SCPS*KILKEEN CSVINEWFNSESSYTSKEKNLVPN AC*EITM*VATNCDFT/SLL*RSENY PKLFHNNETTSQKIHLKIKISRPATS GQWILFSLVWWRARKG*GILMIHN GILY*TIC*IKLHRLP*GMDYPNQPD/ MKSGWDKRMSHTL*F*GKEIVDFD QNQQNKLSTLYLSVQE**HEEFFFR DLKYNKPGSTIKSLVSF/HSLTLFFFF FFEARSHSASQAGVQWGNIGSLQPA PPGLKRSSYLSLLSSWDYRRVPPHP ANFCIFCR/GWGFGVSPCCPGSSGTP VLKWRAHLSLPNC

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3458	8955	A	3727	2	217	SSPSPPHPPASPPSSPSPASPPPPSLP LPSPDFPPLSPCSSLSPFSSFSPPPSPP SPFFSRGSPSPDNFH
3459	8956	A	3728	25	396	ISGRSTFSLFSRQGLSALSPRLE\CSV AISAHCNLRPLPGSSN\GTTGA*HHTR LILYF/LAEMGFHHVVGQAGFEVLT SNPPASASTSARITGMSNRT\GHLFN FHP*MCYKYRCGSLAGRGGSRW
3460	8957	A	3729	80	460	YISLNVTTHLIFFFFFFLRQGL\CSVTQ AGV\QWCNLSLQPLPPRFK\NWDY RCVTPHLANFVFLVEMGF/LPASAS QSAGITGVSHCTQLGVFICICYGSSH GVRQSWHQFCSSKLLVKSGRVGVG LLG
3461	8958	A	3730	1	316	FFFFFETESHIVQAGVQWRDLSSL QPPPPRFKRFSSLSLPSSWDYRHVPP RPA\NFAFLVEMGFHHVVGQAGLELL TPGDPPSSASQSAGMTGVTHCAWP RCLMF
3462	8959	A	3731	3	1717	RPQTLKGHQEKIRQRQSILPPPOGPA PIP\SSTAAGIPRRPRIAWARR/WPLS EPGFRRRESQEEPRAVLAQKIEKET QILNCALDDIEWFVARLQKAAEAF KQLNQRKKGKKKGKKKAPAEGVLT LRARPP\PEGEFIDCFQIKLAINLL AKLQKHIQNPQRR\DVVHFLFGPLD LIVNTCSGPDIAHSVSCPLFSRDAVD FLRGHLVPKEMSLWESLGESWMRP RSEWPREPQVPLYVPKFHSGWEPPV DVLQEAPWEVEGLASAPIEEVSPVS RQSIRNSQKH/RPHFRAHPPGGCPY HQSAPHILTRGYQPTPAMAKYVKIL YDFTARNANELSVLKDEVLEVLED GRQWWKLRSRSGQAGYVP\GNILG EARPEDAGAPFEQAGQKYLGTQP DPQATPKLPGGT/IDELMQHMDDEVN DELIRK\NTTSRAQPQRHFRVERSQP VSQPLTYESG\PDEVRA\FLEAKAFS PRIVENLGILTGPQLFSLNKEELKKV CGEEGFRVYSQLTMQKAFLEKQQS GSELEELMNKFHSMNQRRGEDQLG PAALGWGLRRGSPPTMHGVFLYV YVFCIK
3463	8960	A	3732	1	324	
3464	8961	A	3733	1	581	MDKLETTYSLQRLSQEEIESLNRTI MSFKTKSVINTIPTKKSPGPDRLTAN FYQMCKEELADIIHGLCIRHEMTPV NPGVGQCCTSSYANRRPCFSSLVVD ETYVPPAFSDDKFIFHKDLCQAQGV ALQTMKQEFNLVKQKPQITEEQ EAVIADFSGLLEKCCQGQ\NQEVC AEEGQKLISKTRAALGV
3465	8962	A	3734	39	1935	LATMKWVESIFLIFLLNFTESRTLHR NEYGIASILDSYQCTAEISLADLATIF FAQFVQEATYKEVSKMVKDALTAI EKPTGDEQSSGLENQLPAFLEELC HEKEILEKYGHSDCCSQSEGRHNC FLAHKKPTPASIPLFQVPEPVTSCEA

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						YEEDRETFMKNKFIYEIARRHPFLYA PTILLWAARYDKIIPSCCKAENAVE CFQTKAATVTKELRESSLLNQHAC AVMKNFGTRTFQAITVTKLSQKFTK VNFTEIQKLVLDVAHVHEHCCRGD VLDCLQDGEKIMSYICSQQDTLSNK ITECKLTTLERGQCIIHAENDEKPE GLSPNLNRFLGDRDFNQFSSGEKNI FLASFVHEYSRRHPQLAVSVILRVA KGYQELLEKCFQTEPLECQDKGE EELQKYIRE\GQPWAKGSSGFSKK* GEYYLQTGSSLSLQQ*RPPQLTSSSEL MAITRKMAATAATCCQLSEDKLLA\ CGEGAADII\GHLCIRHEMTPGKPL VFGQVPAPPSICPNRRPHASSTWVV DGNIWSPPCISLMTKFHFSP*RDPGG PSLQGW*ALAKPMKAKRFPSTLV KAKGPQIPGGNNSEAVIARFPQAWL EK\CCQ/GPQEQEVCF AQEGTK\LSK TRALGV
3466	8963	A	3735	95	272	RALQPDTTWE*GSQRRPWL PQVTN KPV L*SKTSKS
3467	8964	B	3736	344	1420	MLLKT VLLLGHVAQVLMLDNGLL QTPPMGWLA WERFCNINCEDEPK NCISEQLFMEMADRMAQDGWRDM GYTYLNIDDCWIGGRDASGRLMPD PKRFPHGIPFLADYVHSLGLKLG IY ADMGNFTCMGYPGTTLDKVVQDA QTFAEWKVDMLKLDGCFSTPEEAA QGYPKMAAGLNATGRPIAFSCSWP AYEGGLPPRVNYSLOADICNLWRN YDDIQDSWRSVLSILNWFVEHQDIL QPVAGPGHWNDPDMLLIGNFGLSL EQSRAQMALWTVLAAPLLMSTD LR TISAQNMDILQNPLMIKINQDPLGIQ GRRIHKGSWMPKGSVCVPGCLRDPG TQDSQGKISHRSVHAASVQQG*
3468	8965	B	3737	49	2119	MALWTVLAAPLLMSTD LR TISAQN MDILQNPLMIKINQDPLGIQGRRIHK EKSLIEVYMRPLSNKASALVFFSCR TELCLIATTSCLGQLNFTGSVIYEAQ DVLLS*
3469	8966	A	3738	139	536	QSLGFIPFRKRQRISISYTFYFETGS YSVAQAGVQWHNLGSLQPRPPGFK QSSCLSPPGSWDHWRA PPHQANFA LLVETGSPHAAQASLKLSSSDPSA LASQSTGITGVSHHGQPYISHTLIIFI GKFY
3470	8967	A	3739	1	213	QFSCLSLPSSRDYRHEQP/PLIFVFLV ETGFYHVGQAGLELLTSGDPPALAS QSAEITGVSPRTRPNNLKS
3471	8968	B	3740	75	729	MEGTAGGERPSVVNGDSGKSGGVG DPREPLSCLQEGSGCHPTTESFEKSV REDASPLPHVCCCKQDALILQRLH HEDGSQHIGLLHPGDRGPDHEYLLV EEAERAMSEREARPNEESVQRNRLI CRTNPYRIFEYLP LSLEEAFFLVYAL GCLSIYYEKEPLTIVKLWKAFTVVQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PTFRTTYMAYHYFRSKGWVPKVG KYGTDLLLYRKGPFFYHAX*
3472	8969	A	3741	1	2649	
3473	8970	A	3742	41	656	PVPRPCCGLRARSWPSSPRAARAAL PHGESALSRLRALLAARASLDLCL FAFSSPQLGRAVQLLHQRGVVRV VTDCDYMALNGSQIGLLRKAGIQV RHDQDPGYMHKFA\VDRRVLITG SLNWTQTQAIQNNRENVLITEDDEYV RLFLEEFERIWEQFNPTKYTFPPKK SHGSCAPPVSRAGGRLLSWHRTCG TSSESQT
3474	8971	A	3743	3	267	FNMESQSLASLKCSGAVSAHCNLCF LGSSNSPASASRVSGITGVLYHTWLI FVFLVQTGFHHVQGAGLELL/NLVI HPPRPPKVLGLQA
3475	8972	A	3744	2	430	FFFETGGAFVTQAGVQWPNLSSLPQ SPPGFKPSSHLSLPSTWDYRYTPPCP ASFCIF\TDTGCHVDQAGLELLASC NLPASASRSAGITGVSHHACPFLLFS FFKSGITSPNYPISHHEIIESNVAPVF LFEDSTAIYVYYF
3476	8973	A	3745	2	316	EFLFFETEFCSVTRLECSGAISAHCK LCLGSRHSPASASRVARTTGTRHH AQRIFVFSVETGFHRVS\RDGLDLL/ NLVIHPPQPPKVLGIRGREPPCPACF FAF
3477	8974	A	3746	1	1053	
3478	8975	A	3747	1	3011	SLQRLPGLMHNLTQFLLDGNFLQSL PAELENMKQLSYLGLSFNEFTDIPE VLEKLTAVDKLCMSGNCVETLRQ ALRKMPHIKHVDLRLNVIRKLIAD VDFLQHVTQLDLRDNKLGDLAMI FNNIEVLHCERNQLVTLDICGYFLK ALYASSNELVQLDVYPVPNYLSYM DVSRRNL\ENVPEWV\CESRKLSF GILGHN\QIC\ELPARLFCM\SSLRKLL GQGHN\QLARLPERLERTSVEVLDV QHNQLELPPNLLMKADSLRFLNAS ANKLESPPATLSEETNSILQELYLT NNSLTDKCVPLLTGHPHLKILHMA YNRLQSFPASKMAKLEELLEEIDLSG NKLKAIPTTIMNCRRMHTVIAHSNC HRGPFPEVM\QLP\EIKCVD\LSCNE\ LSEVTLP\ENLPSPNCRSLDLTGNPR PCPLITKPLELLNNIRCFKID\QPSTG DG\SGAPAVW\SHG\YTEA\SGVKNK LCV\VALSVNNFCDNREALYGVFD GDRNVEVPYLLQCTMSDILAEELQ KKTKEEEYMNVTFIVMQRKLGT GQKLGGAAVLCHIKHDPVDPGGSF TLTSANVGKCQTVLCRNGKPLPLSR SYIMSCEEELKRIKQHKAITEDGKV NGVTESTRILGYTFLHPSVVP QSVLLTPQDEFFILGSKGLWDSLSV EEAVEAVRNPDALAAAKKLCTLA QSYGCHDSISAVVVQLSVTDSFCC CELSAGGAVPPSPGIFPPSVNMVIK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DRPSDGLGVPSSSSGMA\SEISSELST SEMSSEVGSTASDEPPPGVALSENSP AYPSEQRCMLHPIWLSNSFQRQLSS ATFSSAFSDNGLDSDDEEPIEGVFTN GRRVEVEVDIHCSRATEKEKQQHL LQVPSEASDEGIVISANEDEPGLPRK ADFSAVGTIGRRRANGSVAPQERSH NVIEVATDAPLRKPGGYFAAPAQPD PDDQFIIPPELEEEVKEIMKHHQEQQ QQQQPPPPQLQPQLPRHYQLDQLP DYYDTPL
3479	8976	A	3748	1	246	LPTLECSGMISAHCNLR LPGSSDSP ASASQVAGITSAHHYA WL VFVFSV EMGFHHVGQGWRS L D LVIRPPQPP KMLGLQA
3480	8977	A	3749	153	527	LLVFYLP T PSLK GGLRQLDMSLLCQ LYSLYESIQEYKGACQAASSPNWTY ALENGFFDEEEYFPEQNSLH DRRD RGPPRDLSL P APPSPAATGFWSPSR GSWEGCDCWEALPTGHA VI CCFS
3481	8978	A	3750	2	377	IPAASTFFCFLRQSLTLWPHAGVQW CGLSSLHPPPPGFM L FCSLSPSSWD YRRPPRPAKFSVFLVETGFHRVSQ DGLDLMTSDPPALASQSAGITGVS HCTRPKEA YFYFLALDPRCKDGVR
3482	8979	A	3751	2	294	LFLHADRLEYSGMTISHLQPQTPGA QGDPLTSSLPREVGLQ/CVCHHTQL FFF/CIFVETESHHLA\RAGL KLLGSS DPTASPSQSDGITGMSHSCPSTF
3483	8980	A	3752	80	267	RQGLTILPRLVLNSC/RLKLSSHLSL P KYWDYRQEP PCLAIS I IFFKKS LIYY LNLAILYFKCK
3484	8981	A	3753	1	972	
3485	8982	A	3754	1	283	PKPQEIELPEAKNR\PWIFNKILGTTV KLMELKPNTCYCLSVRAANTAGVG KWCKPYKVSPGKRGALGVERS PKP REPGLWRLGTPLCPHDSSG
3486	8983	B	3755	346	472	XRNMN I LQYCPSSDMWTLFETCDV HIRKQQMVSVEETIYIVGG*
3487	8984	A	3756	1	1346	MSAEEMVQIRLEDRCYPVSKRKLIE QSDYFRALYRSGMREALS QEAGGP EVQQLRGLSAPGLRLVLD FINAGGA REGWLLGPRGEKGGGVDEDEEMD EVSLLSELVEAASFLQVTSLLQLLS QVRLNNCLEMYRLAQVYGLPDLQE ACLRFMVVHFHEVLCKPQFHLLGS PPQAPGDVSLKQRLREARMTGTPV LVALGDFLGGPLAPHYPYQGEPPSML RYEEMTERWFPLANNLPDLVNVR GYGSAILDNYLFIVGGYRITSQEISA AHFLQGP/RTNEWLQVASMNQKRS NFKLVAVNSKLYAIGGQAVSNVEC YNPEQDAWNFVAPLPNPLAEFSAC ECKGKIYVIGGYSTRDRNMN I LQYC PSSDMWTLFETCDVHIRKQQMVS EETIYIVGGCLHEIRGPNRRSSQSED MLTVQSYNTVTRQWLYLKENTSKS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GLNFDLCAP
3488	8985	A	3757	3	358	TNSMPPMMSMSYRICAMLKGE/DV QALRRAHQRNVKHMROQLMDRGL PCHPLPPANINPIRV/DPHPCPIALS HPIYSWSLTLPNKPTSVAVFNYLLS CLTIPFIASFVSLFEKLSAILD
3489	8986	A	3758	1	164	GSTTPAMEFASLFFKILLIDCRD/RG LALLPRLVLSSWPQVIFLPWPPKFL GLRT
3490	8987	A	3759	3	280	FFFETESHSAVARLEYRGITLAHCILC RQGSSNSPASDPQVAGTTGTRHRA QLTFV\FLVQMGFFHFGQAGLELPN LGIHPTSASPKCWDLPA
3491	8988	A	3760	3	516	AQHQPMMNIFPYPVGVHAPLMNIQR NPFNIHPQLPLHLHTGVPLMQVATP TSVSQGLPPPPPPPPSQVNYIASQ PRWKRNCTKLQIQEKAAQEVKLA KPFYQNKDITKEEYKEIVRKAVDKV CHSKSGEVNSTKVGNL\VKAYVDQ YEYSRKGSRKLEWGPVSTGKN
3492	8989	A	3761	173	411	
3493	8990	A	3762	438	789	LTWSTPVLPAAPGKYGNFGQ PSSGNTSSSSHSQRPLMAAVKLAES KVSVAVEASADSSKTDKKLQIEK AAQEVKLAIKPFYQNKDITKEEYKE IVRKAVDKCVLLECSIQKM
3494	8991	A	3763	1097	4669	ILLGTSCGYALAHTQEGEEKKQTS GTSNTRGSRRKPAITPTRRSTRNT RAETASQSQRSPISDMSGCDAPGNS NPSLSVPSSAESEKQTRQAPKRKSV RRGRKPPLKKKLRSSVAAPKSSS NDSVDEETAESDTPVLEKEHQPDV DSSNICTVQTHVENQSANCLKSCNE QIEESEKHTANYDTEERVGSSSSESC AQDLPVLVGEEGEVKKLENTGIEA NVLCLESEISENILEKGGDPLEKQDQ ISGLSQSEVKTDVCTVHLPNDFPTC LTSESKVYQPVSCPLSDLSENVESV VNEEKITESSLVEITEHKDFTLKTEE LIESPKLESSEGEIITVDRQSVKSPE VQLLGHVETEDVEIATCDTFGNE FNNIQDSENNLLKNNLLNTKLEKSL EEKNESLTHEPRSTELPKTHIEQIQK HFSEDNNEMIPMECDSECDQNESE VEPSVNADLKQMNENSVTHCSENN MPSSDLADEKVETVSQSPESPKDTI DKTKKPRTRRSRFSPTTWSPNKD TPQEKKRQSPSPRRETGKESRKSQ SPSPKNESARGRKKSRSPKDDIA RERRQSQRSPKRDTTRESRRSELS PRRETSRENKRSQPRVKDSSPGEKS RSQSRERESDRDQRRERERTRK WSRSRSHSRSPSRCRTKSKSSSFGR DRDSYSPRWKGRWANDGWRCPRG NDRYRKNDPEKQENENTRKEKNDIH LDADDPNSADKHNDCPNWITEKI NSGPDPRTRNPEKLKESHWENRN ENSGNSWKNFGSGWVSNRGRGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GNRGRGTYRSSFAYKDQENNRWQ NRKPLSGNSNSSGSESKFVEQQSY KRKSEQEFSFDTPADRSWTSASSW AVRKTLPADVQNYYSRRGRNSSGP QSGWMKQEEETSGQDSSLKDQTNQ QVDGSQLPINMMQPMNVMQQQM NAQHQPMMNIFYPVGVHAPLMNIQ RNPFNHPQLPLHLHTGVPLMQVAT PTSVSQGLPPPPPPPPSQQVNYIAS QPDGKQLQGIPSSSHVSNMSTPVL PAPTAAPGNTGMVQGPSSGNTSSSS HSKASNAACKNWQKGKVSVAVEA SAIYSSKTDKKFAKFEKAAQVVKI WANKPFYQNKDITKEEYKEIVRKA VDKVCHSKSGEVNSTKAAANLVKA YVDKYKYSRKGSLLKKTLEPRVTE KDLG
3495	8992	A	3764	108	253	
3496	8993	A	3765	2	283	RRLFFFFETESRSVSRLCSGNISAH NLH/LPGSSNSPGSASRVAGITGACH HAQLIFVFLVETGFHHVGGAGLEL L/NLMICPPQPPKVLGLQA
3497	8994	A	3766	1	290	RSTFFFFFLERVYCSVTRLCSGTIS AHCNLRPLPGSSGSHASVSQVAGITG AHHHTQPIFVFLVETGFHHIGQAGL ELL/NLMIHPPRPPKVLGLQV
3498	8995	A	3767	234	1449	EPGTHDPHLFLQGLLFWQAGGGEG GDGTGPAGGRQICVPPAALAHVRV PGEFLAQVAAAA*AIHDEQRPGKLH HPPG/ELMQRGVASESYMIVAPPMP SSWSSSGTNGPPSPTNLT*PIVHFIFS APTP/TKKTTTNTAMKTATHIPDVQ SAFCSPHSGTQRGDGLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNACLEAAAGAAAE DSGAARGSLQPAPAPPPGDPAAQA SVSNGEDAGGGAGRELVDLKIIWN KTKHDVKFPLDSTGSELKQKHSIT GIPDESRRRGPPAGPYQQSQRLEL YAQATEALLKTGAAYPCFCSPQRLE LLKKEALRNHQTPR
3499	8996	A	3768	1	8157	
3500	8997	A	3769	1126	1355	
3501	8998	A	3770	1	1611	MGSRCNLNPPPPAHSDDTGKDSFGNI RGAETGQGASACSVTSARVTCGAG SEPHSHRNPGISAQVGLAPSYGAAR GRRRPLALQQSPQERRHVGWNSTR GLLPASLPGTASSQSASATASAALP LKVTGPLARNPTPPWTAALATR GQRPEKGLFPGPAPFSLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNACLEAAAGAAAE DSGAARGSLQPAPAPPPGDPAAQA SVSNGEDAGGGAGRELVDLKIIWN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KTKHDKFPLDSTGSELKQKIHSIT GLPPAMQKVMYKGLVPEDKTLREI KVTSGAKIMVVGSTINDVLAVENTP KDAAQQDAKAEENKKEPLCRQKQ HRKVLDKGKPEDVMPSVKGQERL PTVPLSGMYNKS GGK VRLTFKLEQ DQLWIGTKNGTEKLPMGSIK\NVVS DPI\EGHEDYHNDGRFQLAPTEA\SY YWVYVWPTQYVDAIK\DTVLGKW QYF
3502	8999	A	3771	482	631	AGGWGPQAPDTPWVGPAQAGRL HPLRSTKRS/MSVPATRTTVPLTVM Q*RRVCRWCWGPLGHWEAHGFLV SGDVNHFGGPAALLL
3503	9000	A	3772	1	1579	
3504	9001	A	3773	3	486	DRYMLTRDYLTVKVWDLNMEARP IETYQVHDYLRSKLCSLYENDCIFD KFECAWNGSDSVIMTGAYNNFFRM FDRNTKRDVTL\EASRESSKPRAVL K\PRRVCVGG\KRRRDDISVGQLGTF TKKIL\HTAWHPAENIHLPAATNN LLHLSRGKVNSDMH
3505	9002	A	3774	72	1317	KLLPAPRQPPRPTNGSPRDPTPAQV* VEAPAGSSQ*TAP/ARRPLRAARTLP AAEAAGLTLRGCFHGDGRACAAL RRWPWRQLRGWGFVPAPPLL RTP AELVG/RSPEPRCPGKVSMAEFLTEF LEIPPFNKQYTESQLRAGAGYILED NEAQVDVLESQFSQLLHQINSTRDF ESIRLAHDHFLSNLLAQSFILLKPS VEEKSEPQDFQEADSWGDTKRTPG VGKEDAAEETVKPGPEEGTLEKEE KVPPPRSPQAQEA PVNIDEGLTGCTI QLLPAQDKAIVFEIMEAGEPTGPILG AEALPGGLRTL PQEPGKPKDEVLR YPDRSLSPEDAESLSVLSVSPDTAN QEPTPKSPCGLTEQYLHKDRWPEVS PEDTQSLSLSEESPSKETSLDVSSKQ LSPKALAPFQLGN
3506	9003	A	3775	1	350	FGTRKPGAVGAGEFVSPCESGDNT GEPSALEEQRGPLPLNKTFLGYAF LLTMATTSDKLASRSKLPDGPTGSS EEEEEFLEINPPFNKQYQESQLRAGA GYILKEFKEAQVRSFFV
3507	9004	A	3776	3	318	RRGLTLSSRLEYSGLIKTHWNHLHL GSSNPPTSASQVAGTTGTCHHAQLN FF/CLTFLVATRSHDIAQAGLELLDS SHPPASASHSAGTTGVNHHAWPAV ALLWIN
3508	9005	A	3777	4	378	ARNHHDLCFKKAILFFEMESCSVSQ AGVQWRVFGSLQAPPPGFLPFS/CY RCQPPSPANFFLYFLVETGFLF**RQ GFTVLDRMVSI*PRDPPALASQSA GITGVSPRTRQEGHS*R*EENGIG
3509	9006	A	3778	19	418	VEMGFCQADQAGLELLTSGDPPAS VSQSTGITVLSLSFFFETESRSVAQA GVQWRDLGSLQRPPPGFTPFSCSL PSSWDYRRPPRLANFFVFSVETGF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HRVSQDGLDLLT/S/GDPPASASQSA GDTGVSQAPV
3510	9007	A	3779	3	331	CFIFYFILFYFETESRSVAQAGVQWR HLDSLQAPPPGFTPFSCSLPSSWDY RRP/PPRPANFFVLLVQTGFHRVSQD GLDLLT/S/GDPLASASQSAGITGLSH RARPAQVS
3511	9008	A	3780	659	1092	AYNIFQFANRTNTGENLPKTLVIKYYI SSTFRSFFFFFFFFLRQSRVAQAGVQ WRNLGSLQPPPGFTPFSCSLPSSW DYGRPPRPANF/SVFLVETGFHRVS QDGLDLLT/S/GDPPTSASQSAGITG VSHCARPHSVLIKEITQT
3512	9009	A	3781	8	295	GRVSLRHQAGVQWRSLGSLQAPPP RFTPFSCSLRLRSWDHRRPPRPANL LYFLVETGFHRVRQDGLDLLT/S/GD PPALASQSAGITGVSHRAHPTY
3513	9010	A	3782	1474	1870	SARGITGVSHCTRPFSSFFFFFFFFFETE SHSIAQAGVQWRYLGSLQPLPPGFK QFACLSLSSSWDCRHAPRPANFLAF LVEMGFHHL*LELLISSDPPASAFKS ARITGVSHRAWPIRFFLLKNIFKFLN FC
3514	9011	A	3783	60	560	SDNYEKSHNIQEMTGLQSTLLVNN RVQLNFKWELNFFLSFLKQSSTLVA QAGVQWHDLGSLQPPPGVKRFSC LSLPSSWDYRHVPPCLANFVFLFFL VETGFLHVGQAGPELLTSGGPPASA SQSAGITSVTHRPLPEDSAFYQCRL NLWQRSPLECRCSLVLKT
3515	9012	A	3784	3	230	FFFKTESRSVTRLECSGAVLAHCNL QLPGSSNSPASASRVAGITRHVPPH RLIFVFLVETGFHHVGQDGLDLLTL
3516	9013	A	3785	3	4117	
3517	9014	A	3786	1	457	FPVRNLDLSTYICIGQKEEQLPSEYEL YADINHYGGMIGGHYTACAPLPND RSSQRNDVGWRLFDDSTLTTRDQS QAVTRYAYVLFYRRRNSPVERPPK AGHSEHHPDLGPAAEAAASQ/ATRP WPGPRGG/APRGQPLNASPPLWIGQ TPPLKQT
3518	9015	A	3787	1	298	NNQESCSVTEAGVQWHDLGSLQPP PSGFKQFS/CAQLLSSQDHRHMPPCP ANFYVFLIAEMGFYHVSQAGLELL TSSDLPALASQSAGIIGVSHRAWAK
3519	9016	A	3788	3	286	FFFFLFETQSHSHIRLECSGVISDYC NLCLPSSDSLVLASGVAGTMGVR HNARLIFVFLVKMRFHVGPRLGP QIPWTGIWIPSHFGPPQSA
3520	9017	A	3789	1	1422	
3521	9018	A	3790	353	470	IPGVSLYSLFSL/QNIPQSTEILKKL MTTNEIQSNIYT
3522	9019	A	3791	1328	1615	VSLFHAGVQWCDLSSLPAPPPGFKR FS/RLNLLSSWDYRRPLPHPSTFCKF VEMGFHHIGQAGLKLLTSGDPPASA SQSARITGVSHRARNCFYVT
3523	9020	A	3792	2	114	CQPGFVMKGPPHVRVQCQALNKWE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TELPSCSR/VCLPEA
3524	9021	A	3794	1940	2062	
3525	9022	A	3795	785	892	
3526	9023	A	3796	1	2745	
3527	9024	A	3797	1	3297	
3528	9025	A	3798	1	2202	
3529	9026	A	3799	1	2868	
3530	9027	A	3800	1	3237	
3531	9028	A	3801	1	2001	
3532	9029	A	3802	1	2982	
3533	9030	A	3803	1169	3269	VHCRFWILALCQMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDIMIVYLENPTVSAQNLLK LMSNFSKVSQYKINVQKSQAFLYT NNRQTESQIMSGLPFTITSKRITYLGI QLTRDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGGRINLVKMAILP KVIYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRALIAKSSLSQKNKTGGI TLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNYLIFDK PDKNKQWQKDSL FNKWCWENWL AICRKLKLDPFLTPYTKINSRWIKDL HVRPKTIKTLEENLGNTIQDIGMGK DFMSKTPKAMATKAKIDKWDLIK KSFCTAKETTIRVNRQPTWEKIFA TYSSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSEEDIYAACK HMKKCSSSLAIREMQIKTTMRYHLT PVRMVIKKSGNNRCWRGCGEIGTL LHCWWDCCLVQPLWKS VWQFLRD LELEIPFDPAIPLGIYPEDYKPCCYK DTCTRMFIAALFTIAKTWNQPKCPT MIDGIKKMWHIYTM EYYAAIKKDE FMSFAGTWMKLETIILRKLSQGQK TKHRMYSLIGGNLTMRTFGHSAGS HHTPGPIMRCGAGGGIALGEIPNVN DELMGTANQHGT CIPMQQNCTLCT CTLKLV
3534	9031	A	3804	2821	5793	
3535	9032	A	3805	2	256	KRSLSLPSRLECSGVILAHCKLRLLG SRHSPPSDSGAAGTAGARH HARLFF LYFLVFHRVCLDGLDLL/NLVIHLPR SPKVWGLQA
3536	9033	A	3806	1	2406	
3537	9034	A	3807	139	6503	
3538	9035	A	3808	1	3204	
3539	9036	A	3809	77	277	PHPTPCSCFPWSASSPLT*TH\QALT EEDEW*QAKNSGQAAQGQTPALPL GNLGQVTAPLCPRFIC
3540	9037	B	3810	21	219	MMPRSSRTKSCRSSCAWSSCMKE NKLRAEAERLGHELQQA GLKTKE AEQTCRHLTAQVRS LGGTX*
3541	9038	A	3811	1	6359	MTLHATRG AALLSWVNSLHVADP VEAVLQLQDCSIFIKIHDRIHGTEEGQ QILKQPVSERLDFVCSFLQKNRKH SSPECLVSAQKVLEGSELELAKMT

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MLLLYHSTMSSKSPRDWEQFEYKI QAELAVILKFVLDHEDGLNLEDLE NFLQKAPVPSTCSSTFPEELSPPSHQ AKREIRFLELQKVASSSSGNNFLSGS PASPMGDILQTPQFQMRRLKKQLA DERSNRDELELELAENRKLLETKDA QIAMMQQRIDRLALLNEKQAASPL EPKELEELRDKNESLTMRLEHETLKQ CQDLKTEKSQMDRKINQLSEENGD LSFKLREFASHLQQLQDALNELTEE HSKATQEWLEKQAQLEKELSAALQ DKKCLEEKNEILQGKLSQLEEHLSSQ LQDNPPQEKGEVLGDLVQLLETLLKQ EAATLAANNTQLQARVEMLETERG QQEAKLLAERGHFEEEEKQQLSSLIT DLQSSISNLSQAKEELEQASQAHA RLTAQVASLTSELTTLNATIQQQDQ ELAGLKQQAQEKQAQLAQTLLQQQE QASQGLRHQVEQLSSSLKQKEQQL KEVAEKQEATRQDHAQQLATAAEE REASLRERDAALKQLEALEKEKAA KLEILQQQLQVANEARDSAQTSVT QAQREKAELSRKVEELQACVETAR QEQHEAQAQVAEELQLRSEQQKA TEKERV AQEKDQLQEQLQALKESL KVTKGSLEEEKRRAADALEEQQRCI SELKAETRSLVEQHKRERKELEER AGRKGLEARLQQLGEAHQAETEVL RRELAEAMAAQHTAESECEQLVKE VAAWRERYEDSQQEEAQYGAMFQ EQLMTLKEECEKARQELQEAKKV AGIESHSELQISRQQNELAELHANL ARALQQVQEKEVRAQKLADDLSTL QEKMAATSKEVARLETLVRKAGEQ QETASRELVKEPARAGDRQPEWLE EQQGRQFCSTQAALQAMEREAEQ MGNELERLRAALMESQGGQQEERG QQEREVARLTQERGRAQADLLEK AARAELEMRLQNALNEQRFVATL QEALAHALTEKEGKDQELAKLRGL EAAQIKELEELRQTVKQLKEQLAK KEKEHASGSGAQSEAAGRTEPTGP KLEALRAEVSKLEQQCQKQQEQAD SLERSLEAERASRAERDSALETLQG QLEEK AQELGHSQSALASARELA AFRTKVQDHKAEDWKAQVARG RQEAERKNSLISSLEEEVSILNRQVL EKEGESKELKRLVMAESEKSQKLEE RLRLLAQETASNSARAAERSSALR EEVQSLREEAEKQRVASENLRQELT SQAERAEELGQELKAWQEKFFQKE QALSTLQLEHTSTQALVSELLSAKH LCQQLQAEQAAAEKRHREELEHSK QAAGGLRAELLRAQRELGELIPLRQ KVAEQERTAQQRLRAEKASYAEQLS MLKKAHGLLAENRWLGERANLG RQFLEVELDQAREKYVQELAAVRA DADTRLAEVQREAQSTARELEVMT

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AKYEGAKVKVLEERQRFQEERQKL TAQVEQLEVFQREQTKQVEELSKK LADSDQASKVQQQKLKAVQAQGG ESQQEAQRLQAQLNELQAQLSQKE QAAEHYKLQMEKAKTHYDAKKQQ NOELQEQLRSLEQLQKENKELRAE AERLGHELQQAGLKTKEVAEQVTCR HLYLPRLRSLEVAQVAHARPSSFRD LGKFQVATDALKSREPQAKPQLDL SIDSLLDSCEEGTPLSITSLPRTQPD GTSVPGEPASPISQRLPPKVESLESL YFTPIPARSQAPLESSLDSLGDVFDQ SGRKTRSARRRTTQIINITMTKKLD VEEPDSANSSFYSTRSAPASQASLR ATSTQSLARLGSPDYGNSALLSLP GYRPTTRSSARRSQAGVSSGAPPGR NSFYMGTCQDEPEQLDDWNRIAE QQRNRVCPHLKTCYPLESRPSLSL GTITDEEMKTGDPQETLRRASMQPI QIAEGTGITTRQQRKVSLEPHQGP GTPESKKATSCFPRPMTPRDRHEGR KQSTTEAQKKAAPASTKQADRRQS MAFSILNTPKKLGNSLLRRGASKKA LSKASPNTRSGTRRSPRIATTTASAA TAAAGATPRAKGKAKH
3542	9039	A	3812	241	6884	LSGITKMTLHATRGAALLSWVNSL HVADPVEAVLQLQDCSIFIKIIDRIH GTEEGQQILKQPVSERLDFVCSFLQ KNRKHPSSPECLVSAQKVLEGSELE LAKMTMLLLYHSTMSSKSPRDWEQ FEYKIQAEALAVILKFVLDHEDGLNL NEDLENFLQKAPVPSTCSSTFPEELS PPSHQAKREIRFLELQKVASSSSGN NFLSGSPASPMGDILQTPQFQMRRL KKQLADERSNRDELELELAENRKL LTEKDAQIAMMQQRIDRLALLNEK QAASPLEPKELEELRDKNESLTMRL HETLKQCQDLKTEKSQMDRKINQL SEENGDLSEKREFASHLQQLQDAL NELTEEHSKATQEWLEKQAQLEKE LSAALQDKKCLEEKNEILQGKLSQL EEHLSQLQDNPPQEKGEVLGDVLQ LETLKQEAATLAANNTQLQARVEM LETERGQQEAKLLAERGHFEEEEKQ QLSSLITDLQSSISNLSQAKEELEQA SQAHGARLTAQVASLTSELTTLNAT IQQQDQELAGLKQQAQKEKQAQLAQ TLQQQEQASQGLRHQVEQLSSSLK QKEQQLKEVAEKQEATRQDHAQQ LATAAEEREASLRERDAALKQLEA LEKEKAAKLEILQQQLQVANEARD SAQTSVTQAQREKAELSRKVEELQ ACVETARQEQHEAQAQVAEELQL RSEQQKATEKERVAKEDQLQEQL QALKESLKVTKGSLEEEKRRAADA LEEQQRCISELKAETRSLVEQHKRE RKELEERAGRKGLEARLLQLGEA HQAETEVLRLRELAEMAAQHTAES

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ECEQLVKEVAAWRDGYEDSQEE AQYGAMFQEQLMTLKEECEKARQ ELQEAKEKVAGIESHSELQISRQQN KLAELHANLARALQQVQEKEVRAQ KLADDLSTLQEKMAATSKEVARLE TLVRKAGEQQETASRELVKEPARA GDRQPEWLEEQQGRQFCSTQAALQ AMERAEQMGNELERLRAALMES QGQQQEERGQQEREVARLTQERGR AQADLALEKAARAELEMRLQNAL NEQRVEFATLQEALAHALTEKEGK DQELAKLRGLEAAQIKELEELRQTV KQLKEQLAKKEKEHASGGAQSEA AGRTEPTGPKLEALRAEVSKLEQQC QKQQEQADSLERSLEAERASRAER DSALETLGGQLEEKAEQELGHSQSAL ASAQRELAAFRTKVQDHSKAEDEW KAQVARGRQEAERKNSLISSLEEEV SILNRQVLEKEGESKELKRLVMAES EKSQKLEE/RLRLLQETASNSARA AERSSALREEVQSLREVEAEKQ RVA SENLRQELTSQAERAEEELGQELKA WQEKFFQKEQALSTLQLEHTSTQA LVSELLPAKHLCQQQLAEQAAA EK RHREELEQSKQAAGGLRAELLRAQ RELGELIPLRQKVAEQERTAQQ LRA EKASYAEQLSMLKKAHGLLAENR GLGERANLGRQFLEVELDQAREKY VQELAAVRADAETRLAEVQREAQS TARELEVMTAKYEGAKVKVLEERQ RFQERQKLTAQVEELSKKLADSD QASKVQQQKLKAVQAQGGESQQE AQRFQAQLNELQAQLSQKEQAAEH YKLQMEKAKTHYDAKKQQNQELQ EQLRSLEQLQKENKELRAEAERLG HELQQAGLKTKEAEQTCRHLTAQV RSLEAQVAHADQQLRDLGKFQVAT DALKSREPQAK\PQLDLSIDSLDLSC EEG\TPLSITSKLPRTQPDGTSVPGE PASPISQRLPPKVESLESYFTPIPAR SQAP\LESSLDSLGDVFLDSGRKTR SARRRTTQIINI\TMTKK\LDV\EEPDI SAPNLSFYS\TRSAPASQASLRATSS TQSLARLGSPDYGNSALLSLPGYRP TTRSSARRSQAGVSSGAPPGRNSFY MGTCQDEPEQLDDWNRIAELQQRN RVCPPHLKTCPLESRPSLSLGTITD EEMKTGDPQETLRRASMQPIQIAE GT\GITTRQQRKRVSLPHQGGPGTPE SKKATS\CFPRPMTPRDRHEGRKQAS TTEAQK\KAAPASTKQA\DRRQSM\ AFS\LNTPKKLGNSLLRTG*PQRKA LSK\ASPNTSRG\TRRSRPNJATTTASA ATA\AAIGCHPSRPRGKGKALKGPV PVSGPHLCSPMVAVTWSSAYCPSQ CLLSAPRPTVAKPLETVMPARTLA WSLVLHWRLLGAGPGGLEHGQCG RSPYLASFLLKAKSLLHHNQI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3543	9040	A	3813	1	3466	EKEKAAKLEILQQQLQVANEARDS AQTSVTQAQREKAELSRKVEELQA CVETARQEQHEAQAQVAEELQLR SEQQKATEKERV AQEKDQLQEQQLQ ALKESLKVTKGSLEEEKRRAADAL EEQQRCISELKAETRSLVEQHKRER KELEEERAGRKGLEARLQQLGEAH QAETEVLRLRELAEAMAAQHTAESE CEQLVKEVAAWRERYEDSQQEEAQ YGAMFQEQLMTLKEECEKARQELQ EAKEKVAGIESHSELQISRQQNELA ELHANLALALQQVQKEVRAQKLA DDLSTLQEKMAATSKEVARLETLV RKAGEQQETASRELVKEPARAGDR QPEWLEEQQGRQFCSTQAALQAME REAEQMGNELERLRAALMESQGGQ QEERGQQEREVARLTQERGRAQAD LALEKAAAELEMRLQNALNEQRV EFATLQEALAHALTEKEGKDQELA KLRGLEAAQIKELEELRQTVKQLKE QLAKKEKEHASGSGAQSEAAGRTE PTGPKLEALRAEVSKLEQQCQKQQ EQADSLERSLEAERASRAERDSALE TLQGQLEEK AQELGHSQSALASAQ RELAAFR TKVQDHSTAEDWKAQV ARRRQEAERKNSLITILEEEVSILNR QVLEKEGESKELKRLVMAESEKSQ KLEERLRLQAETASNSARAAERS ALREEVQSLREEAEKQRVASENLR QELTSQAERAELGQELKAWQEF FQKEQALSTLQLEHTSTQALVSELL PAKHLCCQLQAEQAAAEKRHREEL EQSKQAAGGLRAELLRAQRELGELI PLRQKVA\EQERTAQQLR AEKASYA EQLSMLKKAHGLLAEENRGLGERA NLGRQFLEVELDQAREKYVQELAA VRADAETRLAEVQREAQSTARELE VMTAKYEGAKVKVLEERQRFQEER QKLTAQVEQLEVFQREQTKQVEEL SKKLADSDQASKVQQQKLKAVQA QGGESQQEAQRLQAQLNELQAQLS QKEQAAEHYKLQMEKAKTHYDAK KQQNQELQEQLRTLEQLQKENKEL RAEAERLGHELQQAGLKTKEAEQT CRHLTAQVRTLEAQVAHADQQQLRD LGKFQVATDALKSREPQAKPQLDL SIDSLDLSCEEGTPLSITRSGGSLPPY VCLWSACCLSGCILVR
3544	9041	A	3814	35	266	
3545	9042	C	3815	383	628	MDPSAGVTIVTCLASLFSGR LVRFR CSHDWRNYTERVLLFQWVELKTKC WRHTEAGLKPSHYFLEKMKKTLRE SQATYDRI*
3546	9043	A	3816	2	513	DIYGGDYERFGLQGS AVASSFGNM MSKEKRDSISKEDLARATLVITITNNI GSTA\WLCALNENIDRVVFGNFLR INMVSMKLLAYAMDFWSKGQLKA LFF\VEHQGYLGAVGALLGTVQND

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						LMTSRRRGSGRETASQKGQRTKKL LLEKVKVALGRKPSHLWQMNLLGFC
3547	9044	A	3817	29	175	KSRPGTVAHACNPSTLGSRGGRIPAE QEFKTSLGNTVSEPCLYLRKNN
3548	9045	A	3818	171	419	KFFPFQSLWWERRAFPLKGEDMAA LLCQDEKKDQVERSSTAFHGEIFGT SVPENG\HHPKKQSDGMEEYKTFGL GLTNVKKNR
3549	9046	A	3819	2	1209	WPSKETAF\NTTQMPC\QSASTWS SYEHNSESYLLREHVSELDSSFHVS LSLPSDVPLHFHFETLLKKTEIKGNL AENKFVDEYIISPSPVHSTLNQWRN GYSPICKPQIRSESSAQLLQGRKKRH LSETALGERTKL\KEFDFHHTESGSH SNFTAVSNVNVLSRIQNSSRNTARR R\LRSESSYD\DNIVIPMSL\VAPAK LEKLQYKEILTPSWRMVVLQPLDE YNLGKEEIEDLSDEVFSLRHKKYEE REQARWSLWEQSKWHRNSRAYS KNVEGQDLLLKEYPNFSSSQCA AASPPGLPSNQDLCA\GLPSLNQS QETKSLWWERRAFPLKGEDMAALL CQDEKKDQVERSSTAFHGEIFGT PENGHHPKKQSDGMEEYKTFGLGL TNVKKNR
3550	9047	A	3820	7	447	
3551	9048	A	3821	1	373	EQQVLRSTCLGVGAKV/L/VEGMVL QYSTQKGILT/ENHIQEINAQ/TTGLR /KTMLLLDILPSRGPKAFDT/FLDSLQ EFPWVREKLKKAREEAMTDLPAGL EEKGRTGRRMGWGAGEEKGQKCQ TVGMRT
3552	9049	A	3822	1	708	TPVWWNSLWGRFPNSQDSGCSFSP PPQRYVVADGEMEARDKQVLRSLR LELGAEVLVEGLVLQYLYQEGILTE NHIQEINAQTTGLRKTMLLLDILPSR GPKAFDTFLDSLQEFPPWVREKLKK AREEAMTRPCLAVDRLTGIPSHILN SSPSDRQINQLAQLGPEWEPMVLS LGLSQTDIYRCKANHPHNVQSQVV EAFIRWRQRFQKATFRTLDNGLR AVEVDPSLLLHMLE
3553	9050	A	3823	791	1090	HFLHGPLAQEDKSERERWQ\HLAD\ LADFALA\MKDTLTNNNQSFNNFM LRIGEHTPAGLPSRLPSHAGAWPP TRRDMRLRTTEAIRVGRFTHSQGKE T
3554	9051	C	3824	172	243	MRPSHGPSEQLCSTLSPPIKPRPT*
3555	9052	A	3825	1	615	
3556	9053	A	3826	1	596	PGWEKRMSRSSVVNTQEALPTAAIP RDAKGRVYYFNHITNASQWERPSG\ NS\SSGGKNGQGEPAAV\RC\SHLLV KHSQSR\RPSSWRQ\EKITRTKGGGP GSLINGLHPEDSSSGEEDFESLASQF SDCK/SSAKARG\DLGAFQQKVRLQ KPFLKTPRFAL\RTGGDERGPCFTD\

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						SGIHILPHLSEGGEPRPGLGAGQGG
3557	9054	A	3827	1	295	ETVFHSVTQSGMQWHNLASLQRLP LRLKQTSLSLLSSWDCRHMPPNL A/NF/CVLRDKISPFPCGWASNPPG LKQCIGILKYPQALTPYELINIWEGI
3558	9055	A	3828	131	771	MGVILEPSGTTVPLVSSV*LLVWDH GPTRIVGLIIRLGPR/YPLVSSSSKSG RTMPNILDIIASAVENKIPPSKTSKI NVKPELKEEPEESIISAVDENNKLYS DIPHSWICDALQKAFTDKEELLKQQ ASNLHEQKKAGVIFEAEVITLLTS VLKTSSASRTSLSSRHQFAPGATVL YKGDKMVLNLDNRVPTCEKIEA ILKELEKPAP
3559	9056	A	3829	1	655	MPVNAGGKVQESQKPPTLIPEPKDS QANFKSSSEQSLTEWWRPNNNLSK EKTEWHVEKSSGKLQAAMASVIVR PSSSTKTDSMPAMQLASKDRVSERS SAGAHKTDCLKLAAGETGRILPN VNSDSVHTKSEKNFQAVSQGSVPSS VMSAVNTMCNTKTDVITSAADTTS VSSWGGSEVISS/CIKYHFLYIIRM CIFKKCQSASGSKTRMQGYLE
3560	9057	A	3830	1	515	LTLENQIKEEREQDNSESPNGRTSPL VSQNNEQGSLRDLLTTTAGKLRV GSTDAGIAFAPVYAMGAPSSKSGRT MPNILDIIASVVENKIPPSKTSKINV KPELKEEPEESIISAVDENNKLYSDIP HSWICEKHILWLRIIIIVIGSFSKNV GNKDSLQWFLVCIRK
3561	9058	A	3831	6	226	RKGGFFVDFVRVSNQVAVNMYK QLGYSVYRTVIEYYASNGEPDEDA YGKLPSMAVSPRSRNSYILSTDCSI
3562	9059	A	3832	37	611	SGGGAMTTLRAFTCDDLFRV/FNNI NLDPLTETYGIPFYLAHWPEYF IVAEAPGGELMGYIMGKAEGSVAR EEWHGHVTAHSVAFRRRLGLAA KLMELLEISERKGGIFLVDLFVRV SNQVA\VNMYK\QLGYSVYR\TVIE YYFGPATGEP**GTLIDMRESTFPRD TGERNPIIPLPHPGGGLEDH
3563	9060	A	3833	1	191	MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWPQLST/FQQMWISKQEY DESGPSIVHRKCF
3564	9061	A	3834	2	1203	LSRRCQLSHSVLPPLRRRVSLPVAM EEEIAALVIDNGSGMCKAGFAGDD APRAVFPSIVGRPRHQGMVGMGQ KDSYVGDEAQSKRGILTLKYPIEHG IVTNWDDMEKIWHHTFYNELRVAP EEHPVLLTEAPLNPKANREKMTQIM FETFNTPAMYVAIQAVLSLYASGRT TGIVMDSGDGVTHTVPIYEGYALPH AILRLDLAGRDLTDYLMKILTERGY SFTTTAEREIVRDIKEKLCYVALDFE QEMATAASSSSLEKSYELPDGQVITI GNERFRCPEALFQPSFLGMESCGIH ETTFNSIMKCDVDIRKDLANTVLS GGTMYPGIADRMQKEITALAPST

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						MKIKIIPPERKYSVWIGGSILASLST FQQMWISKQEYDESGPS\VHRKCF
3565	9062	A	3835	3	412	SRFPEGLFQPPFPGMKSCGIHETTF HSH/IKFDVAIR\KDLYANTLLPGGN HQVSGALLTGMQKEIHAPAAQATL RFKIIAPPGSASTRW/VGSGVGSILASL STFQ\QMWISKQEYDESGPLHSSTA KCFLNGLSQIA
3566	9063	A	3837	3	480	SHITVLTNLVNGLNAPVKRHRLAN WIKSQDPPVCFIQETHLTCRDTHRL KIKGWRKIYQANGK/QKKAGVAIL VSDKTDFKPTKI/KRQGHYIMVKGS MQQEEQVLRDPQRDLDSHTMIMGD FNTLLSILDRSTRQKVNKDIQELKSA LHQADLIDIYRTLH
3567	9064	A	3838	1	834	MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEITNCLSDHSAIKLELTIKKLTQN RSTTWKLNLLNDYWKYKQPSN KHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPIRSEIEAITNSLP T/KKSPGPDGFTAIFYQ\MLEVLAR AIRQEKEIKGIQLVKEEVKLSLFADD MIVYLENPIVSAQNLLKLIGNFSKVS GYKI/NVQKSQAFLYTNNRQTESQI M
3568	9065	B	3839	1	543	MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEITNCLSDHSAIKLELTIKKLTQN RSTTWKLNLLNDYWKYKQPSN KHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPIRSEIEAITNSLP TKK*
3569	9066	A	3840	1	1470	MEQSWVENDFDELREEGFRRSNFS EVKEESRTQPKEAKNLARRDTHRL KIKGWRKIYEENGKQKKAGVPILVS DKTDFKPTKIKRDKEGHYTMVKGSI QQEELTILNIYAPNTGAPRFIKQVLR DLQRDLDSHTIIMEDFNTPLSTLDRS TRQKVNKDIQELNSALQQVDLIDIC RMLHPKSTEYTFFSAPHHTYSKIDH RVGSKALLSKCKRTEITNCLSDHSA IKLELRIKKLTENRSTAYNLNLL NDYGVHNEMKSEIKMFFETNENKD TTYQNLWDTFKAVEIQTIREYYKH LYRNKLENLEEMDKFLDTYTLPRV NQEEVESLNRPIRSEIEAITNSLP KSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYDASIILPKPG KDTTKKENFRPISLMNIDAKIMNKIL ANQIQQHIKKLIHHDQVGFIPGMQV WFNIGKSINVIQHINRTKDQK\NHRH SIDAEKAF
3570	9067	A	3841	2807	4148	
3571	9068	A	3842	2	1516	WRKIYQANGK/QKKAGVAILVSDK TDFKPIKIKRDKEGHYIMVKGSIQQ

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						EELTILNIHAPNTEAPRFIKQVLSDL QRDLDSHTIIMGDFNTPLSTLDRSTR RKVNKDTQELNSALHQVDLIDIYRT LHPKSTEYTFLSAPHHTYSKTDHIV GSKALLSKCKRSDIITNCLSDHSAIR LELRIKLTQNRSTTWKLNLLND YVWHNEMKAEIKMFFQTENKDT TYQNLWDTFKAEEVKSLNRPITGSE IVAIINSLPTKRSPGPDGFTVEFYQR CRKAFDKIQRPF TLKTLNKL AIDGM YLKIIRAIYDKPTANVILNGQKLEVF PLKTGTTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLRKEKVKLSLFVD DMIVCLENPIISVQKLLKLISNFSKV SGYKINVQKSQAFLYNNRQTESQI MSELPFTIASKRIKYLGIQLTRDVKG LFKENYKPLLNKIKEGTNKWKNP CSWIGKINIMKMAILPKETPSHMQR HT
3572	9069	A	3843	3	120	FIIDKKQKQLKSPSIDEWIK\KMWYI HKIEYHSAIKGIK
3573	9070	A	3844	2	244	SRLSFPSSWDYICAPPHLANFCIFLV ERSVAMLPRLVSSSWAQAILPPWP PKAQGFTGMGHHHAQSAAGLYIFSG LGSNAI
3574	9071	A	3845	1	2616	
3575	9072	A	3846	1	773	QTSPMIPSIVVHCVNEIEQRGLTETG LYRISGCDRTVKELKEKFLRVKTPV LLSKVDDIHAICSLKDFLRNLKEPL LTFRLNRAFMEAAEITDEDNSIAAM YQAVGELPQANRDTLAFLMIHLQR VAQSPHTKMDVANLAKVFGPTIVA HAVPNPDPVTMLQGHQGVQPKVV E\RLFLGLWEYWEFSFMDGWEQG GTFDPLHVIENSNAFSTPQTPDIKAV PGGGLCVHFTAGEAEIQKGPSCGQ NKSTAAFNY
3576	9073	A	3847	1	422	CGRVRACGRVREPSSQIHNNMANL FIRKMVNPLLYLSRHTVKPRALSTF LFG\SIR\SAAPRGCGNPGAAVR\SL SPGLPA\HHL PACGWGFKKQDCPLR KRCKDCYLVK\RRGRWYVYCKT\H PRHKQKTRCRTLFPPESTR
3577	9074	A	3848	1959	4060	RFFSFFFFFFETESHVAQAGVQWCN LGSLQAPPPG\SRHSPASASRVAGTT GAHHHARLIFVFLVETGFHRISQDG LDLLTS*SARLGIPKCWDYRCEPPH LASI
3578	9075	A	3849	1	1320	
3579	9076	A	3850	1239	1733	ALFFSFFFFFFETESRSVAQAGVQW RDLGSLQAPP\PGSRRSPASASRVAG TTGARHRIFFVFLVEMGFHRDLDFP TS*SA\QGLQA*ATAPGPFLFFFFFF LRRSLTLLPRLECNGAILARNLYL LGSSNSPASASRVAGIAGMHHR LIFCILVEMGFHHL
3580	9077	A	3851	131	436	VTHLHQKKGSVFFFFFFETESCPV

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						AQAGVQWRDLRSLQAPPPG\SRHSP ASASRVARTTGAHHYTRLIFVCLV ETGFHHVSQDGLDLQDQFPWSLFLF CPP
3581	9078	A	3852	56	192	KFLFSPKALNSVRKFFQYFPPPKKR/ CPSQNSQVG/CLKSPP*GEKF
3582	9079	A	3853	1	230	FQLHQHLLNPKHDYRGWAKWNR NSLYEKMKEGERRK\RRSAIPYLQG QRLDNVVAKKSVQFFPLRVRDPG VKSSC
3583	9080	A	3854	3	126	SCCGVGNQFKGPGGGGGG/RGGG/RR NVSGGGAGGRGWKNERKER
3584	9081	A	3855	1	1021	MPRLEAFVNNQTCPKKECGAASEG DTIGKQSELSFGKAKMARETHWP KVGKLRSTVVKQLPKTFQAISSTET KDQGPVVPAPVKGEPIVPAPVKDE GPMVSAPIKDQDPMVPEHPKDESA MATAPIKNQGS MVSEP VKNQGLSG\ PGPVKDQDVVPEH*KGHDSA\LV APW*RIKGPVVPSPVKNQDPILPV LVKDQGPTVLQPPKNQGRIVPEPLK NQVPIVPVPLKDQDPLVPVPAKDQE P/TLPG/PLGSETAAPVPAHSHSPPPA GSSPAPPRAPGSGRLRLPCSLAPRDLG TRDRAGTVSGALRTMRHPTGGLCQ KGPCWVPPPPLLQIQHFGPP
3585	9082	A	3856	1	448	SSRKDQGLVVS GPVKDQDVVPEH QRSRFSCQV VAPVKNQGPVVPESV KNQDPILPVLVKDQGPTVLQPPKNQ GRIVPEPLKNQVPIVPVPLKDQDPL VPVPAKDQGPVPEPLKTQGP/KGT LSLPTVSPLPRVMIPTAPHTYEIESSP
3586	9083	A	3857	1	573	DPQFISGSPESPIRLWCVGLGNTKVT FTNPKNPVRAVVIHPRHYTFASGSP DNIKQWKFPDGSFIQNLSGHNAINT LAVNFDGGLVFGAANGPMHLWDW ETWAPIFKRVHA\AVQPG\SLDSESG IFACAFDQ\SESRL\TAEADKPIKV YREDDTATEETHPVSWKPEIHKRR FLMNVEFFLSLFFSF
3587	9084	A	3858	1	589	EDLRKCTFIFIIGGPGSGKGTQCEKL VEKYGFTHLSTGELLREELASESER SKLIRDIMERGDLVPSGIVLELLKEA MVASLG DTRGFLIDGYPREVKQGE EFGRRI GDP\QLVIGKE\CSPDT\MTN RL\LQRSRSLPVDDTTK\TMAKRLE AYYR\ASIPVIAYYETKTQLHKINAE GTPEDVFLQLCTAIDSIIF
3588	9085	A	3859	1	557	KLLSPKQPLLRAQLKTLVRLLCFSH AFVGLSKITTWYQYGFVQTQGPKA NILVSGNEIRQFARFMTEKLNVSHT GVPLGEEYILVFSRTQNRLLNEAEL LLALAHEFQMKTVTVPWRITPLTD VVRLVSNASMLVSMHGAQLVTTLF LPRGATVVELFPYAVNPDHYTPYK TLAMLPGHGTSSM
3589	9086	A	3860	323	656	NEELMPKGRLYPPLANIQEV SINIAI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KVTEYLYANKMGFPDQTQEPEDKA KYVK/EKGTWAEWNMDSLLPDVY EWPEICNQAPPVNTEIEALPLINTFV CSRGTPFFQTRKR
3590	9087	A	3861	1411	1799	GYLQFSFSFFLFFFFFFFLRWSLTLS PRLECSSVISTHCNLRPGSSDSRAS ASQVAGTTGAHHHARLIVCVLVER VFHHVGGAGLEVLTSGGPPTSASQS ARITGMSHHTRPVICSFQFSDDLPEHY F
3591	9088	A	3862	1	1007	MDGGHLFSNLTGKEEVHKGAKLH PNGYRMAQGSETLVARGGPCRSVE PSAASPQELRGWWEAQALKRWGL MGGVWVMEVDPSWLGAISIVSSS ASRLKSVWHIPCPHFLLRPQLKE AQRKKQLEERCVEESIGNAVLT WNNEILPNWETMWCSRKVRLDWW QGIPPSVRGKVWSLAIGNELNITHEL FDICLARAHERWRLSTGGSEVENE GLCVAVCAQQGHVGVMGFGSDEP SAVSPCEKGKSLAAWVLIFVDFRVG LQKSFQKRKERESTKLQQLWSWCL MLTYFAAFEVFFFEENLPKLFHFHKK NNLTPDIYLID/W*FRLLVGC
3592	9089	A	3863	1	1857	
3593	9090	A	3864	1	840	GIPAADR/EASLELIKLDISRTFPNLCI FQQGGPYHDM LHSILGAYTCYRPD VG YVQGM SFIAA VLILNLD TADAFI AFSNLLNKPCQMAFFRV D HGLMLT YFAAFEVFFFEENLPKLFHFHKKNNL TPDIYLIDWIFTLYSKSLPLDLACRI WDVFCRDGEEFLFRTALGILKLFED ILTKMDFIHMAQFLTRLPELPAEE LFGPSIATIQMSRNKKWAQVLTAL QKDSREMREGKSVPTLRLQREFAL GTNQSPMPRLCCFRLTPGQPRRTD AL
3594	9091	A	3865	3	288	FFFEMESLYVTRLNCSGTITISVHC NLCFPGSSDPASASQIAGITGRHH AQLILVFLVEMGFC/HISTKQMEVIH PPWPPKVLGLQVVTHDVL
3595	9092	A	3866	285	489	
3596	9093	A	3867	3	425	GSSDPPASAFQVAGSISVCHHTQLIF VFLVEVEFHVSQASLQL/RDLSLPS SWDYRRPPPRPANFFVFLVEMGFH HLNKAIKSFACNEIQPLSAVSVARA GWGVFEYVS VYFLCSNSDYFSSNPS IANWMREWPLRLSLF
3597	9094	A	3868	1	156	APHPAN/FAFLVEMEFHDVGQGD QLLASSDLPASASQSAGITGVSHCN WI
3598	9095	A	3869	1	526	LAESGEGVLVSGGSLRLPCIASRFIF SSYYMSGVRQAPGKGLEWVSFIRA TSVRGRFTMSRDESKNITYLQMKSL RRGMFRGDLG/DWPGGDGHWGAL RIWEPLWIFRCLWKMGLRLGASDG VTEPGGLGSHIWTRCLNKPGLVLM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AEECVSGAVSVGLQDRCTAANRAI FSLEL
3599	9096	A	3870	2	353	
3600	9097	A	3871	136	315	FKYVLSFLFLASGDGESLDEDESEFTL ARDFEIGHFFRERIVPRAVLYFTGE AIEDDDNV
3601	9098	A	3872	132	1552	GDKNIQMADHSFSDGVPSDSVEAA KNASNTEKLTQVMQNPVLAALQ ERLDNVPHTPSSYIETLPKAVKRRIN ALKQLQVRCAHIEAKFYEEVHDLE RKYAALYQPLFDKRREFITGDVEPT DAESEWHSENEEEKLAGDMKSKV VVTEKAAATAEPPDPKGIPEFWFTIF RNVDMSELVQEYDEPILKHLQDIK VKFSDPGQPMFVLEFHFEPNDYFT NSVLTKTYKMKSEPDKADPFSFEGP EIVDCDGCTIDWKKGKNVTVKTIK KKQKHKGRTVRTITKQVPNESFFN FFNPLKGKSVASGDGESLDEDESEFT LASDFEIGHFFRERIVPRAVLYFTGE AIEDDDNFEEGEEGEEEGLEGDEEG EEDDDAEFNPVKVLIFFLLIHTFSRR DPSQPAECKQQYAEAGAWQTGCR DSRPVGGASVLAQAQSRGQSLHL TRFQVHDFHFHFSFLLILNLYSGN
3602	9099	A	3873	171	324	
3603	9100	A	3874	3	383	
3604	9101	A	3875	2	314	FFFFISALKALFAFLQILLFQVNVLR TAHIVISFINLLSVTPSKAFLLAFIF CREDYSFTAYATISYLKIGPKANLL NNEAYVITMQVTKSTQNSFRVNG Y
3605	9102	A	3876	3	319	TESRSVPQLGVQWRDLGSLQPPPPG FTRFSCSLPSSWDYRHTPPRPANFL VFLVETGFRHVGQTGLELLTSGDPP ASASQSAGILCVLCTSTLGNHREHI YRMV
3606	9103	A	3877	118	1341	
3607	9104	A	3878	1	214	GFTSSLACMQMGEMFMGFTCQTH LLALGCALFTAYLGVGMANFMAE GTCERRIVGKKKASITKDHQQRRI
3608	9105	A	3879	1	176	MRTFALLTAMLLVA/HAQAEPLQ ARADEAAAQEQPGADDQEMAHAF TWHESAALPLSA
3609	9106	A	3880	3	125	AASTFLFPNLKNSLRGSLRTFSSVT NVRKTALTWLNSQDI
3610	9107	A	3881	1169	1512	YTQKNWHLFCFIFLRWSFVLVAQP GVQWCNLSSLQPLPPRFR*FSCLSL SSWDYRCAPPRPANF/SVFLVETGF HHVGQADLELLTSGDLPTSASQSAG ITGVSHCTWPDILYEI
3611	9108	A	3882	43	347	AGVQ*CDLG*LQLPLGFK*FSCLSL PSSWDYRRLPPRPANF*FLVETGFH HVGQADLELLTSGDSPASASQSAGI TGMSHRAGPI*KSFLKYSTNKLRTT
3612	9109	A	3883	10900	11295	KPWVNETGKLFQDSYSSISHILSGF SFPSFFSETESCSVTQAGVQWHDLS

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						SLKPLPPGFKQFSCSLPSSWDYRR VPTRPANF/SVFLLETEFHRVSQDGL DRLT/S/GDPPSSASQSAGITGVSHRA RPHSPHF
3613	9110	A	3884	3	227	RFSCSLSSSWDYRAPPPRLANFCI LVETGFHHAGQTGLELLTSGDPPAS ASEIAGITGMSHHTQPGQLLWECC
3614	9111	A	3885	2	296	KWSSALVAYAGVTWHHLGSLRSP PGFKRFCCLSLPSSWDYRHAPPPA/ NFFVFLVKTGFLHVGQAGLELPISG DPPALAPKQSAWIRGVSHRAQPQN
3615	9112	A	3886	1	162	LGGLVFPSEVVCK/RKLDGMQLIKV HLDKAQQNNVENKAETFSGVCKK HRDLMA
3616	9113	A	3887	2	474	
3617	9114	A	3888	2	592	STGKFSQEKAMFSSSAKIVKPNGEK PDEFESGISQALLELEMNSDLKAQL RELNITAAKEIEVGGGRKAIHFVPVP QLKSFQKIQVRLVRELEKKFQWES MSVFIAQRRILP/KPTRKSRTKNKQ KRPRSRTLTAVHDAILEDLVFPSEIV GKRIRVKLDGSRLIKVHLDKAQQN NVEHKVETFSGVYKKHRDLMA
3618	9115	A	3889	1	93	GFTMLP/RLVLNSWVQMICLPWPPK MLSLQA
3619	9116	A	3890	1	252	PTLEQYAMRAFADALEVIPMALSE NSGMNPIQTMTEVRAR/QDMKQQH VIETLIGKKQQISLATQMVRMILKID DIRKPGSEEE
3620	9117	B	3891	18	1121	MASMGTLAFDEYGRPFLIKDQDRK SRLMGLEALKSHIMAAKAVANTMR TSLGPNGLDKMMVDKDGDTVNTN DGATILSMMDVDHQIAKLMVELSK SQDDEIGDGTGTVVVLGALLEEA EQLLDRIHPRIADGYEQAAARVAIE HLDKISDSVLVDIKDTEPLIQAKTT LGSKVVNSCHRQMAEIAVNAVLT ADMERRDVFELIKVEGKVGGRLE DTKLIKGVIVDKDFSHQPMPKKVED AKIAILTCPFEPKPKTKHKLDVTSV EDYKALQKYKEKFEEMIQQIKETG ANLAICQWGFDDDEANHLLQNNLP AVRWVGGEIELIAIATGGRIVPRFS ELTAEKLGFAGLDKRISFGDT*
3621	9118	A	3892	1	282	LPSSHTIPGYP/NPLHPRFPSSRLPP GIIGGEYDQRPTLPYVGDPISLIPGP GETPSQFPPLRPRFDPV/GPNDRFPF RPSRGRPTDGRLSFM
3622	9119	A	3893	3	166	PRPFPKSRLPPGIIGGEYDQRPNPILP /GRGGPNDRFPFARPSRGRPTDGRLS FM
3623	9120	A	3894	101	1926	SPVRGRRRLGRELLGPAAVPVAAS GSRPLGPPAAVMRLRVRLKRTWP LEVPEPETLGHLSHLRQSLCTW GYSSNTRFTITLNYKDPLTGDEETL ASYGIVSGDLICLILQDDIPAPNIPSS TDSEHSSLQNNQPSLATSSNQTSM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QDEQPSDSFQGQAAQSGVWNDDS MLGPSQNFEAESIQDNAHMAEGTG FYPSEPMCLCESVEGQVPHSLETLY QSADCS DANDALIVLIHLLMLESgy IPQGTEAKALSMPEKWKLSGVYKL QYMHPLCEGSSATLTCVPLGNLIVV NATLKINNEIRSVKRLQLLPESFICK EKLGENVANIYKDLQKLSRLFKDQ LVYPLLAFTTRQALNLPDVFGLVVLP LELKLRIFRLLDVRVLSLSAVCRDL FTASNDPLLWRFLYLDRDNTVR GQD TDWKEL YRKRHIQRKESPKGR VFM LLLPSSTHTIPFYPNLHPR/PPV SSRL\PPG\NGGEYDPKTNTPMGLD PISSLIPWVLGETPQPSFPPTETHALN PSWPPISRD PNPQSCPGAEGGPPN/R TRFPPLRPQPGGRANLMAGLVISCG LDLLIFISWSLPPVFCFLNYRCQRPW GADLRVLFS
3624	9121	A	3895	2	442	LSQLCGDPQRFDDFLRAYVEKYKF TSVVAQDLLDSFLSFFPELKEQSVD CRAGPPLAEPDLSQGSSLTRPVEAL FQL/WTAEPDQAAASASAI DISKW RTFQTALFLDRLLDGSPLPQEVVMS LSKCYSSLLDSMNAEIRIRWLQIV
3625	9122	A	3896	1	1035	GEFLVIDVIHEVAHSWFGNAV TNAT WEEMWLSEGLATYAQRITTETYG AAFTCLETAFRLDALHRQM KLLGE DSPVSKLQVKLEPGVNP SHLRNLFT YEKG YCFVYLSQLCGDPQRFDDF LRA YVGE\YKFTSVVAQDLLDSFLS FFPELKEQSVD CRAGLEFERWLNAT GPPLAEPDLSQGSSLTRPVEALFQL WTAEPDQAAASASAI DISKWRTFQ TALFL\DRLLDGSPLPQEVVMSLSK CYSSLLDSMNAEIRIRWLQIVVRND YYSLT/FHRVRRFPGRARCHACYTIP LYEDLCTGALKSFALEV FYQTQGR L HPNLRRAIQQILSQGLGFQHRARP
3626	9123	A	3897	2	912	CSRSSRTGGW WPAPCSAASRRPTPG PAAAAAATTD/VVTAGCGFGKDFR KGLLKKGACYGDDACFVARHRS A DVLGVADGVGGWRDYGVDP SQFS GTL MRT CERLVKEGRFVPSNP I GILT TSYCELLQNKVPLLGSSTACIVLD RTSHRLHTANLGDSGFLVVRGGEV VHRSDEQQHYFNTPFQLSIAPPEAE GVVLSDSPDAADSTSFVQLGDIILT ATDGLFDNMPDYMILQELKKLKNS NYESIQQTARSIAEQAHELAYDPNY MSPFAQFACDNLNVRGGKPDDIT VLLSIVA EYTD
3627	9124	A	3898	2	220	YMSKKFSALLQSQERNCLIIINWCSS LCLRVRLYL RQVTVIPRICKVSD\SP CAPEADAMFAFNADGVGDAKG
3628	9125	A	3899	1	346	SANATTKTSETNHTSRPRLKNVDRS TAQQLAVTVGNVTVIITDFK\EKTRS SS\TSSSTVTS\SAGS\EQQN\QSSSGV

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QRAPDKGLPPRSLPTPKGDMSIAVN DEIFPEIATWNCEKL
3629	9126	A	3900	76	368	
3630	9127	A	3901	1	1182	MFAKGRGSAVPSDGGQAWEKLASV VVEYLLHVRVQKSAETFLSEIRWEK NITLGEPPGFLHSWWCVFGDLYCA APQRRDTCEHSSEAKAFHDYSAAA APSPVLGNIPPNDGMPGGPIPPGFFQ GPPGSQPSPHAQPPPHNPSSMMGPH SQPFMSPRYAGGPRPPURMGNNQPPG GVPGITQPLL\NSMDPTRQQGH\N MGGSMQRMNPSRPLGPMGPRPHR ITGSGMRPPPNSLGPA\MP\GINMGP GAGRPWPNPNSANSIPYSSSSPGTY VGPPGGGGPPGTPIMPSPADSTNSS DNI\YTM\NPNVPPGGSRSNFQMGGP STGPMDSMGGMEPHHMIG\SLGSG DIDGLPKIFPNNISGISNPPGTPRDDG ELGGNFLHSFQNDNYSPTMTMSV
3631	9128	A	3902	2	470	IPTFGLPGSIQSDNGP\SFISQITQQVS QSLGIQWRLHPCWPQTSGKVERAN GILKAQLTKLTLEVQKPWDL\LLPH RHWESIRRP/GPKGTLLSFSSIWSLIY GTPFPLT\NRPPSNSQLGGIPSQQSSL MEVIFLWPTRPTRAFFPKPHGGGLPIP K
3632	9129	A	3903	69	523	PLGCASSQSIASRNTLCTTASSCCP QVLAHS\KAAEYMTRWKVQQMPH SQDRALQSVFCAPFHS**LVALPTG HR*MTPAQFSECFQATSGGSD*DPF LAPSFL\VPGLPVAPG\LLPLGPVHS RATMEEGQATHEELTVFIGLRPGVR GS
3633	9130	A	3904	101	1469	RTHPTFFHPGTGPTSAPPSGALEGTA GTITSNEWSSPTSPEGSTASGGSQAL DKPIDNDGEGVWSPDIEQSFQEALA IYPPCGRRKILSDEGKMYGRNELIA RYIKLRTGKTRTRKQVSSHQVRLAR RKAREIQAKLKDQAAKDQALQSM AAMSSAQIISATAFHSSMRLARGPG RPAVSGFWQGALPGQAETSHDVKP FSQQTYAVQPPLPLPGFESPAGPAPS PSAPPAPPWQGR\SVASSKLWMLEF SAFLEQQQDPDTYNKHLFVHIGQSS PSYLRPYLEAVDIRQIYDKFPEKKG GLKDLFERGPSNAFFLVKFWADLN TNIEDEGSSFYGVSSQYESPENMIIT CSTKVCSFGKQVVEKVETERYE NGHYSYRIHRSPLCEYMINFIHKLK HLPEKYYMMNSVLENFTILQVVTNR DTQETLLCIAVFEVSASEHGAQHH IYRLVKE
3634	9131	A	3905	1	1290	
3635	9132	A	3906	2	270	ISLADLKEGPHTHLKPPDYSVAVQR SKMMHNSLSRLPPASLSSNLVACVP SKIVTQPQRHNLQPFHPKLGDVTD DSEED\ENEQVSAV
3636	9133	A	3907	2	288	RWGLALSLR/AGAQWFHHSGLQPQ

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						PPMLKSSSRSLPSSRNHRHTQPCPA NFFIFVEMGFHHVAQAGLELLSSLT VWASQSAGITGVSHRTHPLLS
3637	9134	A	3908	3	222	FFFETESRSVTRLECSGTISAHCKLH LPGSCHSPASASRVAGTTGAHCHTQ RIFVEMGFHRVSQDGLDLKLN
3638	9135	A	3909	3	175	GTSPKDCEVRDFCPSEGLYST*WGG SILPSLDT/FKKMWVSKKKYEEDGA RSIHRKTF
3639	9136	A	3910	2	533	RAAEFFEFETFNVPALFISMRAVLSLY ATGRTTGVVLDSEGDVTHAVPIYE GFAMPHSIMCIDIADRDVSRFLRL YLRK\EGYDFHSS\SEFEIVKAIKERA CYLSINP\QKDETLETEKAQYYLPD GSTIEISAPQERLYSTWIGGSILASLD TFKKMWVSKKEYEEDGARS IHRKT F
3640	9137	A	3911	1	1213	EFGALRRTRLGSSFPRRRDSSAMES YDVIANQPVIDNGSGVIKAGFAGD QIPKYCFPNYVGRPKHVRVMAGAL EGDIFIGPKAEHRGLLSIRYPMEHG IVKDWNMERIWQYVYSKD\QLQT F\SEHPVLLTEAPLNPRKNRERAAE VFFETFNVPALFISMQAVLSLYATG R\TTGVVLDSEGDVTHAVPIYEGFA MPHSIMRIDIAGRDVSRFLRLYLRLK EGYDFHSSSE\FEIVKAIKERACYL FKTPKRD\ETLETEKASVTTWLDGS TIEIGPFR\FRAP\ELLFGPRI*LEKESE G\HEVPGVPRFRKSDMGPAGARLF SNIVL/SQGGSTPVQKFSSLPISGFGD RLLC*VKKLAPKDVKIRISAPQERH VYPRGLGGSILASLDTFKKMWVLQ KGD MR*DGSTIEIGPFRIPGPLSCSSG PEFDWKRKVKASHEVPGVPRFRKS DMGPAGARLFSNIVLFREALPLFKS SPLCPFQVLVTGSFVIVKKLSSKRCE DQDICTSGETCISTWIGGLHPCLP HLRRCGCSKKEI
3641	9138	A	3912	2	262	LEKRSHSVTKLGYSGVIIAHCSLNF LSSSQPPTSASQTAGTTGICHSTQLIF KIFLVEMG/LHYVAQAGLDLLGSSN VEPPKVLLGL
3642	9139	A	3913	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFD CG KPQVEPKKCPGRVVGCV AHPHSW PWQVSLRTRSPRPSYKVLGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLSPNYVVA DRTECFITGWGETQEHFYFN
3643	9140	A	3914	1	387	TPEKEPPLWHAFTKEELVQKLSST TKSADQLNG\LLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKP GSERESLLPVINT

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						MLQLSPEEKGKLAAVAQGLQETSIP KKK
3644	9141	A	3915	360	885	NV FVLLEANQRTSTVTLATVSASGQ MPSTEFGLDSSIQKLI AIAH FILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSSLGVHPG*PCRMKALGTSP SSGQSTPTLGISRCLHRS AFQTLF
3645	9142	A	3916	1669	4914	
3646	9143	A	3917	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQRVL*HL/QPVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPW CY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGCV AHPHSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN
3647	9144	A	3918	1	387	TPEKEPPLWHAFTKEELVQKLSST TKSADQLNGLLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK
3648	9145	A	3919	360	885	NV FVLLEANQRTSTVTLATVSASGQ MPSTEFGLDSSIQKLI AIAH FILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSSLGVHPG*PCRMKALGTSP SSGQSTPTLGISRCLHRS AFQTLF
3649	9146	A	3920	1669	4914	
3650	9147	A	3921	1	246	FLETEFHSAQAGVQWCHLGS LQP PPPGFKQLS\CLSLPSSWDYRGTPPY LANFCIFSRDGVSLCWPGWSQTPDL KQSSGNL
3651	9148	A	3922	10	476	DRVLLSVAQAGLQWRDLGSLQPPP P/GFKRFSCSLSPNSWDYRCVPPCLA NFFVFLVETGFHHVGQAGLELLTSG DPPLPQPPKVLGAGITGMSHTWLI SLIFYQTKWRQTAIASVGIPGSPLCH PLPLIRKGVAGKAVLCPRKDGHTH KTQLRP
3652	9149	A	3923	2	465	ARARADSARAARA EFEDIMKRNRA ISSSPISKAVSGASAGDYSDAIETLLT AIAVIKQSRVAK\DERCRVLISLKD CLHG\IEGQVPTVWGAQLGALS RKR HPFPGERSPASRSRETSRRHRDLLHN EDRHDDYFQERNREHERHRDRER DRHH
3653	9150	A	3924	3	218	LPPPLSNIHSTLSTPFLPPAPL/SP/YP SRASPPSTYSPLPTPPPLPTSQPSTPT LPLPTPCSTPSGQALFF
3654	9151	A	3925	1379	2175	TTAGIQMPIKAPGVLPQTPASGGST

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						AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWYCY TTNPRKLYDYCDVPQCAAPSFDCCG KPQVEPKKCPGRVVGCVAHPHSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN
3655	9152	A	3926	1	387	TPEKEPPLWHAFTKEELVQKLSST TKSADQLNGLLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK
3656	9153	A	3927	360	885	NV FV L L E A N Q R T S T V T L A T V S A S G Q M P S T E F G G L D S S I Q K L I A I A H F I L N H R E L G F L E K A S S K S T L G F S P A S D E T F G P V S D H I I W G W Q T S W D Y F V S D D G R T A * L * Q G N I F S C G L Q E Q P R H F Y F L N M R F / D D S L L G V H P G * P C R M K A L G T S P S S G Q Q S T P T L G I S R C L H R S A F Q T L F
3657	9154	A	3928	1669	4914	
3658	9155	A	3929	1	1542	
3659	9156	A	3930	3	1771	
3660	9157	A	3931	2	1869	RLVVVEAKMAAAQAAAAQAAAA QAAQAEAADSWYLALLGFAEHFRT SSPPKIRLCVHCLQAVFPFKPPQRIE ARTHLQLGSLVLYHHTKNSEQARSH LEKAWLISQQIPQFEDVKFEAASLLS ELYCQENSVDAAKPLLKAIQISQQ TPYWHCRLLFQLAQLHTLEKDLVS ACDLLGVGAEYARVVGSEYTRALF LLSKGMLLLMEKRLQEVHPLLTL GQIVENWQGNPIQKESLRVFFLVLO VTHYLDAGQVKSVPCKLQQLQCCI QTISTLHDDEILPSNPADLFHWLPKE HMCVLVYLVTVMHSMQAGYLEKA QKYTDKALMQLEKLKMLDCSPILS SFQVILHEHIIMCRLVTGHKATALQE ISQVCQLCQSPRLFSNHAAQLHTL LGLYCVSVNCMDNAEAQFTTALRL TNHQELWAFIVTNLASVYIREGNRH QEVVLYSLLERINPDHSFPVSSHCL RAAAFYVRGLFSFFQGRYNEAKRF LRETLKMSNAEDLNRLTACSLVLL GHIFYVLGNHRESNNMGG\PAMQL ASKIPDMSVQLWSSALLRDLNKAC GNAMDAHEAAQMHQNFSSQQLQD HIEACSLPEHNLITWTDGPPPVFQFQ AQNGPNTSLASLL
3661	9158	A	3932	2	614	
3662	9159	A	3933	1	4992	VSSNNVLLNSQADDRVVINKPESAG FRDVGSEEIQDAENSAKTLKEIRTL MEAENMALKRCNFPAPLARFRDIS DISFIQSKKVCFKEPSSTGVSNGDL LHRQPFTEESPSSRCIQKDIGHTQTNL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KCRRG IENWEFISSTTVRSPLQEAE KVSMAL EETLRQYQA AKSVMRSEP EGCSGTIGNKIIIPMMTVIKSDSSSD ASDGN GSCSWDSNLPESLESVSDVL LNFFPYVSPKTSITDSREEEGVSESE DGGGSSVDSLAAHVKNLLQCESSL NHAKEILRNAEEEEESRVRAHAWNM KFNLAHDCGYSISELNEDDRRKVEE IKAELFGHGRTTDL SKGLQSPRGMG CKPEAVCSHIIIESHEKGCFRTL TSE HPQLDRHPCAFRSAGPSEMTRGRQ NPSSCRAKHVNLSASLDQNNSHFK VWNSLQLKSHSPFQNFIPDEFKISKG LRMPFDEKMDPWSELVEPAFVPP KEVDFHSSSQMPSPPEPMKKFTTSITF SSHRH SKCISNSSVVKVG VTEGSQC TGASVGVFN SHFTEEQNPPRDLKQK TSSPSSFKMHSNSQDKEVTILAEGR RQSQKLPVDFERSFQEEKPLERSDF TGS HSEPSTRANC SNFKEIQISDNHT LISMGRPSSTLG VNRSSSRLGVKEK NVTITPDL PSCIFLEQRELFEQSKAP RADDHVRKHHSPPQH QDYVAPDL PSCIFLEQRELFEQCKAPYVDHQMR ENHSPLPQQQDSIASDLPSPISLEQC QSKAPGVDDQM NKHHFPLPQQGD CVVEKNNQH KPKSHISNINVEAKFN TVVSQSAPNHCTLAASASTPPSNRK ALSCVHITLCPKTSSKLD SGTLDERF HSLDAASKARMNSEFNFDLHTVSS RSLEPTSK\LLTSKPVAQDQESLGFL GPKSSLD FQVVQPSLPDSNTITQDL KTIPSQNSQIVTSRQIQVNISDFEGHS NPEGTPVFADRLPEKMKTPLSAFSE KLSSDAVTQITTESPEKTLFSSEIFIN AEDRGHEIIEPGNQKL RKAPVKFAS SSSVQQVTF SRGTDGQPLLLPYKPS GSTKMYYPQLRQIPSPDSKSDTT VESSHSGSND AIAPDFPAQVLGTRD DDL SATVNIKHKEGIYSKR VVTkas LPVGEKPLQENADASVQVLITGDE NLSDKKQ QEIHSTRAVTEAAQAKE KESLQKDTADSSAAAAAEHSAQVG DPEMKNLPDTKAITQKEEIHRRKKT PEEAWPNNKESLQINIEESECHSEFE NTTRSVFRSAKFYIHPVHLPSDQDI CHESLGKSVFMRHSWKDFFQHHPD KHREHMCLPLPYQNMDKTKTDYT RIKSLSINVLGNKEVMDTTKSQVR DYPKHNGQISDPQRDQKVTP EQTT QHTVSLNELWNKYRERORQQRQPE LGDRKELSLVDRLDLAKILQNPIT HSLQVSESTHDDSRGERSVKESWG RQQQRNKLQKKRFRFSLEKSHKNT GELKKS KVLSHHRAGRSNQIKIEQI KFDKYILSKQPGFNYISNTSSDCRPS ESELLTDTTTNILSGTTSTVESDILT QTDREVALHERSSSVSTIDTARLIQA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FGHERVCLSPRIKLYASSITNQQR\RYLEKRSKH\SKESAGLTGHPLVTSEHTRRRHIQPPTSATACRQPLMTFCFYGFAYSGPFI
3663	9160	A	3938	2	354	NRILVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIFPEKPLALSGKSFLQLEALLPPRQKVITDDMDQVELKEFCPNEQNWRQHREAYEEDEDGPQAGVQFQTA
3664	9161	A	3939	204	374	DHGFLIPLTQGDQKGP\RVHPL*ACYHWNQREKVISSCIGCICMSQIKDPLVKKKKK
3665	9162	A	3940	39	385	AGVQWRDLSSPQPPPPGFKRVSCSLPSSWDYRPQ\RLANFC/DFLVEMGFCHVDQ\AGLELLTSGDPPASASQSGITGVSHRTQPCLLFLKTKTWSGKWEKDGMFWEMNGAQDQQE
3666	9163	A	3941	1	200	FETGSYSVT\RLVFSVQISAH\CNLCLPGSPDPPTSASEVVGTSVCHR\TQLI VIYPLQLPKLFRLOV
3667	9164	A	3942	2	458	LFYGVYFLFPLNSCILFVSFTVNHLQIFFFGGGMKSWSVRRLECSGVILAH CNLRLPGSSDSPASASRVAGTTGTC HR\ARLIFVFLVEMG\FHHVG/RRDGLGSPDLVIHPPR\TPKGVGG\QGVSHC GPGPSPQGFY\KIKELGSSQGGEQFP
3668	9165	A	3943	1	2499	
3669	9166	A	3944	855	2479	PGGSGPGFPTLEGSSKAGRELIGYEPGSSGVGAPLTPHKMKKRKELN ALIGLAGDSRRKKPKKGPSSHRLRTEPPDSSESSEEEEEFGVVGNRSRFAKGDYLRCCIKICYPLCGFVILAACVVACVGLVWMQVALKEDLDALKEKFRTMESNQSS\FQEIPKLNELLKSKQKLEKIESGEMGLNKVWINITEMNKQISLLTSAVNHLKANVKSADLISLPTTVEGLQKSVASIGNTLNSVHLAVEALQKTVD\EHKKTME\LLQSDMNQHFLKETPGSNQIIPSPSATSELDN KTHSEN\KQDILYLHNSLEEVSALVGYQRQNDLKLEG\MMNETVSNLTQRVNLIESDVVAMSKVEKKANLSFSM MGDRSATLKRQSLDQVTNR\TDTVKIQSIQKEDSSNSQVSKLRE*LQLISALTNK\PESNRPPETAD\EEQVESCTSKPSALPKFSQFLGDPVEKGCPKLR\TYS P*QGVSKH*KIFQDLFR\KTGQD\VDGKLT\YQEIWTS\LG\SAMPEP\ESLRAF D\SDGDGRYSFLELRVALGI
3670	9167	A	3945	336	519	AALPCEPAFSP\QEVRGLQDRGQ NQTQRPFFL\NVVQA\VSQEG\ACV\YAVSELRK\EWGRPQ
3671	9168	A	3946	252	2104	LCASSCFICPPIRPSVCP\PAAPLLGCRAMARGYGATVSLVLLGLGLALAVIVLAVVLSRHQAPCGPQAF\AHAAVAADSKVCSDIGRAILQQQGS\PVDA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TIAALVCTSVVNPQSMGLGGGVIFT IYNVTTGKVEVINARETVPAHAPS LLDQCAQALPLGTGAQWIGVPGEL RGYAEARRRHGRLPWAQLFQPTIA LLRGGHVVPVLSRFLHNSILRPSL QASTLRQLFFNGTEPLRPQDPLPWP ALATTLETVATEGVEVFYTGRLGQ MLVEDIAKEGSQLTLQDLAKFQPEV VDALEVPLGDYTLYSPPPPAGGAIL SFILNVLRGFNFSTESMARPEGRVN VYHHLVETLKFARGQRWRLGDPRS HPKLQNASRDLLGETLAQLIRQQID GRGDHQLSHYSLAEAWGHGTGTSH VSVLGEDGSAVAATSTINTPGAMV YSPRTGIILNNELDLCCERCPWGS TPSPVSGDRVGGAPGRCWPPVPG RSPSSMVPSILINKAQGSKLVIGGAG GELIISAVAQAISKLWLGFDLRAA IAAPILHVNSKGCVEYEPNFSQEVQ RGLQDRGQNQTQRPFFLNVVQAVS QEGACVYA\VSDLARKSGEAARS
3672	9169	A	3947	2	97	GLGRWLT/PVIPTLWEAKKGRSPEV RSSRPVKS
3673	9170	A	3948	3	308	PEDSDEKSLSSSVVHVRRPSRRVP RMPRGSRSTSRMAPPASRAPQMR AAPRPAPVAQPP\QPCLYEIKQFLEC AQNQGDIKLCEGFNEVLKQCRLAN GLA
3674	9171	C	3949	38	154	MXSNSFWSPRTRVTSSSVRVSMR CCYDFILCELIRIKS*
3675	9172	A	3950	1	192	GSNAEP/ARPDLT/YQEP/QGTQPAQ QQQPCLYEIKQFLECAQNQGDIKLC VGFNEVLKQCRLANGLA
3676	9173	A	3951	1	254	LMARMQTLKLAVLWASAIGHTWV HAFTGAFSGGSNAEPARP/DITYRSL YEIKQFLECAQNQGDIKLCGFNEV LKQCRLANGLA
3677	9174	A	3952	1	142	
3678	9175	A	3953	1	325	FFFEMESCSVAHAGVRWA/DLSSLQ SPFPGFKRFSCGLLSSWDYRRLPP HPANFYFLVDTFHHVGGAGLELL T/S/GDPPASASQSAGITGTSHRAP VNTFNRPPAS
3679	9176	A	3954	3	304	HEGREKRRVLGAEAGGGRSCEIGV PLEWWRPLMRVRVMCC/LMLML RWGASFAWYCCFLSFCNWLASSET TGLMITFMLRISALLMRSLQNPEAM TLPW
3680	9177	A	3955	3	961	LLLLNSRPRRRDRLVTLESWANDPD YLKRQVGFCQWSLDNFLKEGRQ LTYEKNLSSIRAMLSNDVSEYK ISPHGLEARCDASSFESVCCSFCVD AGVWDYEVTVVTSGVMQIGWATR DSTFLNHEGYGIGDDEYSCAYDGC RQLIWYNARSKPHIHPCWKEGDTV GFLDLNEKQMIFFLNG/TPA/RPPEE QVFSSTVSGFFAAASFMSYQQCEFN

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FGAISPFKYPPSMKFSTFNDYAFLTA EEKIILPRHRLALLKQVSIRETAGS LCCDEVADTQLKPCGHSCLCMDCA LQLETCPLCRKEIVSRIRQISHIS
3681	9178	A	3956	4	101	RQSLAMLSRLA\NSWPQVILLPWP PKVLGLQA
3682	9179	A	3957	21	338	HPVLAITLSIFIVAFAYAEELDEIQ P/CIMMKTNLKLGIEGMCLNSIKAIY /DKSNANFILNKEKLKAFFLRSGTRQ IRPNFQ/PLLFNIVLEVLAKEIRQEEI KV
3683	9180	A	3958	90	360	ALICLVDIESGENSTTRPFASHDQV CIALLRTA\GILCLETFFIDSPSHGSRH FLFVLSSPPLTLFPLLHIYLLAVVPI VSPLLSLSDPP
3684	9181	A	3959	1	424	CGRRFSTRSDLTKHRRTDTG\EKPN RCELCGKRFTCVSNLNVHRRNHAG HKPHKCPECSKAFSVASKLALHRKT HLGERPAECARVGQVLQPAPLS QHQRGPHAPPAPLPPLPSSPAVGHC PQSFEGGRLEQEKAKGSL
3685	9182	A	3960	153	328	SIASYFTLVCHLLRKCHPRLGTVAH TYNPSTLGGRGRWIMR\QEFETSLT NMVKPCRY
3686	9183	A	3961	1	936	
3687	9184	A	3962	1	1023	
3688	9185	A	3963	15	337	RINNTISWLIYVCKFCLSSFSIYLIIIII IIFFETESHVAQAGVQWRNLGSLQ PPPPRFKRFSCLSFPSSWDYRCPPPR PANFCIFSRDGVSPCWPGWFRTPDL R
3689	9186	A	3964	3	1105	HASALTPVVCMLSAIAFSNVFEHYL GDDMKRENPPVEDSSDEDDKRNQG NLYDKAGKVRKHATEQEKEEGLG PNIKSIVTMLMLMLLMFVHCTW VTSNAYSSPSVVLASYNHDGTRNIL DDFREAYFWLRQNTDEHARVMSW WDYGYHIAGMANRTTLVDNNTWA NNSHIALVGKAMSSNETAAYKIMR TLDVDYVLVIFGGVIGYSGDDINKF LWMVRIAEGEHPKDIRESDYFTPQG EFRVDKAGFPTLLNCLMYKMSYYR FGEMQLDFRTPPGFDRTRNAEIGNK DIKFKHLEEAFTSEHWLVRIYKVKA PDNRETLDHKPRVTNIFPKQKYLK KTTKRKRGYIKNLVFKKGKKISK KTV
3690	9187	A	3965	1	181	ANVVFTQLLIWYGVDVRSRDARGL TALAYARRAGSQECADILIQHGCS AEGCLSSTCY
3691	9188	A	3966	640	961	DGVSASCCPGLGVQWVRFGLSL\QP SASWGFKQFSCLSLPSSWDYRRALP PPRPANF/SVFLVKMGFLHVG\QAG LELLTSGHPAASASQSAGITGVSHR TRPAASILI
3692	9189	A	3967	2	334	VGLYGRIEASSPMGEGNRW*SGTPA NQG*QEQGIARPKPRGEPGLRNEGG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PGAILPGRWAGV*GPTGQEGR*RGSGESCPCPAQSSCSHRVAGLDVGGSHGHSAAFPATP
3693	9190	A	3968	1	361	ARARLRHLRDLRAPAGPVGGLCAAGTACGWPGPGPLLGERVRAFLRR*RAQHLLHHHRVRAPLPGWREAAGGAPPFLGTYGPESQVRLRDAVVPEAGGQDSGSSGSASLRPRSSFSCSCS
3694	9191	C	3969	151	373	MPTAVXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXVLPFLV LEVMOCLCPVLLLYDPNSKTRYV FFKTR*
3695	9192	A	3970	50	441	IPSPPDGFFSNLGRKPFPCNFSCQ NILLTRKILLKSFLYPFFFLRWSLA LPPAVLSAHCNLCPPGSSDSLASAS* VAGITGVHHQAWPVLPLVLEVMQ CLCPVLLLYDPNSTPRYVFFKTRT FIA
3696	9193	A	3971	3	224	FLRWSLALPPAVLSAHCNLCPPGSS DSLASAS*VAGITGVHHQAWPVLPL LVLEVMQCLCPVLLLYDPNSFV
3697	9194	A	3972	1	214	PIQFKQRLPFGFLFVFVF*EGVLLCH PGWTAVTEDRSWLTATSTSWAQVI LQSSCLSLPGS*DYRQCLPGV
3698	9195	A	3973	154	341	KNFFRGQFWFVA*AGVQWGHFRSL QPQPSGVKQFFPLGLPKPLDCRCES HRVPFLFLGLETL
3699	9196	A	3974	3	379	FALVAQAGVQWCSFDSLQPPPPGF K*FSCSLSPSSWNYRHLPPRLANFV FLVEMGFHYVGQASLELLTSGDPPA SASQSAGIRGLSHCTWPHVSGFIMQ YEYTLCFMVFIMSFWRNCRKVAKY LK
3700	9197	A	3975	2	35	LKQAPCLCLPSS*DYRHLPPCLSNF* NFL*R*GLSLLPRLVSNS*PQAICPRR PPKVLRL*AQTSPLPLTK
3701	9198	A	3976	1958	2316	IHSSPTKATFFLRQSLALSPRLEYS AISAHCNLCFPGSSDSRALAS*AAG TTGACHHIRLIFLFFVFLVETGFHH VGQAGLELLVSSDLPLVLSARITG VSHHAQPPPKLLNALL
3702	9199	A	3977	2	80	SLCICMCVCACIRTHA*MYVCVCV HTHACMNATSPSWVF
3703	9200	A	3978	123	452	KTGSNFAPQLEAQGGNLG*LNPWP PG*KQFSGLTLLITWINGAPPPPRAN FGIFNKKGVTPCGQGGPKTRDLGIG PSKPPKGLEFRAQPPEPALMGKFYP MVNLSNVPPF
3704	9201	A	3979	3	250	AIAAH*NLHLLGSSNSSASVSRVAGI TGARHHTQLIFVFLVETGFHHVCQA GIEFLTSGDTSTSASQSARITGMSHH TWPQKQ
3705	9202	A	3980	2	257	PRSSPTCPACLCVQVNPPAQDPEDP APQLSPQPQDPAKPPQPYNPYPY PNLGCGL*PQNYCIIVCMVSIVYYH MGHETVKSQ
3706	9203	A	3981	2	147	LVEMGFHHVSQAGLKLLDSGNLSA

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						S*RSAGITGISHRAHPPNSTNIYA
3707	9204	A	3982	3	446	QVVRGFGFRVSKQMGIPANFPEQV VDNLPADISTGIYYGGASVGSQDVH KMOVSI*WNPYYKNTKKSMETHIM HTFKEDFYGEILNVAIGD*LRPDKN FDCLESISPVGQDGD*AKIRLELPE HLRI*EDTFFQVSLNRTMIVTDDK
3708	9205	A	3983	1	162	FFFRVKASICCPGWSTVAQ**LTAA SDSWAQKSSCSFLWSSWDNRRLP HLANK
3709	9206	C	3984	131	442	MNIPLSMSLVVSNMQDVFWXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXX*
3710	9207	A	3985	141	429	TGSHFVAQAGMQWCNLWSMQLLP AGLR*FPYLSLPSSWDYRHAPPCST HFLYFFVEMGFCHVAQVGLELLAS SDVPTYASQSAGITGVSNHPRPF
3711	9208	A	3986	1577	1879	
3712	9209	A	3987	1	219	EM*SCRVTQAGVQWCNLSSLQLPS PGFKQFSCLSVPSGWGYRCMPHP ANFCIFSRDRASPRWPGWSQTPDLR
3713	9210	A	3988	1	414	FF*TGSCFVSQAGTQQQDHSSLQP* TPGLKPSSHLCLSSWDNRHLIFKFF VEMGSRHVAQAGLQLLGSNNPPTL AS*SARIISWSHRAQPTCTLCSWLC DSGAGTAESFLWQPALSRVANRGC CRRPGKLKEKQGT
3714	9211	A	3989	3	666	FFVETGFCHVGQAGLELLGSGNLPA AASQSAGITGMSHRVRQHS*YETHR KVFYS
3715	9212	A	3990	1	436	FFFFFLRQNLTLSPRL*CSGTILAH NLQHPGSSDSPASASQVAGITGVRH HIWLIFVFLVEMRFHHVQGASLELL NSGYLPTSASQSAEITGVSHCAQLQ PGILMHGLRRLTDLDDNVHHPRSRL KVTSSSAHPGAASSFLHL
3716	9213	A	3991	167	563	SESASEFSIFYLFIIIIIIETRSCSVA QTGVQWCDHGLLQPRPPWFRPSCH LSLLSSRDYR*APHPANTFNFFLE IGSHYVAWGSLELLGSSDPPASASQ SVEIIGVSHRGPDSQKSFIHLSPRFP
3717	9214	A	3992	3	456	
3718	9215	A	3993	78	129	
3719	9216	A	3994	96	251	MDOYSRNSPLEVNGQQLLGWYQH ALRCKWNF*APLCYCSTVFNSQPT HTEE
3720	9217	C	3995	94	351	MKRISTTQYYHCQDYDLRHSKHM CLVSTAFQKVPLYKYLEILQENLD PQKDSRWFSVISSPRSQNVKVR HLQSCLTSHCKH*
3721	9218	B	3996	1	431	MAVASTKSRWETGEVQAQSAAKT LSCKDIVAGDMSNKSFEQKGGSK TSSTITAQIAFLQGERKGQENLKD LVRMIRMLEYALKQKRAKYHKLK YGTELNQGAMKPPSYDSDEAQQQA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MRSVHGPLHLSAPPASQQKRPTE *
3722	9219	A	3997	772	1391	IANNKDALRKTWNPKFTLRSHFDGI RALAFHPIEPVLITASEDHTLKMWN LQKTAPAKK*EYSTLTLEFYFK*HA
3723	9220	A	3998	3215	3491	SAKVLRPTFFFFFFFFFAIESHCVT QAGVQWCNLAQLQSPTEFK*FSC GLPSSWDYRCVPPHPANFYIFSRDR VSPCWPGWSKTPDLK
3724	9221	A	3999	1	779	MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEK VPETTTTRFWAPGVEAPGDDAERRR REASGPATRHSPPLTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSSTVQPVAAAATPSY ALIGSSLWPVNERGRQESRTCIIDQ SAWHVGRAEIRKLLPYCSTQGGLK YSDVTSGMVKDPPDVL/DRQKCLD ALAALRHAKWSSEIRF
3725	9222	A	4000	1	1286	MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGGPGLGLGV RPGMPPQPQGPAPLRPDSSDRYV MTKHATITYPTEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLLSRIAE NLPKQLAFISPEKYDIKCAVSEAAI LNSCVEPKMQVTITLTSPIREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLOSCVHIR ILRDLQCRVP/TWS/DFPSWAMELLV EKAISSAS\SPQSPGDALRRVFECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PDPASRED/LSTSQCHSLPLETS LAFPPRYHKVLGMDPITRK*AQR NI\HNRRKRRRD\SDGVDGFEEAGK KDKKDYDNF
3726	9223	A	4001	2	379	DLPASATQONAGITGVSHHIWPRJIFL LW*KTFTILTFLSVQYSSSNYIHPVC NRALELFKSYKTETKLNFPSPPPPI VNLHCIFFF*GLTFLLGFFSLPKYRG FTNFVSPCTVAMLTRGGGGGEF
3727	9224	A	4002	229	445	RPGPNFGLLETLTWGLKGTWLWNP PKNWELGAHPPTPGNFWIF*KGGF WNVSQGGSKTRGLRELPPFSWKKG
3728	9225	A	4003	192	529	HEVLNFLTSCVLTTLVFLIADIHWS CRTRSLPFVATTLEVLPLSLIGLCHH TILVFISNAFFI*KAYFVTSSFIMFP*S FFLFNISVLSYMYLTFSHLTSFVIAY FSYSHI
3729	9226	A	4004	330	754	SDLSQKESSSSLSKFLVTEKNSSLGS GGCDMANKENELACAGHLPEKLH HDSRTYLVNSSDSGSSQTESPSSKYS GFFSGGFLRDHETMAQVLFSDMR LNVALTFWRKRSISELVAYLLRIED LGVVVDCLPVLTNCLQE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3730	9227	A	4005	296	861	VSQDHETMAQVLF SRNMRLNVALT FWRKRSISELVAYLLRIEDLGVVVD CLPVL TNCLQEEKQYISLGCCVDLL PLVKSLLKSKFEE*CY*WVLTGLQA VIKRWWSSELSSKTEINDGNIQILKQ QLSGLWEQENHLTLVPGYTGNI AK DVDA YLFPVTIEGFHLLKSIWFFKTS LELYNLQKKKVS
3731	9228	A	4006	2	265	NNFFSFSETESHSVTQAEAQWYD NS SLQP*ILGLKQSFCLSLPSNWDHRC APHPQFSFLIPGLYVSQFILGNKPSS LPCQMFKSAV
3732	9229	A	4007	3	295	HFNLSHRSAQAKGNRYKEAEALT N AAVHVDDMPNALNALIDLRAHNLG QDPVNFKRLSHCLLVTLAAHLLAEL TPAVHA*LDKFLASVSTVLTSKYT
3733	9230	A	4008	1	1077	
3734	9231	A	4009	3	285	ETESRLATQAGVQCCDLGSLQPLSP GFK*FSCFSLPSSWDYRYPSCQAN FCILVEMGFHHVGQASLELLTSGDP PASASQSARITGVSHRAQ
3735	9232	A	4010	1	338	VIATYHGGGLCTQKSQPPPPQALWSA STSTINLMVSTEPLALTETHICKLPK D*GTCRDFILPWDYDSNTKSCARF WYGRCSANENDFGSQSECEKVCAP VLCKPGVISEMAT
3736	9233	C	4011	269	526	MLARLVSNSLPQVIHHTQPRVGSPT RIPTLSLNLPLPLALTSLRWDRHQLR GQGHWGAQELRAITGFKDHQVWQ TLNCSLCV PKP*
3737	9234	A	4012	2	51	
3738	9235	A	4013	83	5229	
3739	9236	A	4014	3	45	EVVHALRCRWWWSWGLKLDLLTPEP EPICGPALLSRSSLRGSHPTAFLLPP QVSQ*RGELGPSTFRAFRAEFPTSRG SKDNKEKNQQEQDMAKPATGTGQ G*GADGGAGA
3740	9237	A	4015	3	323	LLWKVESSWRDQKDIMSWEWDKR RRRHHLTDRSQLCSKV FQVDCDLI EWGTWIINLKQYNAYHCEGECHNP VG*KFHQSNHAYIQVGCQVLGEE AVIWHWGTGL
3741	9238	A	4016	2	279	FFF EAKSHSVTRMLECNGAISAPC NLHLP GSSDSPASASQVVGITGVYH HTQLIFISVETGFCHVGQDGLNLPD LMIHPPWPPKVLG*QA
3742	9239	A	4017	166	939	
3743	9240	A	4018	2	225	KELTGRRCAEPHPRPSPQLLTEEPF TKGRFSGEWRGRNAASMTGPFAE HSNQLWNISAVPSWSKVNQGLIRM YKAEP*EGADRKALCRASPPPIPPV TDRGAIYKRPI LWVERQERSVYED WPICRALQPAVEHQRRPFLVQSEPG SHPHV
3744	9241	A	4019	142	1336	KARGDCKHPGRCWPEQMAEGERQ PPPDSSEEAPPATQNFIPKKEIHTVP DMGKWKRSQAYADYIGFILTLNEG

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						VKGKKLTFEYRVSEAIEKLLALLNT LDRWIDETPPVDQPSRFGNKAYRT WYAKLDEEAENLVATVVPHTLAA AVPEVAVYLKESVGNSTRIDYGTG HEAAFAAFLCCLCKIGVLRVDDQIA IVFKVFNRYLEV MRKLQKTYRMEP AGSQGVWGLDDFQFLPFIWGSSQLI DHPYLEPRHFVDEKAVNENHKDY MFLECILFITEMKTGPFAEHSNQLW NISAVPWSASKVNQGLIRMYKAECL VEKFPVIQH/FSKFGSLPIHPVHVGL GGAKPKEPPRGTVSCCLPFPTPAVA PPSPSPSVSSRLMRGCLLGLGGEMG LRGLRA
3745	9242	A	4020	80	283	
3746	9243	A	4021	61	626	DLICVIGVPEEEKETGAKNIFKEIMG ENSPHLVKDVIVHIEEIHSDEN*** Q*KSYK**QKGIIKLRVDLLETMEA KCSRTPSLKCLGKESFGESWESRILH PAEISHRNECHMKIILDFKSEKGPDA VAHTCNPSILGGHTAGGSLEARSFE TNLPETLSLLKKLNLKEKEFVASYP PLVEMLK
3747	9244	A	4022	18	161	TSFKNPPPPPPGGLKKIPSPPPKKK KFKDVS*PTYFYLNLASSVT
3748	9245	A	4023	30	262	NRRQAGPFAKLGRPSPKGGFPNFF KSSSSKSSF*KNPKGQGWGFPLIPG FQGPQVGGSLGAPGLKPPWGTPQN PF
3749	9246	C	4024	193	366	MYNYRSIPKNKYTYTYTKSYPNKIF SRLILYIPLGTVSQISTLNCVPRFVLL TWKAL*
3750	9247	A	4025	3	258	TIDSLKGLPCKQNEPWHTIQCGYL GNSSKWN*YQSGKDFIRIAFCVCIC I/CYF*E*IYSCT*IPVRNTLNELNPLA KCPCPFH
3751	9248	C	4026	164	313	MEGTRIFGKWVKLIQSIPNRNSCTTI DLFLKINIIHTQKAILMKSFDP*
3752	9249	A	4027	9	373	DRVSLCRPTLEVQWRDLGSLQPPSP QVQSNPALSLPSSWDYRRVPPCPS *FFVFLSRRWRFRHVGQTALFLIKM MGKKILKIKSNYTLGLYVGPSYSER MIKPQEFESSLGQHCKTPSQK
3753	9250	A	4028	1	336	DRILLHRPCWSTLARS*LTIPSNHLG SVFPSPALLES*DCRHTPTTPD*FLKI FL*RRGLTVFPRVLNVAWTQAIQPL PLKALGLQDTFFKNINCDRLKVSEY YSDTEIEI
3754	9251	A	4029	514	742	LPKC*DHRHEPPHQAFFNFVEMG SCHVPQSGQLQLGSSDLPASAFYSA GIAGMSHHTWPPYLFKSRHKSFRFCP S
3755	9252	A	4030	1	264	QAQGKHGSGFGPPFAGLKGFPGGLGF PRTGNSGGFPQGGKYKGLIKNGVP PSFQGGF*IPGPGSHQRLGFRG*VGR AL*TPGFRATLF
3756	9253	A	4031	7	417	RQDLALSPRLECSDTIIAHCISIKLLG

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						SNGAPSAAS*VAGTTGTRHHAQLIF LKIFVETRSLYVAQASCVFPASSNPP TSASQSTGITGMSCCARPTSYVPGS DLSVLCILTHLILKIPLYRRYYYFVS LTYSKAEVQ
3757	9254	A	4032	123	376	KTGSNFVPPQAEAQGGNSG*LNPLPP G*KQFSGLTLLITWINRAPPPPRANF GIFKKKGVSPPC*GGLKTPNSGFSPF KPPKGLE
3758	9255	A	4033	3	292	QWHKHGLLQPQPPGLK*SSHLSPR SWDHRHVSPCLTNFF*FSVSMGSCY VAQAGLKLASSDPPASASVGTIG MSTT*SKTTLYTEKLANIILTK
3759	9256	A	4034	1	230	FFF*TDSCSVAQAGLQWRDYRPEPP CPANFITIKVQNKSVTFPARNLNK MRGASIMLYPIGLSLNDLMQLLSEGF
3760	9257	A	4035	3	189	SWDYRRRLPHARLIFVFLVGTGFHHV VQAGLELLTS*FTRLGLPRCWDYRR EHIAPGHIWY
3761	9258	A	4036	2	148	PGSSNPPTSASQLAGTAGTHHA*LI FVCLVETGFCHVA*AGV*VKFF
3762	9259	A	4037	348	696	AEEQDKKGRQ*ERGKEWERETETK IYSRIKGNREGQAKKKWGHGELIH KTKDEKRKKSEEDKKLRWRKR*TN SQKD*IRKRLHKETANSER*EEKHK ERKQWRRGPKARRAISRG
3763	9260	A	4038	1	295	QNQFFIFIYFKTESGSVTRLEYSGVIS AHCNLCHPGSSQSPASAS*AAGTTG AHHHIQLLFVFLVETGFHHVQGAG LELLTSSDLPASASQSAWGLQV
3764	9261	A	4039	6	151	SQGLALLPRLISNPWVQAILLPWPP KVLGL*AEIAQNKMQK
3765	9262	A	4040	101	318	SNHTLGTS*HFFETVSCCIMLHRVE CSGAVIAHCNLELLGSSDSPASTS*V AGTTAVYHHTGLSWLLNLH
3766	9263	A	4041	210	306	SWPGTVAHICNPSALGGQGGWIA* GQAFRQA
3767	9264	A	4042	2	147	DFSVKTL*ARREWRDIFTVMKEKNF YPRKVYALKIPFKNEATKKVEV
3768	9265	A	4043	160	525	NTQTRSFGRNLMAQAQSSHKALTK KVMTCNPSETVHDSQECFFVLFFET VLVCLPGWSAVMLVRCSLCLLSSW DYRRVPPHLG*FLYF**R*CLTMLA RMVSNS*PQVIHLPRPKLLGLQA
3769	9266	A	4044	3	72	KTQVHFQGWQHSVHIITHPCWEKL ALSITPLR*DNRKLQAWNRPRLGPT CLFPRALALMCVLM**NIHEYNSFQ RVLWVLLVNC*ISKVGSTLCISSHIP AGRS
3770	9267	A	4045	313	358	
3771	9268	A	4046	7	308	AGGRRARAPHLGGRGAARGRL*RV RGHRERGLRAAPVPRPQQLRRGA AAGAVQPGQGVGRAGPPEGSEGSV AGVGLDLSSCYHHSSDFYICHPMP ISS
3772	9269	A	4047	92	390	ETGSHSVNLAGLQWCDHNSLQP*T

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						PGLKQSSYLSLLSS*DYRWVPPCPA NF*IFFVEIRSCHISQAGLDLPRSPD PVWGSQSAGTIGMSHHAQPREIC
3773	9270	A	4048	65	375	SQLTATSTSRVQ*HDLSSQPPPPGF KRFSLSLPSGCDYRHPPPHLANFL YFLVETGFCHVGQAGLELLTSSDLP ALASQSAGITGVRYCAWPTFLIMKT CIPSFPLPSTSPIPLP
3774	9271	A	4049	12	292	DIVSPVA*TRMQWHNLGSLQPPPPR FKQSLCFLPSWDYRCVPPCPAIF VFLAEMGFCHIGQAGLELLASSNPT TLASQSAEPPHLAATDF
3775	9272	A	4050	40	343	SSSSLILSSSVIYLLNLSDFLVLLY FLVFRFSVCSFCFFVKNFNLIFYF FKHIKNICFKVCV*RLGFLDPLCAYF GCLLFL*VFSHVLSLHIPDDL
3776	9273	A	4051	97	282	
3777	9274	A	4052	3	336	FFETGSRFVTHAGVKWHNHDSLHP QPPRLK*FSYFSLLLSSWDHRHVPP RPANLVYLL*RGGPSMLPRASLEF PGLQVNSSLPSALPKVLGITG*GHRP RPKVTFHQRG
3778	9275	A	4053	3	294	CCFGDGVSLCRPGWSIECSGNHSSL QAVEPPRLR*SSRLSLGSDWPSHV PLHLANF*TFCTHGVLA MLPLAGLK TPWAQTIPPHLSLPKVLGLQG
3779	9276	A	4054	16	308	MPQPN*SNPPVNCRLPRGPPSQVP PRIHLSPKYSPSEASAPDLQKKGNL QAPRRPGEVLETPRKPESSCMKFPF* REIKLPPPRLTSPVHSMVL
3780	9277	A	4055	445	448	IS*HCDASASIFRKKQRKQINKHPTL ASRVLGLAMEMQDETWCSSGQSET VN*SQTAQNHPQPGS*PAGVCLWV ASSQHFTPQPLKKKPNPDSAKLNSA SDSLTEVILCKIFSAWQTDK
3781	9278	A	4056	3	284	CLSLSSWDYKCLPPRLGYFLYF** RRGFTVLARMVVISRMVVISRMVIS *RRDPPASASQNAGITGVSHCARPK EQKLFYPEVSCLYLGLY
3782	9279	A	4057	428	636	DYHIVSLHLHF*FLETGSHSVTQAGI QWCDHSSL*PRTPLKQSSCLSLPE* LGLQE*VTVPGSYSLFF
3783	9280	A	4058	2	113	FFGRDGVSLCCPDWS*TPGLKGSSC LGLPKCWDYRRE
3784	9281	A	4060	36	359	RSGVQNGFHAQEVLSVRLCFSTEAL GQNPMPPFAPPGATSSPGPRPSCHL HSQKL/TLLHAQTLVTPLPL*GLGLS AWRTL AGGAPGLHPFTTHALSTPET IPGAYRRT
3785	9282	A	4061	17	168	APGMVSGVLSACVVNGWSPGAPPA SVLQA/PQT*PF*SRPHVTSQPLLKA PH
3786	9283	A	4062	2	375	FFFFFFENHTNLLSYSSRGSGVQNGF HQPEVLSVRLCFSTEALGQNPMPPF APPGATSSPGPRPSCHLHSQKLPLLH AQTLVTPLPL*WPPWITQGPPQST GHLPTTEILKLKHHRRVPFCHAR

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3787	9284	A	4063	309	620	
3788	9285	A	4064	3	218	LRQSYSVTQAGVQWRNLGSLQPLP PGFKRFSCLSLRKS*DYRRPRLPNFC ILVKTGVHPCWSGWSQTLDLR
3789	9286	A	4065	1	170	NPKATPPQIVNGDQYCGDYELFVE AVEQNTLQEFLKLA*VKPVQSSPAG LHHHTPL
3790	9287	A	4066	29	483	RRLPAVQLPLTAALCPPARLSTPSM SGPARSTARRATGFREIKVPSKSEVT RILÆGKRIQYQLVDISQDNALRDEM RALAEQPQGHPTPDLSTGDQYCGD Y/DASFVEAVEQNTVAG\FPGSLGL KFKPCSRVSPCWSDSHHQHSPPAFQP GQ
3791	9288	C	4067	33	236	MRHHAWLIFVLLVETGFHHVQGAG LEHLISGGPPTSASQSAGITGVSHHA WPIYLFILLSGPSRLCF*
3792	9289	A	4068	1	205	AIGTDKGTWRPSEDDPGNLPEIFLFI LGPTADYV*RERQRSIELESFYRRV WGSPGGEGTGDLDDEFDF
3793	9290	A	4070	2	44	LSSWDYRHVPPRLANFCIFSRDGGF TMLARLVLNS*PQVIHPPQPP*VL*L QACATTPG
3794	9291	A	4071	173	369	CSTLI*IRKVWLGAVAHAYNPNTLR GRGGRIA*GQVFKTSLGNNVKTCLF LPSPHNQQSLSGFLL
3795	9292	A	4072	1	336	
3796	9293	A	4073	1	200	
3797	9294	A	4074	11	392	
3798	9295	A	4075	1	191	
3799	9296	A	4076	84	264	
3800	9297	A	4077	2	446	DSARNSRVDGCE/IDRQKGTNDSLM MLMRELEDRFASEASGYQDNIARL EEEIRHLKDEMARHLREYQDLLNV KMALDVEIATYRKLLGEESRINLPI QTYSALNFRETSPEQRGSEVHTKK TVMIKTIETRDGEVVSEATQQQHEV L
3801	9298	A	4080	3	196	SRAKGPKNYNFGQGPPTKVKGPLA SPFFPLLPFPRPPWFPPPF*NPIFPW W*KGPKKPFLN
3802	9299	A	4081	1	187	SIRLFFFCFFF*AETGFRHIGQAGFGL LTSSVPPALASQSAGIIGVSHRARC SSLIVLHL
3803	9300	A	4082	156	326	KLEICRRARVSLKIGFIRPGTVAHAY NPSTLEGRGRQIT*DQEFETSLANM VKPCLY
3804	9301	A	4083	3	448	
3805	9302	A	4084	1	4249	AAATIRYLKTTMAWKTLPIYLLLLL SVFVIQVSSQDLSSCAGRCGEGYS RDATCNCDYNCQHMECCPDFKR VCTAELSCKGRCFESFERGRECD AQCKKYDKCCPDYESFCAEVHNPT SPPSSKKAPPPSGASQTIKSTTKRSP KPPNKKKTKKVIESEEITEHSVSEN QESSSSSSSSSSSTIWKIKSSKNSAA NRELQKKLVKDNKKNRKTKKPTP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KPPVVDEAGSGLDNGDFKVTTPDT STTQHNKVSTSPKITTAKPINRPSL PPNSDTSKETS LTVNKETT VETKET TTTNKQTSTDGKEKTTS AKETQSIE KTS AKDLAPTSKVLAKPTPKAETTT KGPAL TTPKEPTPTTPKEPASTTPKE PTPTTIKSAP TTPKEPAP TTTKSAPTT PKEPAP TTTKEPAP TTPKEPAP TTTK EPAP TTTKSAP TTPKEPAP TTPKKPA PTTPKEPAP TTPKEPTPTTPKEPAP TKEPAP TTPKEPAP TAPKKPAP TTPK EPAP TTPKEPAP TTTKEPSPTTPKEP AP TTTKSAP TTTKEPAP TTTKSAPTT PKEPSPTTTKEPAP TTPKEPAP TTPK KPAP TTPKEPAP TTPKEPAP TTTKKP APTAPKEPAP TTPKETAP TTPKKLTP TTPEKLAP TTPKEPAP TTPPEELAPTT PEEPTPTTPEEPAP TTPKAAAPNTPK EPAP TTPKEPAP TTPKEPAP TTPKET APTTPKGTA PTTLKEPAP TTPKKPAP KELAP TTTKEPTSTTS DKPAP TTPKG TAP TTPKEPAP TTPKEPAP TTPKGTA PTTLKEPAP TTPKKPAP KELAP TTTK GPTSTTS DKPAP TTPKETAP TTPKEP APTTPKKPAP TTPETPPPTTSEVSTPT TTKEPTTIHKSPDESTPELSAETPK ALENSPKEPGVPTTKTPAATKPEMT TTAKDKTTERDLRTTPETTTAAPKM TKETATTTTEKT TESKITATTTQVTST TTQD TTPFKITTLKTTTLAPKVTTTK KTITTT EIMNKPEETAKPKDRATNS KATTPKPQKPTKAPKKPTSTKKPKT MPRV RKPTTPTRKMTSTMPELNP TSRIAEAMLQTTTRPNQTPNSKLVE VNPKSEDAGGAEGETPHMLLRPHV FMPEVTPDMDYLPRVPNQGIINPM LSDETNICNGKPVDGLTTLRNGTLV AFRGHYFWMLSPFSPSPARRITEV WGIPSPIDTVFTRCNCEGKTFFFKDS QYWRFTNDIKDAGYPKPIFKGFGGL TGQIVAALSTAKYKNWPESVYFFK RGGSIQQYIYKQEPVQKCPGRRPAL NYPVYGEMTQVRRRRFERAIGPSQT HTIRIQYSPARLAYQDKGV LHNEVK VSILWKIGLPNVVTS AISLPNIRKPD GYDYYAFSKDQYYNIDVPSRTARA ITTRSGQTL SKVWYNCP
3806	9303	C	4085	258	362	MFYRNLMKVRAELNCSAILIEIKA KVLTLFHSN*
3807	9304	A	4086	2	236	QSYNSDSLFFLR SFALVTQAGVQ WRDLGSLQLPSPGFK*FSCLSLPSS WVYRCPPDPANFLVLVETGFHHV GQGWS
3808	9305	A	4087	224	464	KIFLFFFFFKRQGLT LSCRLDCSVQ *HNHYPLQSRTPELKQSSCLSHPKY WD*RHEPLCLAPKKEDTLQEQL EIR LLIY
3809	9306	A	4088	129	315	ILKILWIFRIFLLSIKCF*TNMHVCV

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						SCLFIFLTVSFIEQTF*ISFFYASWIML LMSFFF
3810	9307	A	4089	1	190	FFF*IGPHSVAQAGVRWCDLGSCSL NLPGSSDPPASASQVAGTTGVHYYT QLIFKFFIEMRAP
3811	9308	A	4090	1	5229	
3812	9309	A	4091	1	7044	
3813	9310	A	4092	170	422	
3814	9311	A	4093	1	3230	
3815	9312	A	4094	3	151	DTATCCAKWNTEDKVSHVSTGGG AS*ELLEGKALPGVDATSTIYYFPAF
3816	9313	A	4095	2	1446	SLRSARRQSAPSLTESPTSLPSCISK MSLSNKLTLDKLDVKGKRVVMRV DFNVPKNNQITNNQRIKAAVPSIK FCLDNGAKSVVLMShLGRPDGVPM PDKYSLEPVAVELKSLLGKDVLFK DCVGPEVEKACANPAAGSVILLENL RFHVEEEGKGKDASGNKVKAEPK IEAFRASLSKLGDVYVNDAFGTAHR AHSSMVGVNLPQKAGGFLMKKEL NYFAKALESPPFLAILGGAKVAD KIQLINNMLDKVNEMIIGGMAFTF LKVLNNMEIGTSLFDEEGAKIVKDL MSKAENGVKITLPVDFVTADKFD ENAKTGQSTWASGITPG\WMGLDC CPSS\RYAE\AVTRAKQMVWNGP V\GYFE\WEAFA\RGTKALMDEVVK A\TSRGLPPSP*GGWRPLPTCCAQM ETREDKSQPM*ATGGWCPVWQLE G*SPFLGVDALSQYLGTFPALLSPC AQPPKVNLGIFLHPLGH
3817	9314	A	4096	1	747	MDSSRARQQLRRRFLLPDAEAQL DREGDAGPETSTAVEKKEKPLPRLN IHSGFWILASIVVTYYVDFFKTLKEN FHTSRSPESPAPRRGGVRASVPQKL AEMLSQYGLIVFVAGLLLLLAWA VHAAGVSKSDLLCFLTALMLLQL/P VDAVVRGPQLRAPPLPPQGHARG CRLAARQRPPTVSTGRGEHVDSPPP AQRRLYLPLRLGAEFASEPPSAPA HRA\TPPPVEVTPTEAGRFRQAKG ALS
3818	9315	A	4097	1103	1295	EQEGTGLERRRGSPMSKDWPPPHL TPPQGPCGIPVHSLSPPSFSPGPRNS K*ARRSTAPVDCK
3819	9316	A	4098	1	1302	MVAGSDNYHEVSLHDGVIGARGCP PPSPSARGASPRPPGGCARQPTA GRDAEQPVWADRVRGGAAGL GRARRGLAESDLLCFLTALMLLQM LWYVGRSSAHRRLFRLKDTAGAG WLHRLWIPPAFGCRPEYDNGLEEI VFGFEPWIIVNLAMAFSIFYAMHA AASLFEVYSGISETSVLGDWSKPSTF DSKASGLRHLKTSKGKSSLVNASIP TPPSPFRPSQPSEPASQPAKPAKPAK PVSQPSQPSQT\PGKPAKPAKPPKPA KPPASQASQASQPGMPAKPAKPAK

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						K/PKPGMPAKPARQPSQPAKTAKPA NQPSQSASQASQPASQPSRPACQPT KSARQPRQPSLPAKRANATYQRS HSASQDRHASEPTSQPSSQHSARP AATSQPDSDRAANQSAVEQARQPSA KHSGKQQADSEAAAGS
3820	9317	A	4099	684	902	
3821	9318	A	4100	143	551	TNEFPFHRSRPPQIQTS*AHFPHLITD PDLLSPLSPSHHRSRPPEPTSPISPQIQ TC*AHFPHLITDPDLLSPLSPSHHRS RPPEPTFPISSPVISWAPAI SFPNCCC KQTATDSSGFHFCLIVLIAKSPKRISP G
3822	9319	A	4101	14	209	ASFKVWLIWE*RPWHGTYPSCKNW GKFASGSVTIWFKLPSGPLALSGIL MRLLLLSLSLHENSVS
3823	9320	A	4102	126	265	
3824	9321	A	4103	74	196	NLGMLAHAYNSRN LGGQVRTII*G QKFETSHENISRCLV
3825	9322	A	4104	1	217	NIYMFLICFVLIFNFLNELIT*KHIVIF ICWILSLLLLTLH*FWCHKFHVSW NLEFCIFYFGFKIKLDTFT
3826	9323	A	4105	3	268	DRVLLCCPGWSAVSQS*LTAPQTPG FK*SSHLSPSSWDYRHIPPHLAKK QKYFK*RWSLPVLPRLV*NSWAQAI FPCQPPKGLGLQA
3827	9324	A	4106	3	263	DSLALSLRLECSGVISAHCNLCFLGS NNSPAAASRVAGTTGACH*DWLIFE FLVETGFHHIGQAGLELLTEVICLP WPPKVLGLQM
3828	9325	A	4107	22	208	SFSIQGPLLLKPNS*PGVVAHSYNPS TSGGQGR CIT*GQEFESSLVHMAKP HLYQKIQKICR
3829	9326	A	4108	122	339	EKGFWFCAQGGK NLP GGNSLEPSA SGLKEIFGLNLLNWE*RGGP KTPG NFWIWKKGGV*PLWPGWG*NPGL
3830	9327	A	4109	2	210	KEKIFPSPGFKHPPPPPF*KTPLK GK RIFFSPPRKNWPPQRIFKKAPPSSSSS SSSSSSSAQI*SFNSP
3831	9328	A	4110	3	76	ATSESLDVMA SQKR*SRSGSPMARR
3832	9329	B	4111	1	2142	MGGAGSPQVILVSHT PQSASAACEE IAYQVAGVSGNLAPGNQPEKEGRA HQCLECDRAFSSAAVLMHHSKEVH GRERIHGCPVCRKAFKRATHLKEH MQTHQAGPSLSSQKPRVFKCDTCE KAFAPKPSQLERHSRIHTGERPFHCT LCEAFNQKSALQVHMKKHTGERP YKCA YCVMGFTQKSNMKLHMKRA HSYAVAVAMGGTAQCPPGATA CL GTAICPSGLRAQRPSNLSVPEAAKP KSGRNRKIEAPT WALSTSKDPQTEG LRNPQTCVQIRSNPFCFAQGFSLIS ELRTL NCFVGLCDSQSGKQQLGFYS GQPATEAWQKYS LAVCILRSEQEIS ATRLGLKNTNVNKL DGGCGAWNF LGGMSEHNSPPSGRAILLPVVFTEV FPGPWTPEQGS HICRMNLAPTQAF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPKTGFPIDPQELLQGPIERTIWPGT VYTFRSAIVTARAVWVRPRMDRRA DLSSATQSASAEKFGGRVSAGHCA LPLPARPVTASVYGRRLARLRGLED SYPSALSAQVFLDSPAVGCGLETRL FIEAALGPPCRATVTSRGHLLDISIT KSPGRPCFLSVCLHGSDQQKRKGA AATAKRKSKGGGVNVEGRLCTWPP EDPPKSWSLAFGPLQEKTELNLHP RCWARCLSHWELPPGPRGRAQAPD WTGSKSFREQLLTFTLWGVQEKISK HQANQGKEAPAYTGLEDSDPGGLC AV*
3833	9330	A	4112	1	551	
3834	9331	A	4113	3	288	CIGLGVVAHACGPGTLGGRGGRIT* AREFGTSLGNIARSHLYKKRKNSES QMSLHLLTDLTPYISAAFASPVDA DTQLSACTFQLKETPMPSF
3835	9332	A	4114	3	344	VQYYGPAT*VQDGS*GYRTHMYMI NQIWLQAVLKIITNKTGRALTILTQ QETQMRNAIYQNRALDYLLAAEG EVC RKFNLCCLHIDNQGQVFEDI VRDMTKLAHVPMQV
3836	9333	A	4115	6	185	LAGHDRVRL*SQLFRRLRREDCLSS GGRGCSEP*SHHHTPVWKTCLGPV SKEKKYNQIV
3837	9334	A	4116	1	176	QSIFQICIFFKFTVYMFKTFKFQTV FLCGRCWFL*KGLIIFFTLYFKTFHH IVRGIK
3838	9335	A	4117	1	312	GGEKNQDFTFKMESPSDSA VVLPST PQASCLSLPSN*DYRHPPPCPANFCI FSRDWVSTHVGPWSRTPDPQVIH RLGLPKTIRGSEEGIPDEYQLKGTLI YKL
3839	9336	A	4118	1	112	GKTFKQKQKQEQKKQK*ELK*KAM GKGPLAAGEIKKS
3840	9337	A	4119	3	355	SQSTKNLPSLARDMDIQIEAQRSP KRSPPRHIFELTKVKDKEKNPKVPV EKHQVIYKGFIRITAETSQARKKW DDISKFLKEKKKYRSKILCTANQSIR N*VEIASHSGSCL*SMILTA*PATVA HAYNP
3841	9338	B	4120	638	3862	MKGTCVIAWLFSSLGLWRLAHPEA QGTTCQQRTEHPVISYKEIGPWLRE FRAKNAADFSQLTFDPGQKELVVG ARNYLFRLQLEDLSLIQAVEWECDE ATKKACYSKGSKEECQNYIRVLL VGGDRLFTCGTNAFTPVCTNRSLSN LAEIHDQISGMARCPYSPQHNSAL LTAGGELYAATAMDFPGRDPAIYR SLGILPLRTAQYNSKWLNEPNFVS SYDIGNFTYFFRENAVEHDCGKTV FSRAARVCKNDIGGRFLLEDTWTF MKARLNC SRPGEVPFYYNELQSTFF LPELDLIYGIFTTNVNSIAASAVCVF NLSAIAQAFSGPFKYQENSRSALP YPNPNPHFQCGTV DQGLYVNLTER

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NLQDAQKFILVHEVVQPVTTVPFSM EDNSRFSHVAVDVVQGREALVHIIY LATDYGTIKKVRVPLNQTSSSCLLE EELFPERRRREPIRSLQLHSQSVLV GLREHVVKIPLKRCQFYRTRSTCIG AQDPYCGWDVVMKKCTSLEESLS MTQWEQSISACPTRNLTVDGHFGV WSPWTPCTHTDGS AVGSCLCRTRS CDSPAPQCGGWQCEGPGMEIANCS RNGGWTPWTSWSPCSTTCGIGFQV RQRSCSNPTPRHGGRVCVGNREE RYCNEHLLCPPHMFWTGWGPWER CTAQCGGGIQAARRRICENGPDCAGC NVEYQSCNTNPCPELKKTPWTPW TPVNI SDNGDHYEQRFYRTCKARL ADPNLLEVGRQRIEMRYCSSDGTSG CSTDGLSGDFLRAGRYSAHTVNGA WSAWTSWSQCSRDCSRGIRNRKRV CNNPEPKYGGMPCLGPSLEYQECN TLPCVDGVWSCWSPWTKCSATCG GGHYMRTRSCSNPAPAYGGDICLG LHTEEALCNTQPCPESWSEWSDWS ECEASGVQVRARQCILLFPMGSQCS GNTTESRPCVFDSNFIPEVSVARSSS VEEKRCGEFNMFMIAVGLSSSILG CLLTLLVYTYCQRYQQQSHDATVI HPVSPAPLNTSITNHINKLDKYDSVE AIKAFNKNNLILEERNKYFNPHLTG KTYSNAYFTDLNNYDEY*
3842	9339	A	4121	3	124	NVNRPVSSNEIKIIKSLPVKKSP*LN GFNAEFTKHVKNL
3843	9340	A	4122	1	197	GFKQLS*LSLPNSWDHRHTTTTPRE MGFHHVGGAGPELPISGDPPAPASQ SAGITGVSHRTRPRI
3844	9341	A	4123	1	268	QLYHLSLQSSRDHRCEPPRPANFLII CRDEVYVAQAGLKLPSSTDPPASAS KSAGSTGVSHCTQAKFYFF*NLMG EMRGKNNKHLTSFK
3845	9342	A	4124	3	301	TEEIHGVL SWNLVPDNYPPYYHPPP PSYIYGAQHLLRLFVKLPEILGKMT FSDKNLKALLKHFDLFLKHLAEYH DDFFPE*AYVAACEAHYCTHNPRSI
3846	9343	A	4126	2	214	FFFFKEMGSHYVA*AAVKWLF TGA IITL*SLKLLDSNNTPALSECKLIITQ EASVLKIKKVEIKKTKNRN
3847	9344	A	4127	2	382	TMVLSPADKTNVCAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKL RVPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASVS TVLT SKYR
3848	9345	A	4128	2	253	
3849	9346	B	4129	317	683	AHKLRVDPVNFKLLSHCLLVTLAA HLPAEFTPAVHASLDKFLASVMHR ADLQIPLSWSLATGCQK LIEVDDER KLRTFY*
3850	9347	A	4130	1	82	VDGWVDGWVDG*MDR*VGRWID

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GWVDG
3851	9348	A	4131	1	240	ASTFFFFSIDRVLLCCPGWTRTPGFI* SSCFGLPKCWDYRSEPPCLATFFFIK KKYKEEHFILLCQIVNMILLYQPT Q
3852	9349	A	4132	3	180	REPPLPAANFVFFVEMRSHHVRQA GPEPPSSDLPASASQSAGITGVHCH AWP*YTYL
3853	9350	A	4133	2	238	SPCAGILEDDRADYQGTRKTSEYSS VTP*EACHT*EGPIAFISWP*KVPIQL TFNERNRARGFQVPYGYDRGLPG TH
3854	9351	A	4134	7	259	IVTAALFTLAPNQK*SKYPSSGKLIN KFWYIYKME*TSISNKQVSTTYSMQ AWVNLKSITLS*RHKGVYII*SHLYD ILEKTEL
3855	9352	A	4135	141	309	AFDEAIAKLYSVNE*SYKGSTVIMQ LVRVNLAVSATSTGFIVSFVFTYPIIP CYLQ
3856	9353	A	4136	113	205	HNLLMLFDLCLLYWL*LIFLIHELAE NLLN
3857	9354	A	4137	3	215	FETGSCSVTQAGVHWRDHSSLQP*S LGFKQPSNLSLPSSWDYRCTPPHLA NLCIFCKDRVTSYCPGWHPV
3858	9355	A	4138	3	386	
3859	9356	A	4139	1	255	IRLMKEGRMKGQAFIGLPNEKAAA KALKEANGYVLF GKPMVVQFARSA RPKQDPKEG*KKKRTWLFNKVGK WELAPKPMGLDFSL
3860	9357	A	4140	78	153	
3861	9358	A	4141	1	293	LRLPGSSHSPASVS*VAGIAGACHH AWPNFCVFSRDQGFTHVGRAGLGA PDPLDPALPWSPKVMGFTRCEAHP CPSPRMRFLKYVSVPMVMVGRPE
3862	9359	A	4142	3	48	PLPRKSVEPGGGTKYKTEQKKRQE RRDRGSK*RKQKKAATSEEQQRK* AKTQEDGGTKRSPDGEEDPEKKIHR NREGTRKKGQDPRNGVNNKNREK EQN*RTHTS*SQKVRRTRRGNEV
3863	9360	A	4143	1	276	GTRDSV*GGLKLIPIFLMDFWKEPL GPALAHQLQYPGRD*SSDIWIRTA SLHTLPIVGPHLLGDLASFCTLLTPD PCQHVPFRSRADTVEMG
3864	9361	A	4144	1	154	LVWS*EASKIPGGAEEAHPPTTF
3865	9362	A	4145	2	231	FFFESGSRSVTQAGVQ*HSLGSLQPL PPRFK*FSCLSLPSSWDYTHVPTSPA NFCIFSGDGVSSCWPGWSRTPNLR
3866	9363	A	4146	1	303	GTRGSVKEGAKYTSHRDMGLSTFD RDADQWKENCANVYG*GCRYNNC QAANLNGIYYPGGSYDPRNNSAYE TDNGVWVVSFTGAHYSRAARMKI RPLVTQ
3867	9364	A	4147	3	372	HAGLGAHPLHHPVIOQEGFLPAPRG FGYRSEVD*IRIPAESTGQNSQCQLR K*KDDSYFHCYFCGCVCTCRGRL QSSTSHQCQAAL*LLPVCLTMLRC ISSLIYT*NLKTVHSVRLNFIYN

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3868	9365	A	4148	2	98	RRPFFFFFFFASCI*NLISPNVQLSNFT CILRN
3869	9366	A	4149	1	230	SGRPFLFFFQKERVYFIPVVVLFYT VVVQ*LRKNVVRWQKTMEPPRSW LMQLGHTEEGPGYPLLGETETKLFR TA
3870	9367	A	4150	1034	2354	DRVLAPVAQTGVQWHDLSLQPPP PGFKRFFCLSLPSSWDYRRPP*RPAN FC*FLVETGFRHVGQAGLGLTSGD PPASASQSSRITGVSHRARTMGLSR ALYRIPALKVWLLINVELKKQMMMA HVDVTCLINKSPSLTRPMGKRLSAE TGKGQKEKQKQTGAGCAVLPSRGF PPKAHHGRQPLTLAPSPPTFSPSP PHTHTHTHTCSPICPRQSRSFQGPR MPDPPGDATCGAGPGGSAPARAA GPRSAPRRAKARVQARVQARAQAR WVRALTLLAAHPRLQVPARIARR AAQSSSSPPPATPAKSPPEASGAAA PPALGLERFPGASPNHLTRSTCALR HVGAGGAALGGPGAPRLPHRLEV REEGRGRRGDGLGHGGCPEPAWEP GWRLPSTIKLFIKSKVSSEALEMPFL CICEHLLSYTYSRKHRNVI
3871	9368	A	4151	387	478	
3872	9369	A	4152	757	1477	HKENRNSLELRQNOSSPIWALPLHG LERKGLGRDHSSPHLPLLPSERL*K ASASQGPWECCPSRAAGPESGRCD QLWESPMASATWKPYRPQPSRSPQ RQRVVLPLVKGKTPPLFKLLQESV PGDLLPGELSL*PWEKPI*NNFAFNF SQQCKGMFKFPQFRSLARGSNPTSL TGVGPLPLPREFPGEEREGAPQIFKQ NTANGLGPSA*MRAGTAQGCWES* GGNTAPGPGAVNTAN
3873	9370	A	4153	32	255	SRRHDSLHRVTFCISDPHYRKWTNP DGTTSKIFGFVAKKPASPWENVCHL FAKLDPY*PAGAIVTFITNVPTAP
3874	9371	A	4154	1	265	CDTVLLCHPGWSAVAQSQLTTTSA SQIKRFSCNLNPSSQNTRRASHPAN FFYF**R*GFTMLVRLVSNSCPQVIH PPLPPKVLGLQA
3875	9372	A	4155	92	333	FLSFFFF*MGCHSVTQCGVKWHDLS SLQPPHLTFKWFSRLSLLSGWDYRC LAQHQAACCIFSRDGISPF*PCWYQT PDLR
3876	9373	A	4156	16	181	ICSLPSTVDVIEFLDYVVKVSLKL*SI IKICDSDKHTHIHTYGYVYIFSPGK PV
3877	9374	A	4157	1	355	TVSLSCSVAQAGVQWHNLGSLQPL PPGFK*FSCLSLPSSWDHRCPPCLA NFCIFL*RWGFARFCHVGEAGLELL TSSDLHTSDSQAIGTSHHAWPH LLVLTCVCAHTLFRHFYL
3878	9375	A	4158	1	194	FFFFFTISYIFYTLTTCWEFKQLAGN I/HL*GTVAFFYLKLLKLQDRLTNSF SSATTNVLAENS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3879	9376	A	4159	112	270	ILGNSLFKKNYK*YLSPPAAVTHACNP NTLGGQGGPVT*AQEFETSLGNIVR PCL
3880	9377	A	4160	1	211	RFSCLSLLSS*DYRRVPPRPAIFVFL VETRFHYVGQDGLDFLTSCSARLYL PKCRDYRRELLCPAPASLL
3881	9378	A	4161	2	253	ETDSCSVAQTRVQWYDLGSLQQPP PRFKRFSCLSLPNSWDYKCVPTPI* FFLFLVEMEFHCAGQADLELLGSGD PPASAPK
3882	9379	A	4162	198	276	KPFMAQCSF*IYEAFSCTSSEIRY
3883	9380	A	4163	3	193	HFGRPRRADCLRSSV*DQPGQHGET PSTKNTKISQAWWWVPVPTT*EA EAGESLEPGGQRLQ
3884	9381	A	4164	2	515	DTEKMSPWDMELIPNNAVFPEELG TRVPLTDGECKTLIYKPLDGEWGTN PRDEECERIVAGINQVMTLDIASTFV APVDLQAYPMYCTGVAYPTDLSSI KQRLNRFYRRVSSLMWEVRYIEH NTRTFNEP*KPNRPAKSGTDLLLH FIKDQTCYNIPLYNMCKKVL
3885	9382	A	4165	3	418	HEADKTNVVTGKTEVGAHAGEYG AQALERMFLSFPTTKTYFPHFDLSH GSAQVKGHGKKVADALTNVTRIK EMRNALCTLSDLIAHKLLGDSCITL *LLSHCMLVTLAN*PSSEFTPAHTL VAKILAFVSTELTSKY
3886	9383	A	4166	1	191	CLETECRYVSQAGMQWHYPG*LQP *PPGYKLSSHLSLPSSWDYRHVPEH PTNFVYFFVERKSH
3887	9384	A	4167	3160	3732	
3888	9385	A	4168	2	326	PRSGSESFSCQLSPFFFFGDRVSLC GPG*SAVV*LQLM*PGPPKLKQSSC LCLPSSWDHRWAAPHLA*FFKFFFI ETGSYHLPQLVSNPWAQASLLPWP PKVLGLQV
3889	9386	A	4169	2	163	LIFVFVIVGTGFHHVGQAGLECLTSS DPSASASQSAGITGVNHHTRPPSAF GC*T*GTGFHHVGQAGLECLTSSDP SASASQSAGITGVNHHTRPPSAFGC
3890	9387	A	4170	126	348	HISIFETGSYSVTQAGAQLDGHSL QP*PPGLK*SSCLSLPSSWDYRHMP CPANFYIFCRDGVSPRCSCGNF
3891	9388	A	4171	1659	1970	MLKGGAKIRSRRKTGVSHSLHSDL NFFFFWDKSIASHRLEYNGAISAH CNLRLLGSSDSPASAS*VARITGMR HHTQLILVFFSRNGVLPCWPGWSRT PDLR
3892	9389	A	4172	153	278	MRPDTVAHTCNPSTLGGQGGRIT*T HEFETSLGDMMKPYLYK
3893	9390	A	4173	3	254	LQYLVISSKAWPS*KLEDGET*SA GENNNYNTIL*LDLFSHREGKWSKI PYV*AFFALQNNRKLCCQCIIDLALI AVISSQT
3894	9391	A	4174	3	225	SLTHLTATSILLK*FSCLGLPSSWDH RCPPLRLANFFAFLVETDFTMLARL V*NS*PEVIRSPRPSKVLGLRA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3895	9392	A	4175	1	344	GGALSGGTPGFSPSPPGKTAAPGQS GNPPGGF*RVSPSGGSQRRGGFPNGT PAPGPLPSSSSSSKGGFGDCTPRDKS RKGGKPPFS*GGFFPQGSAPVKHLA APTNRYSFHPQK
3896	9393	A	4176	2	201	QPGQYQKHPVLIKNSKIKPFWGDP VVPNAREG*A*KMVEPGKVRVQSA QIKALEFNLGPKKKVPF
3897	9394	A	4177	39	225	KSIQSYAI*YNVTCGFFKSALNGVG SVAFCSHHAEHFLGFVFINHEKSFQ FCQMLLLCMTR
3898	9395	A	4178	322	451	INSTDWAPWLTLVISALWEAEAA/G SRGQEIETILANTVKPRLY
3899	9396	A	4179	234	383	
3900	9397	A	4180	86	216	KQTLGQAWWLTPPIPALWEAEVGR S*DQEIETILPNTVKPHRY
3901	9398	A	4181	1	4123	MEEVEEDRFKENLEGALAGQLLGD EATQALQVLAVELDVVVPALHPQ RLHRLGAALVERQPVREVDHLVLP AVDDEHGRDLGHLLDVREGVEA VGLLGVAEGDAHARGERRVQHHR GTLVARGQVHGGHRADALPVQDD AVRADAVPGGAGAGSAAASNARA PFPPAGVPGPSSGCDPPVSPLSQVSA HWELCGPHILNASYLPARVRKPFLV HWPQGRTFLPAALAHPLGHEEFR QLCPQMSPNFGLESERPVRCQCN PGQHRGWLRRWHPLPPAPSLGSG QVLGHLSTTSSHPGAPSPPGHWCAA PDPADPAPVTRPPRAQSQAARGTHLP PCPCRDPTLLPHALGSDPRQTPSC KAGAWAGRSPQLPPGCHHSNERDT SPVEALGTLWPPPHGSGPRFLQDKG AAGQMAEQTELRAHGHRMAKLRS HRASWASPPDLDAASPHLAPSAA SADGLPATRAQTPRPPTPSRQALP PGSPSPAQGLPGGVDVGIEVPLGR PARAGTVAGGVGEDVAEAGAQ ANVEAAHLAQVHGIAVREEDRVPG TRHAANIHAGDTVAAGALGGEDLD GVQLALAVLEVGTLRQGFVWTLR GTDVETYPFSAPRAASHGVGRHEEL PDPTGPCGGRLLSLTIHGVTRYHAL LWARGPIMSKSQVLGEWEPVQGGK SSENDKWTMSDPGAEAPTCSRAAS GVDKEQQGRWQGLWNSHIKPLKIR MVKQNNIIPGETQILLRFTGWESKV NAKKQLPVGIKCEPMDQENEQTGG HETDGHRIVSVLHFPLISILSYATW GLSLLCIPGSPVCTLLVRFSNVGTR WSLEVRGSPCGFGSNKVCVMTPEI KMVCVCEGKAGKAVGSGGVEGTK EVSTGNAEGPVRHEAVDGGVHLAF ALLQGLLWSLLLGPPLAGWGGGE LDAVPDSTSSATNVSMVVSAGPWS SEKAEMNILEINEKLRPQLAENKQQ FRNLKERCFLTQLAGFLANRQKKY KYEECKDLIKFMLRNERQFKEECLA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EQLKQAEELRQYKVLVHSQERELT QLREKLREGRDASRSLNEHLQALLT PDEPKSQGQDLQEQLAEGLDWH STLSKSSAQKMTKMRMKMFK/CEE DEKVLESSAPREVQKAEESKVPEDS LEECAITCSNSHGPCDSIQPHKNIKIT FEEDKVNSSLVVDRESSHDGCQ/EC SKHSPSPWPHLFCHKRQHGG/DQPA LCPARRQR*TF*KSMRNCA/HQLAE KKQQFRSLKEKCFVTQVACFLAKQ QNKYKYEECKDLIKSMLRNERQFK EEKLAEQLKQAEELRQYKVLVHSQ ERELTQLREKLREGRDASRSLNEHL QALLTPDEPKSQGQDLQEQLAEG CRLAQHLVQKLSPENDEDEDVQ VEEDEKVLESSAPREVQKAEESKVP EDSLEECAITCSNSHGPCDSIQPHKN IKITFEEDKVNSSLVVDRESSHDGC QDALNILPVPGPTSSATNVSMVSA GPLSSEKAEMNILEINEKLCPQLAEK KQQFRSLKEKCFVTQVACFLAKQQ NKYKYEECKDLIKSMLRNERQFKE EKLAEQLKQAEELRQYKVLVHSQE RELTLREKLREGRDASRSLNEHLQ ALLTPDEPKSQGQDLQEQLAEGC RLAQHLVQKLSP
3902	9399	B	4182	1	799	MLQIPKQQQNEKYQVPQFDQSTIKN IESAKGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDADDTSIYM FYQKVGDNIDSWSKNAGRVFKDSD KFDANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHYGKQSLTTAQI HFPLISILSYATWGLSLLCEIPGSPVC TLLVRFSNGGPPMDPGSERKGFCRF RNHHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHPGAQ YANRLSPRVGRFINAAGTTX*
3903	9400	A	4183	260	387	REVGRVRWLTPVIPARWEAEVGRS *GQEIKTILANTVKPRLY
3904	9401	A	4184	1212	1442	
3905	9402	A	4185	3844	4180	KYKKCVGCGGRSL*S*LLRRLRQEN RLSPGGGDCSEPRSSHCTPAWVTER /GDSVSKKKKKNLLTWLVNKLCP CRAWWLTVPVIALWEAEAGRSRGQ EITILANTVKPRLY
3906	9403	A	4186	8	385	
3907	9404	A	4187	2	284	
3908	9405	A	4188	1477	1697	
3909	9406	A	4189	17	385	
3910	9407	A	4190	1	837	GKVVLELERFLPQPFTGEIRGMCDF MNLSLADCLLVNLAYESSVFCTSI AQDSRGHIYHGRNLDYAFGNVLRK LTVDVQFLKNGQIAFTGTTFIGYVG LWTGQSPHKFTVSGDERDKGWWW ENAIAALFRRHIPVSWLIRATLSESE NFEAAVVKLAKSPLIADVNYIAGG TCPREGVVVTRNRDGPDIPLNPL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NGAWLRVETDYYHWKPAPKEDDR RTSANKALNATGQANLKLEALFQIL TVVPVYNNLTIYTTAMSAGSPYKY MTRIRNPS
3911	9408	A	4191	653	727	
3912	9409	A	4192	26	161	
3913	9410	A	4193	3	186	
3914	9411	A	4194	28	186	
3915	9412	A	4195	356	428	
3916	9413	C	4196	35	430	MKSCRXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXSETNSWEATRKNPFSSNSSEAFIS RSQGHKDAKKEFVPLXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXLQSHPLVR*
3917	9414	A	4197	213	394	
3918	9415	A	4198	28	123	
3919	9416	A	4199	1578	1835	SNKSLPHNCIPPQMRNYSRGNLLQY IDYVQLHRNLYAGEIYFHC*RKSL CNSSWREGAVGCLPMDFPRLHLSL SPSSLHCRNKP
3920	9417	A	4200	213	305	
3921	9418	A	4201	1715	1850	
3922	9419	A	4202	4016	4315	
3923	9420	A	4203	28	239	
3924	9421	A	4204	7	216	
3925	9422	A	4205	1	576	
3926	9423	A	4206	1	500	
3927	9424	A	4207	1	1266	
3928	9425	A	4208	1	162	
3929	9426	A	4209	1	229	
3930	9427	A	4210	197	416	
3931	9428	A	4211	1	131	
3932	9429	A	4212	76	274	
3933	9430	A	4213	295	2530	RPATMAARLPVSPARALLLALAG ALLAPCEARGVSLWNEGRADEVVS ASVRSGDLWIPVKSFDKNHPEVLN IRLQRESKELIINLERNEGLIASSFTE THYLQDGTDSLARNYTILGHY YHGHVIRGYSDSAVSLSTCSGLRGLI VFENESYVLEPMKSATNRYKLFFA KKLKSVRGSCGSHHNTNLAANKV FPPPSQTWARRHKRETLKATKYVE LVIVADNREFQRQGDLEKVKQRLI EIANHVDKFYRPLNIRIVLVGVEVW NDMDKCSVSQDPFTSLHEFLDWRK MKLLPRKSHDNAQLVSGVYFQGT IGMAPIMSMCTADQSGGIVMDHSD NPLGAAVTLAHELGHNFNMHDTL DRGCSCQMAVEKGGCINASTGYP FPMVFSSCSRKDLETSLEKGMGVCL FNLPEVRESFGGQKCGNRFVEEGEE CDCGEPEECMNRCCNATTCTLKPD AVCAHGLCCEDCQLKPAGTACRDS SNSCDLPEFCTGASPHCPANVYLHD GHSCQDVGDCYNGICQTHEQQCV TLWGPAGAPAGICFERVNSAGDPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GNCCKVSKSSFAKCEMRDAKCGKI QCQGGASRPVIGTNAVSIETNIPLQQ GGRILCRGTHVYLGDDMPDPGLVL AGTKCADGKICLNRCQCNISVFGV HECAMQCHGRGVCNNRKNCHCEA HWAPPFCDKFGFGGSTDSPGPIRQAG KEARQEAESNRERGQGEPLGSQ EHASTASLTLI
3934	9431	A	4217	2	119	
3935	9432	A	4218	2	147	
3936	9433	A	4219	10	216	
3937	9434	A	4220	245	455	
3938	9435	A	4221	1	2867	MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEESNQATGTSRWG VSKKAPRHLSVPCTRPREARQEAE DSTRLSAESGETDQDAGDVGPDI PDSYYGLLGTLPCEALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAAVVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTITLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRLYVTFNKSIAK QAERVFPNSVICKTFHSMAYGHIGR KYQSKKKLNLFKLTPFMVNSVLAE GKGGFIRAKLVCKTLENFFASADEE LTIDHVPWCKNSQGQRMVEQSE KLVGVLEASRLWDMRKLGECTEE AHQMTHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTLVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVKDKFIRRW VHKEGFSGFKRYVTAAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLPLPHFRVESFSE DEWNLLYAVTRAKRLIMTKSLE NILTLAGEYFLQAE LTSNVLKTGV VRCCVG\QCNNALSPVDTVLTMK KL\PIY*ATGK\ENKGGYLCHSCAE QQHRDPWRFLTASPEQVRAMEPHF GGTSYCPRHEALLFLVF
3939	9436	A	4222	57	302	
3940	9437	A	4223	1	550	DAHIIGRIESYSCKMAGDDKHMFK QFCQEGQPHVLEALSPQTSGLSPS RLSKSQGEEEGPLSDKSRKTLFY LIATL NESFRPDYDFSTARSHFSRE PSLKLVLGNVNC SLFSAVREDFKD LKPQLWNAVGRGDLPLKCDIYS\Y

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NPDLDSDPSREDGSLWSFNFFYNKRLKRNRL
3941	9438	A	4224	11	511	GRTRSIAGEETTQRP GPNC GGNC LC LHTLAINMRICYSQTTPFHPLRLKG QRWPFSSLELFPVGFPRALLVQS TLPKPRPERAFTAPSLFPVTLGFCLG RILCQRLLLCPSCLATALSINGYSRT QECQSWKGRDTGLHKGKLLLEALG GTEGFGDRARAKIEDS
3942	9439	A	4225	1	279	
3943	9440	A	4226	1011	1322	
3944	9441	A	4227	3	468	TPLHVVYNEVMSVGGQKYGIRNAGYY ALRSLRIEKKFAFWGQDINNLTPL ECGRESRVKLEKGMDFIGRDALLQ QKQNGVYKRLTMFILDDHDSDDL WPWWGEPIYRNGQYVGKTTSSAY SYSLEHVC LGFVHNFS EDTGEEQ VVTADFINRG
3945	9442	A	4228	1	1236	
3946	9443	B	4229	1	1742	MKRDNSGGCLPAPASAWPARPRQQ AEWRALTRGPANHCIISTLGEPPE TPLIGLRTFQCCRLVTDGRVLAGTV SSEPTDGFRSPAPGPGRRTSAMVLL KLGKTPGEFFPFLGSSSQPPSHELNI GKRLDDTKILPGNMKDNFWEMGD TGPCGPCSEIHYDRIGGRDA AHLVN QDDPNVLEIWNLVFIQYNRFGNCVE LQASAAFNWNNQRCKTRNRYICQF ADLRRNLNIINDDITGRVHKDRKLL TGDS PF AANALGKLAAQEMMAAY AVSLPKLTALLRVFSTVVR SIGERFS PIRVLRLLRHTTPNYIYQRLIPYVCV LPTTELSINLNMLTENDIPLFRALFL NNITDADARVLLQKRPREGWLTTD AFLYWAQQDFSGVKPLVAQHWEW MTFSADSVSSVHTLTDDLPLESLAD QPGAGNVHLLIPPEGLLYRSLTLPN AKYKLTAQTLQWLAEETLPDNTQD WHWTVVDKQNESVEDCLIPLFGKP QKGKCLEKSVWAAGRPF SYAGDK NRQLTRYSDTRWHEDSVNRWFSV MVGPSVRVNEWFSAYAMAGMAYS RVSTFSGDYLRVTDNKGS*
3947	9444	A	4230	1	638	
3948	9445	A	4231	1377	1746	
3949	9446	B	4232	1	1716	MSQYYQPORPPEHIELD SHAKFFPH HHLQVADSA AHLAASPLRRTHRAL TWAQALPQEEGSGAPSPGAPSPPT KSFGRTMSASAVFILDVKGMESC YVVQDVLNSWSPAIPLLQPPKVSDD SGGHIEECQCLPVYSFLYKTIEVGI LRILQGAGGGEHPDNFVIVYELLDE LMDFASRRPPTARSCRIHHS AEQQA GDGQVTGAPTVTNAVSWRSEGIKS MQRQRPSENRNRYHQAQVFLSGMP ELRLGLNDRVSSSLAAKGQFKKSQ WPTVWRYLCLYPAMRLPQIQDQCG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QRQVCAGRNVVIWSIKSFPGGKEYL MRAHFGLPRWKRKRWRAGPPSGSS LDPLLHRLWDPGPMKIIKSGYQA LPWVRTSPRVAIPTSYQLEGRDGG LNTGFLTAPDADFRGRAGEEPAGR AGVSGWGAGTESSAAGCTAAAPRE GCSASARLLRADSAAGLGRAGGFA GRQCRHAAGGGCAGDRLSGAAAR GDVQECAAFCCTGWCIPSTLRQD GAAGFIVPPQSPFEGHDVWQHRHR PELLKQGASPNVQDTSQTVQSMTQ PALDSWTP*
3950	9447	A	4233	1	372	
3951	9448	B	4234	48	1158	MSASAVFILDVKGKPLISRNKGDV AMSKIEHFMPLLVQREEGALAPLL SHGQVHFLWIKHSNLYLVATTSKN ANASLVYSFLYKTIEVFCEYFKELE EESIRDNVVIVYELLDELMDFGFPQ TTDSKILQEYITQQSNKLETGKSRVP PTVTNAVSWRSEGIKYKKNEVFIDV IESVNLLVNANGSVLLSEIVGTIKLK VFLSGMPELRLGLNDRVLFELTGRS KNKSVELEDVKFHQCVRLSRFDND RTISFIPDGFELMSYRLSTHVKPLI WIESVIEKFSSHRSVEIMVKAKGQFK KQSVANGVEISVPVPSDADSPRFT SVGQRQVCAGEKRRYFGVLSLSGG AREYLMRAHFGLPKCEKERX*
3952	9449	B	4235	153	458	KKDLSLEEIQKKLEAAEERRKSHEA EVLKQLAEKREHEKEVLQKAIEEN NNFSKMAEEKLTHKMEANKENRE AQMAAKLERLREKDKHIEEVRKTK NPRPC*
3953	9450	A	4236	3	182	
3954	9451	A	4237	49	607	NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASGQAFELILS PRAKEFVPEFPLSPPKEEGFFPGGKF REN*EAAVEERRQSP*SCSS*RQLAE KLRAPRKKCFQKAIEENNFFQ*NGQ KRKLTPHKMEANKETPERPQMAIA KLEPFAEEKDKAH*KKCGKNKESK DPADETEAGLI
3955	9452	A	4238	1	356	TELQQEQLQTVVGTYHGSPDQSHQ VTGNHQPPQONTGFPR/SNQPYYN SRGVSRRGSRGARGLMNGYRGPAN GFRGGYDGYRPSFSNTPNSGYTQSQ FSAPRDYSGYQRDGYQQNFIP
3956	9453	A	4239	1	2206	RLPPAFSSLSLRSEDALGHQPQRERS KSSGPPPPSGSSGSEAAAGAGAAAP ASQHPATGTGAVQTEAMKQILGVI DKKLRNLEKKKGKLDYQERMNK GERLNQDQLDAVSKYQEVNNEF AKELQRSFMALSQDIQKTIKKTARR EQLMREEAEQKRLKTVLELQYVLD KLGDDDEVRTDLKQGLNGVPILSEEE LSLLDEFYKLVDPERDMSLRLEQY EHASIHLDLLEGKEKPVCCTTYK VLKEIVERVFQSNYFDSTHNNHQNGL

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						CEEEEADSAPAVEDQVPEAEPEPAE EYTEQSEVESTHEYVNRQFMAETQFT SGEKEQVDEWTVETVEVVNSLQQQ PQAASPSVPEPHSLTPVAQADPLVR RQRVQDLMAQMGGPDNFIQDSML DFENQTLDPAlVSAQPMNPTQNMD MPQLVCPVHSESRLAQPNQVPVQP EATQVPLVSSTSEGYTASQPLYQPS HATEQRPQKEPIDQIQATISLNTDQT TASSSLPAASQPQVFQAGTSKPLHS SGINVNAAPFQSMQTVFNMNAPVP PVNEPE\TLKQ\Q\NQSQ\A\SYNQSFSS \QPSPS*QQTELQ\Q\EQ\QT\VG\TY HGS\QDQSHQ\VTGNHQQ\PPQ\QNT GIST*AIRPYNSRGVSRGGSRGAR GLMNGYRGPIANGFR\GGYDGLPAP SFLCLKLPNSGY\SHSPQFQCLPRDYL WPIQRDG\YIQQNFKRGSGQSGPRG APRGRG\GPPRPNRGMPQMNTQQV K
3957	9454	A	4240	1	151	
3958	9455	A	4241	5	120	
3959	9456	A	4242	1	315	EQMVSEdVPC/D/HRVHARIIGSR/G KAIRKIMDEFKVDIRFPQSGAPDPN CVTVTGLPENVEEAIDHILNLEEEYL ADVVDSEALQVYMKPPAHEEAWP CPLRTCSTV
3960	9457	A	4243	107	4057	PFCCGFPGLCVGVRSTMSSVAVLQTQ ESFAEHRSGLVPPQIKVATLNSEES DPPTYKDAFPPLPEKAACLES AQEP AGAWGNKIRPIKASVITQVFHVPLE ERKYKDMNQFGEQEQA KICLEIMQ RTGAHLELSLAKDQGLSIMVSGKL DAVMKARKDIVARLQTQASATVAI PKEHHRFVIGKNGEKLQDLELKTAT KIQIPRPDDPSNQIKITGTKEGIEKAR HEVLLISAEQDKRAVERLEVEKAFH PFIAGPYNRLVGEIMQETGTRINIPPP SVNRTIVFTGEKEQLAQAVARIKK IYEEKKKKTTTIAVEVKKSQHKYVI GPKGNSLQEILERTGVSVEIPSDSIS ETVILRGEPEKLGQALTEVYAKANS FTVSSVAAPSWLHRFIIGKKGQNLA KITQQMPKVHIEFTGEDKITLEGPT EDVNVAQEQIEGMVKDLINRMDYV EINIDHKFHRHLIGKSGANINRIKDQ YKVSVRIPDSEKSNLIRIEGDPQGV QQAKRELLELASRMENERTKDLIIE QRFHRTIIGQKGERIREIRDKFPEVII NFPDPAQKSDIVQLRGPKNEVEKCT KYMQKMVADLVENSYSISVPIFKQF HKNIIGKGGANIKKIREESNTKIDLP AENSNSETIIITGKRANCEAARSRLS IQKDLANIAEVEVSIPAKLHNSLIGT KGRLIRSIMEECGGVHIHFPVEGSGS DTVVIRGPSSDVEKAKKQLHLAE KQTKSFTVDIRAKPEYHKFLIGKGG GKIRKVRDSTGARVIFPAEDKDQD

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LITIIGKEDAVREAQKELEALIQLND NVVEDSMLVDPKHHRHFVIRRGQV LREIAEEYGGVMVSFPRSGTQSDKV TLKGAKDCVEAAKKRIQEIIEDEA QVTLECAIPQKFHRSVMGPKGSRIQ QITRDFSVOIKFPDREENAVHSTEPV VQENGDEAGEGREAKDCDPGSPRR CDIIISGRKEKCEAAKEALEALVPV TIEVEVPFDLHRYVIGQKSGIRKM MDEFEVNIHVPAPELQSDIIAITGLA ANLDRAKAGLLERVKELQAEQEDR ALRSFKLSV\TVDPKLHSPGLSGRK GASNSQI\RGLKHDVNIQFPDKD\D ANQHQD\QITFTGYEKNHSSLPGDAI LRIVG\ELE\QMVSE\DVPLNHRVSR PASFGARGKSHPPKIMYEF\K\DIRF PNKSGAPKTPNCVNC*RGFPIENVE ESHSTQHPSILEEE\YLADVVDSEA LQ\VYMEPP/AHTEEAKGNFSRG\FD VRDAPL\TA\SSSEKAS\DMSSSEEFP SFWG*RWLPKTLP\WGPKTIMIKKE QNPLPAC
3961	9458	A	4244	11	323	
3962	9459	A	4245	3	171	
3963	9460	B	4246	148	405	XKLSVERKDPLAALAREYGGSKRN ALLKWCQKKTQGYAKRNLLAFE AAESVGKPSLELSEMLYTDRPDWQ SVMQYVAQIYKYFET*
3964	9461	A	4247	2	438	AVGGNGGCPRPSRVTSQSTCRFGPR TASHSASRAGLCTASR*VPGWV*CL HFQPLQMPTRDSSFSPDYSAPGRGC GQAGRCGAEHRRPGHRSSCC*NW* CQCShNLVSSSGTISVEHCAWNHRI PGPRLPEGLFFPH*VCFVISM
3965	9462	A	4248	3	256	
3966	9463	A	4249	3	444	
3967	9464	A	4250	3	828	VKGVPGVKAERFIE*RMTAKHCALS LVGEPIMYPEINRFLKLLHQCKISSF LVTNAQFP AEIRNLEPVTQLYVRVD ASTKDSLKKIDRPLFKDFWQRFIDS VKALAVKQRTVYRLTLVKA\WNV \ESLQAYAQLGSLGNPDFIEVKGV YCRESSASSLTMAHVPWHEEVVQF VRELVDLIPEYIACEHEHSNCLLIA HRKFKIGGEWWTWDYNRQELIQ EYEDSGGSKTFSKDY MARTPHWA LFGASERGFDPKDTRHQRKNKSKAI SGC
3968	9465	A	4251	1	384	
3969	9466	A	4252	3	1225	
3970	9467	A	4253	1	864	
3971	9468	A	4254	1	1266	GNSPPSELKWKAKSEDLRHRGLKA QAEIKGSTQQIGFTTDPMARSSPYP TDVARVVNAPIFHVNSDDPEAVMY VCKVAAEWRSTFHKDVVDLV CY RRNGHNEMDEPMFTQPLMYKQIRK QKPVLQKYAELLVSQGVVNQPEYE

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						CVSMHGVRNKPSYNSTKSSMDGLI LHPATGLVFVLSKQCEEIHQPVVWT CEQREAENATAEENRVLLAMVNPT VFFDIAVDGAEPLGRVSFEVGRAAA CGNGAQKVGRGRENFRCEPLERK GFGL*GVPCFHRLFPRVLCVQGGL QQRHNGNWWASPIWGRKFERLK NFHP*KPYGSPGILSPWQNA GPQTQ MVPQFFICTAQDCSGWNGQAMWV FGTSERKAMNIVEAHWSRFGISR\N GKTQQRSPFADCGQLLISLTCVFIF NHPDHSL
3972	9469	A	4255	3	275	
3973	9470	A	4256	125	315	
3974	9471	A	4257	3	292	
3975	9472	A	4259	1	3045	MDKFLNTYTLPRLKQEEVESLNRPI TGSDIEAINSLPTKKKSRTRWIHSRI LPEVQGGAEKEGILPNSFYEASIIIP KPASDTTKKENFRPISLMNINAKILN KILAKQIRQHIKKLIHHDQVGFIPGM HGLFNICKSVNIQHINRTNDKNHMI ISIDAEKPFDKIQHFMLKTLNKL QNLKLIGNFSKVSQYKINVQKSQA FLYTNNRQTESQIMNEFPFTIASKRI KYLGIQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCS\WEKTTLKFI W\NQKRAHIAKSIIISQKNKAGGITLP DFKLYCKATVTKTAWYWYQNRDI DQWNRTESEIMPHIYNHLIFDKPD KKKKWKGKDSLFNKWCWENWLAIC RKLKLDPFLTPDTKINSRRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYA AKKHKMKK CSSSLVIREIQIKTTMRYHLTPVRMA IIKKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKS VWRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVILLHVFWDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLPCSSAC RRPIVGLQLVMINSNGNFQVIAMEGT VASECCHGNGKLTWHRPVLSVCSF SRCTVQAAGGSAILEDGDPLLAPL GSTPQAAVCRGPRGRELRAAPADS HLFQRDLWPFNKVIVHGEKGSNQT SQGLLNTGSEMTIVLENPKYHSGPP VRVSPDGGQVIEVLADPSYTGPTA LNNVFFAFQCNFYFDHIPENC GFSD PSDPQNLQKGEGCPSLVRASTAPPQ EKATEQPLLCKTTESPFGMTVGPCT DETLDHGAPSKHVPGTAHNELALL DLRVIKSAGSA AVHHKLKVLHWS SLSNNKGTGRLYEQVA
3976	9473	A	4260	1	2526	
3977	9474	A	4261	1	3111	

MISSING AT THE TIME OF PUBLICATION

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						VDTIAADESFSQVDFGGRLMKDYG ACMSLLSVRVFFKKCPISVQNFAVF PETMTGAESTSLVIARGTCIPNAEEV DVPIKLYCNGDGEWMVPIGRCTCK PGYEPENSVACKGPVNNTEKAKSG EMWFSPEEYGWEYA AFLALRKCSQ CPEDAVAASGA VALENLMEHGHIR LDKASKDSESSTPHDPTLLFHSGPQP NFRHFQGWNTVTSEGLIHLPKSKT QSQCPLFGGSLDSRIDIGGAWYFC HTHTASSASTPSEEAGSLADPSNETE SLLFACTALCSPWECQLILDASLFQ GIMLMPRAVQFFKCWDKVTVRNQ WRMHSHGPSCLGVSFQKGLCQEM VYISTRGSSSGLRPLVLSLHGWA VD TAIHTCIPFPTDIIWIQDLIAGLKDEW FDTHPGRRIGRPAQLCSSRSGVH
3980	9477	A	4264	1	2653	MGD FNTPLSTLDRSMRQKV N KDIQ ELNSALHQADLIDIYRN LHPESTEY T FFSAPHHTYSKIDHILGSKAPLSKYR RSEIKINCLSDHSAIKLELRIKLTQ NRSTTWKLNNLLNDYVWHNEMK AEIKMFFETNENKDTTYQNLWDTL KAVCRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQT HSKASRRQEIS KIRGELKEIETQKT LQKINESRGWFF EKINKIDRLARLIKKKREKNQIHAI KNDKGDMSTNHT EIQT TIREYYKHL YANKLENLKEIDKFLETYS LPRLNQ EEVESLNR PITGSEIAI NSLPNKR S PGPDGFTAKFYQRYKEELLISNFSK VSGYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMKYLGIQPTRD MKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKNWKKT TLKFIWNQKRARI AKSILSQKNKAG GIMLPDFKLYKATITKTAWYWYQ NRDIDQWNRTEPSEIMPHIYNHLIFD KPDKNKKWKGDSL FNKWCWENW LAICRKLKLD PFLT PYTKINSRWIKD LNVRPKTIKTLEENPGNTIQDIGMG EDFMSKTPEAMATKAKIDKWDLIK LKSFCTAKETTIRLNRPPTEWEKIFA IYSSDKGLISRIYNELQQIYEKKTNN PIKKWAKDMNRHLSKEDIYAAKRH MKKCASSLAIREIQIKTTMRYHLTP VRMAIHKSGNNRCWRGCGEIGTLL HCWWDCCLVQPLWKS VWRFLRDL ELEIPFDPAIPLLGIYPKDYKSCCYE DTCTHMFIVALFTIAKTWNQPKCPT MIDWIKKMWHIYTMEYYADIKKDE FMSFVRTRMKLETIILSKISQEKKT KHRMFSLIGGN
3981	9478	A	4265	1	2988	
3982	9479	A	4266	1	2515	MGD FNTPLSTLDRSTRQKV N KDTQ ELNSAPHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKTDHILGSKALLSEC KRTEIITNYLSDDSAIKLELRIKNLT

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						QNRSTTWKLNLLDDYWVHNEM KAEIKMFFETNENKDTTYQNLWDA FKAVCRGKFVALNAHKRKQGRSKI DTLTSQLEKEKQEQTHSKASRRQE ITKIRAELEKEIETQKTVQKINESRSW FFERINKIDRQLARLIKKKREKNLID AIKNDKGDITTDPTIEIQTIREYYKH LYANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPIGSEIVAIINSLTTK KSPGPDGFTAIFYQRAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLENPIV SAQKLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLLKEI KEDTNKWKNI PCSWVGRINIVKMAI LPKVIYRFNAIPIKLPMTFFTELKKT TLNFIWNQK\RAHIAKS/VLSQKNKA GGITLPDFKLYYKATVTKTAWYWY QNRD TDQWNRTEPSEIMPRIYNYLI FDKPEKNKQWGKDSL FNKWCWKN WLAICRKLKLDPFLTPYTKINSRWI KDLNIRPKTIKLEENLGITIQDIGM GKDFMSKTPKAMATKAKIDKWDLI KLKSFACTAKETTNRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMRYH LTLVRMAIHKSGNNRCWRGRGEIG TLLHCWWDCCLVQSLWKS VWQFL RDLELEIPFDPAPILL
3983	9480	B	4267	1	2634	MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQGDLIDIYRTLHPKSTEYI FFSAPHHTYSKIDHILGSKALLSKCK RTEIITNDLSDHSAIKLELRKLNLTQ NCATTQKLNNLLNDYWVHNEMK AEIKMFFETNENKDTTYQNLWDAF KAVCRGKFIALHAHKRKQERSKIDT LTSQLEKEKQEQTHSKASRRQEIT KIRAELEKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQIDAI KNDKGDITTDPTIEIRTTVREYYKHL YANKLENLEEMDTFLDTYTLPRLN QEEVESLNRPIGAEIVAIINSLPTKK SPGPDGFTAIFYQFRKGLRQNSTT FMPKTLNKLIGDGYLKIRAIYDKP TANIILNGQKLEAFPLKTGTRQGW LSPLLFNIVLEVLAIRAIRQEKEIKGIQ LGKEEVKLSLFADDMIVYLENPIVS AQNLLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIASKR IKYLGQLTRDVKDLFKENYKPLLK KIKEDTNKWKNI PCSWVGRINIVKM AILPKVIYRFHAIPKLPMTFFTELEK TTLKFIWNQKRACIAKSILNQKNKA GGITLPDFKLYYKAI VTKTAWYWY QNRDIDQWIRTEPSEITLHIYKYLIF DKPEKNKQWGKDSL FNK WY WEN WLAICRKLKLDPFLTPYTKINSRWI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KDLNIRPKTIKLEENLGFTIQDIGM GKNFMSKTPKAMATEAKIDKWDLI KLKSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPLKKWAKDMNRHFSKEDIYAA KKHMKKCSPLAIREMQIKTTMRY HLTPVRMTIISQETTGAAGEDVEK*
3984	9481	A	4268	1	2429	
3985	9482	A	4269	1	2745	
3986	9483	A	4270	1	3210	MVKGSIQQEELTILNIYAPNTGALRF IKQVLRDLQRDLDSHTIIMGDFHTP LSTLDRSTRQKVNKDIQELNSALHQ EDLIDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEITNC LSDHSAIKLELRIKNTQNRSTTWK LNNLLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDTFKA VCRGKF IALNAHKRKQERSKIDTLTSQKEL EKQEQTTHSKASRRQEITKIRAEKEI ETQKTLQNINESRSWFFERINKIDRP LARLIKKKREKNQIDAIKNDKGDI TDPTEIQTIREYKHYANKLENL EEMDKFLNTYTLPTLNQEEVESLNR PITGAEIVAINSLPTKKSPGPDGFTA EFYQRYKEELVPFLPKPFQSIEKEGI LPNSFYEASIIIPKPGRDTTKKENFR PISLMNIDAKILNKILAKRIQQHIKN LIHHDQVGFIQGMQGWFNIRKSINVI QHINRAKDKNHMIIISDAEKAFDKI QQPFMLKTLNKLDDMIVYLENPIVS AQNLLKLISNFSKVSGYKINIQKSQA FLYTNNRQTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENHKPLL EIKEDTNKWKNIPCSWVGRINIVKM AILPKVIYR/FNAIPIKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSERTPHIYNYL IFDKREKNKQWGKDSL FNKWCWE NWLAI CRKLKLD PFLTPYTKINSRW IKDLNVRPKTIKLEENLGFTIQDIG MGKDFISKTPKAMATKAKIDKWDLI IKLKS FCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSPLAIREMQIKTTMRYH LTPVRMAIIKSGNNRCWRGCGEIG TLLHCWWDCCLVQPLWKAVWRFL RDLELEIPFDPAIPLGIYPKDYKSC CYKDTCTRRKQLDCAEPVEPRKVG DGEWSLTKWTRPGSRALPWPPEQA KPYPPTLPTLAQDF
3987	9484	A	4271	3	3655	
3988	9485	A	4272	1	3615	
3989	9486	A	4273	1	4038	
3990	9487	A	4274	1	3317	MGDFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLQPKSTEY TFFSAPHHTYSKIDHIVGSKALLSKCK

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						RTEIITNYLSDHSAIKLELRIKNLTQS RSTTWKLNLLNDYWVHNEMKA EIKMFFETNENKDDTTYQNLWDAFK AVCRGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQEITKI RAELKEIETQKTLQKINESRSWFFER INKIDRPLARLIKKKREKNQIDTIKN DKGDITTDPTIEIQTIREYYKHLA NKLENLDEMDFLHTYTLPRLNQE EVESLNGPITGAEIVAIIDSLPTKKSP GPDGFTAIFYQRYKEELVPFLKLKLF QSIEKEGILPNSFYEASIIPLKLRDGT TKKENFRPLSLMNIDAKILNKILAK RIQQHIKKLIHHDQVGFIPGMQGW NIRKSINVIQHINRGKDKNHMISID AEKAFDKIQPFMLKTLNKLIGDGT YFKIIRAIYDKPTANIILNGQKLEAFP LKTGTRQGCPLSPLLFNIVLEVLR AIRQEKEIKAQNLLKLISNFRKVS KINVQKSQAFLYTNNRQTESQIMRE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNI PCSWI GRNIVKMAILPKVIYRFNAIPIKLPT TFFTELEKTILKFIWNQKRAHIAKTI LSQKNKAGGIMLPDFKLYYKATVT KTA WY WYQKRDIDQWNRIELSEIIP HIYNHLIFDKPDKNKKWGKDSVFN KRCWENWLAICRKLKLDFTLTPYT KINSRWIKDLHVRPKAIKTEENLGI TIQDIGMGKDFTSKTPKAMATKAKI DKWDLIKLKSFTAKETTIRVNRQP TKWEKIFAIYSSDKGLISRIYKELKQ IYKKKTNNPIKKWAKDMNRHFSKE DIYAANRHMKKCSSSLAIREMQIKT TMRYHLTPVRKAIKKSGNNRCWR GCGEIGTLLHCWWDCKLVQPLWK TVWQFLRDLELEIPFYPAIPLGIYP KDYKSCCYKDTCTRMFIAALFTIAK TWNQPKCPTMIDWIKKMWHIYTM EYYAAIKNDEFMSFVGTWMKLEIII LSKLSQEQKTKHGIFSLIGGN
3991	9488	A	4275	959	2955	
3992	9489	A	4276	1	2870	MKA EIKMFFDTS ENKDDTTYWNLW DAFKAVCRGKFIALNAHKRKQERS KIDTLTSQLELEKQEQTHSKASRR QEITKIRAELEIETQKTLQKINESRS WFFERINKIDRPLARLIKKKREKNQI DAIKNDKGDITTDPTIEIQTIREYYK HLYANKLENLEEMDFLDTYTLPR LNQEEVESLNRPI TGSEIVAIINSLPT KKSPGPDGFTAIFYQSWAETQPKK ENFRPISLMNIDAKILNKILAKRIQQ HIKKLIHHDQVGFIPGMQGWFNIRK SINVTQHINRAKDKNHMISIDA EKA FDKIQPFMLKTLNKLIGDGT YFKII RAIYDNPTANIILNGQKLEAFPLKTG TRQGCPLSPLLFNIVLEVLR AIRQE KEIKGIQLGKEEVKLSL FADNMIVY

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						LENPIVSAQNLLKLISNFSKVSQYKI NVQKSQAFLYTNNRQTESQIMSOLP FTIASKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSGÆG RINIVKMAILPKNWKKTTLLKFIWNQ KRARIAKSILSQKNKAGGITLPDFKL YYKATATKTAWYWYQNRDLQW NRTEPSEITPHIYNYLIFDKPDKNKQ WGKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNIRPKTI KLEENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKQESFCTAK ETTIRVNRQPTKWEKIFATYSSDKG LISRIYSELKQIYKKKTNNPIKKWAK DMNRHFSKEDIYAAKKHMKKCPSS LAIREMQIKTTMRYHLTPVRMAIHK KSGNNRCWRGCGEIGTLLHCWWD CKLVQPLWKS VWRFLRDLELEIPFD PAIPLLGHPKDYKSCCYNDCTRM FIAALFTIAKTWNQPKCPTIIDWIKK MWHIYTM EYAAIKNDEFVSFVGT WMKLEIILSKLSQEQTTHRIFSLIG GN
3993	9490	A	4277	1	2982	
3994	9491	A	4278	1614	4577	TEPKTKTT*LSQ*MQKKPLTKFSNPS C*KLSIN/IVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTTAS KRIKYLGIQLTRDVKDLFKENYKQL LKEIKEDTSKWKNI PCSWVGRINIV KMAILPKVIYRFNAIPIKLMPFFTE LEKTTLLKFIWNQKRACIAKSILSQ NKAGGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPHIYN YLIFDKPEKNKQWGKDSL FNKWC WENWLAICRKLKLDPFLTPYTKINS RWIKDLNVRPKTIKLEENLGIIQDI GMGKDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPRKW EKIFATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKEDIY AAKKHMKKCSPLAIREMQIKTTM RYHLTPVRMAIHKKSGNNRCWRGC GEIGTLLHCWWDCKLVQPLWNSV WRFLRDLELEIPFDPAIPLLG IYPND YKSCCYKDTCTRM TITSVEEKSQSE KLSYIFLKEKICLMYVGLLNILVSL GKVPFWLYLGSRLATPPTSSQLFFIG GKERSPDEQGV DILIVLIFRYPSTDS AEQIKKKIEKALYQSLKTKQLSLTIN KPSFRLTRCGIRMTSSNMPLPASSST QRIVQGRETAMEGEWPWQASQLI GSGHQCGASLISNTWLLTAAHCFW KNKDPTQWIATFGATITPPAVKRN RKIILHENYHRETNENDIALVQLSTG VEFSNIVQRVCLPDSSIKLPKTSVF VTGFGSIVDDGPIQNTLRQARVETIS

MISSING AT THE TIME OF PUBLICATION

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						LPCLMIPSQMMLLENFSAAPGHRCW THMLDNGSAVSTNMTPKALLTISIP PGPNQGP HQCRRFRQPQWQLDPN ATATSWSEADTEPCVDGWVYDRSV FTSTIVAKWDLVCSSQGLKPLSQSIF MSGILVGSFIWGLLSYRFRGKPMLS WCCLQLAVAGTSTIFAPTFVIYCGL RFVAAF GMAGIFLSSLTLMVEWTTT SRRAVTMTVVGCFAFSAGQAALGGL AFALRDWRTLQLAASVPPFAISLIS WWLPESARWLIKGKPDQALQELR KVARINGHKEAKNLTITPPPPPIPI PSPTAPPLSTPTITTAITPSPAPPPIPS LTPQPPSLQNISTTFTTIVTIGNSTIIN STHTVTSITHHLHLHVARTHLMGVL DVSGETECVYLKVLMSVKEEVAS AKEPRSVLDLFCVPVLRWRSCAML VVKYAVLGRDLTSSLARSFLLISY YGLVFDLQSLGRDIFLLQALFGAVD FLGRATTALLSFLGRRTIQAGSQA MAGLAILANMLVPQDLQTLRVVFA VLGKGCFGISLTCLTIYKAELFPTPV RMTADGILHTVGR LGAMMGPLILM SRQALPLLPLYGVISIASSLVVLF LPETVQGLPLPDTIQDLESQKSTAAQ GNRQEAVTVESTSL
4009	9506	A	4293	3672	3967	LQPPPHGRRGLLHHLSPGHGPHHP VTPQTRSPAQP/PGQMGP RAPLGCC LPPPPRPPTCRREK*TTETRFSPCWR TRPWGPGPPRPLSRGGPLPCAPA
4010	9507	A	4294	1773	2213	AHWLHLRLPHHRAQWAAALQPG PAGWGWSWQPQLCSAGRLCHGAI GRP/LSIFCWTWDLGASSCGHPAAR SMMASGVTWTSRGMGEKRVSSTPF PIFFPAASPPPPSRLPNCPFCHRTLAE RAQHLASVRPGLHLSSPTCCMKCSC
4011	9508	A	4295	1	616	
4012	9509	A	4296	93	502	EERKRPHLGAWWENRKCFFSFQPD FKAAECRETVARPSLSIPQDCLSVSL ADTNQCLLEVRLARGVCRRAHLS PPVCIQSPLSQGH*LLCSK*SASIIGA GLANFQGTDSLVAEHPVSWIHNNSN FVFHPGYFRL
4013	9510	A	4297	1537	2360	TCCTNVVWGAPPHRDSRVSDRVHS QKSRRACYGQRNKRPGG*G*ILISA KKQLSPRR*LKVWPMRSASLQSM PLASPSVCPGGLLFLWP*QALLPS DCG/PLSLTRLSR*GGPPRPHWCSR FRWLCARVLL
4014	9511	A	4298	1	493	MEAPAELLAALPALATALALLLAW LLVRRGAAASPEPARAPPEPAPPAE ATGAPAPSRCAPEPAASPAGPEEP GEPAGLGELGEPAGPEPEPGDP AAPAEAE/PGGGGEAGTHRGRGP LPTPGAPAAA VPRRARERGRGLQ PRLPPGSAEPAARRKCR
4015	9512	A	4299	2	418	
4016	9513	A	4300	8808	9100	RKVLFFFFFEMKSRSVARLGCSGTI

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						SAHCNLCPLPGSSDSPASASRVAGMT GAHNHIQLIFVFLVGMGFHHVGGQA GLELLT*VIHPPQSPKVLGLQV
4017	9514	A	4301	3	101	
4018	9515	C	4302	5673	5894	MWQLTPAILALGEIEAGGLFEPRRV KLAWPAQEELVSTKNTKISWVWW RAPVVPATQEA EVGGSLELERSRLQ *
4019	9516	A	4303	1	241	
4020	9517	A	4304	58	180	
4021	9518	A	4305	2	325	FFFFFFFFFETESLSVTQAGEPGHD LGSLEPPPPRFKQFSCSLPSSWIYR HVPPCPANFFFFLVETGFHHVGGQAG LKLLTSNDPPASASQSSGIRGVSHLT RLVS
4022	9519	A	4306	206	386	
4023	9520	A	4307	2	260	
4024	9521	A	4308	5	227	
4025	9522	A	4309	676	1076	FLLCFPPCLSPKFFLFLLGKIYSQSN WCVIVNWRIELGWMFNKICDSKIIF SLGSFLCKIKAHWGLWKSPTTSFQE RSPFFSSLFRAMRAKPSRSM/RLFF ELLVKSLPVASPV EPLSVIAEQSSQI CPCHGI
4026	9523	A	4310	3	205	
4027	9524	A	4311	3	345	
4028	9525	A	4312	118	7473	
4029	9526	A	4313	1	297	
4030	9527	A	4314	366	504	
4031	9528	A	4315	1	2899	MDAPKAGYAFEYLIETLNDSSHKKF FDVSKLGTKYDVL PYSIRVLEAAV RNCDFGLMKKEDVMNILDWKTQKQ SNVEVPFFPARVLLQDFTGIPAMVD FAAMREAVKTLGGDPEKVHPACPT DLTVDHSLQIDFSKCAIQNAPNPGG GDLQKAGKLSPLKVQPKKLPCRQ TTCRGSCDSGELGRNSGTFSSQIENT PILCPFHLQPVPEPETVLKNQEV EFG RNRERLQFFKWSSRVLKNVAVIPPG TGMAHQINLEYLSRVVFEEKDLLFP DSVVGTD SHITMVNGLGILGWGVG GIETEA VMLGLPVSLTLPEVVGCEL TGSSNPFVTSIDVVLGITKHLRQVG VAGKFVEFFGSGVSQLSIVDRITIA NMCPEYGAILSFFPVDNVT LKHEH TGFSKAKLESMETYLKAVKLFRND QNSSGEPEYSQVIQINLNSIVPSVSG PKRPQDRVAVTDMKSD FQACLNEK VGFKGFQIAAEKQKDIVSIHYEGSE YKLSHGSVVIAA VISCTNNCPYSVM LAAGLLAKKAVEAGLRVKPYIRTS SPGSGMVTHYLS SSGVLPYLSKLGF EIVGYGCSTCVGNTAPLSDAVLNA VKQGD LVTCGNFIWKKNFEGRLC DCVRANYLASPLV VAYAIAGTVNI DFQTEPLGTDPTGKN IYLDIHWPSR EEVHRVEEHVILSMFKALKDKIEM

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GNKRWNSLEAPDSVLFPPWDLKSTY IRCPSFFDKLTKEPIALQAIENAHVL LYLGDSVTTDHISPAGSIARNSAAA KYLTNRGLTPREFNSYGARRGND VMTRGTFANIKLFNKFIGKPAPKTIH FPSGQTLDVFEAAELYQKEGIPLIL AGKKYSGNSRDWAAKGPYLLGV KAVLAESYEKIHKDHILIGIGIAPLQF LPGENADSLGLSGRETFSLTFPPELS PG\ITLNIQTSTGKVFSVIA SFEDDV\ EITL\YKHG\GLLNFV\ARKFS
4032	9529	A	4316	1	178	
4033	9530	A	4317	165	403	PSSRSRAPSPPTLCGASCCPTCPAC FPAPSRRAGAAGGAG*RPRGGPTST TCYGPTETWLYQLQTVGSRNTTTRT PKST
4034	9531	A	4318	3	404	
4035	9532	A	4319	3	217	
4036	9533	A	4320	3	423	SFFIHRTKGKGPLMSSSFKKLYFSLT TEALSFAKTPS/CQGQGC DKTRSRV TLQEWNDPLDHDLEAQLIYRHLLG VEAMLWERHRELSGGAEAGTMPTS PGKVPEDSLARLLRVLQDLREAHSS SPAGSPSEPNCLELQ
4037	9534	A	4321	2	3040	DPGVWLPPSRDPAMAKRSSLYIRIV EGKNLPAKDITGSSDPYCIVKVDNE PIIRTATVWKTLCPFWGEEYQVHLP PTFHAVAFYVMDEDALSRDDVIGK VCLTRDTIASHPKGFGSGWAHLTEVD PDEEVQGEIHLRLEVWPGARACRL RCSVLEARDLAPKDRNGTSDPFVR VRYKGRTRETSIVKKSCYPRWNETF EFELQEGAMEALCVEAWDWDLV RNDFLGKVVIDVQRLRVVQEEGW FRLQPDQSKSRRHDEGNLGS LQLEV RLRDET VLPSSYYQPLVHLLCHEVK LGMQGGQQLIPLIEETTSTECRQDV ATNLLKLFLGQGLAKDFLDLLFQLE LSRTSETNTLFRSNSLASKSMESFLK VAGMQYLHGVLGPIINKVFEEKKY VELDPSKVEVKDVGCSGLHRPQTE AEVLEQSAQTLRAHLGALLSALSRS VRACPAVVRATFRQLFRRVRERFPG AQHENVPIAVTSFLCLRFFSPAIMS PKLFHLRERHADARTSRTLLLLAKA VQNVGNMDTPASRAKEAWMEPLQ PTVRQGVAQLKDFITKLVDIEEKDE LDLQRTL SL*APPVKEGPLFIHRTKG KGPLMSSSFKKLYFSLTTEALSFAK MPSSKKSALIKLANIRAAEKVEEKS FGSHVMQVIYTDDAGRPQTAYLQ C/KGV PFCVRVQSHWEK**YQGHQI YLAGSGIPTSVAKGPAAAEIQPTPAS WAPTIPVPSVGTSGAAATKKTRQC VNELNQWLSALRKVSINNTGLLGS YHPGVFRGDKWSCCHQKEKTD TDF RSVPQTGVQWRDLGSLQSPPPRVK QFSCNLPSWDDRHSPPSLANFFV

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						F*LEMGFHHVSQAALVLLLLLLLLL FDTESRSIIQAGVQWCNLGSLQSPFP RLG*FSCLSLPSTTGASHCTQLSQGC DKTRSRVTLQEWNDPLDHDLEAQL IYRHLLGVEAMLWERHRELSGGTE AGTVPTSPGKVPEDSLARLLRVLQD LREAHSSSPAGSPSEPNCLELQT
4038	9535	A	4322	308	658	
4039	9536	A	4323	1	2662	MAKRSSLYIRIVEGKNLPAKDITGSS DPYCIVKVDNEPIRYRPHQDRGA LSLSSARALPAKGTATVWKTLCF WGEEYQVHLPPTFHAVAFYVMDE DALSRDDVIGKVCLTRDTIASHPKG FSGWAHLTEVDPDEEVQGEIHLRLE VWPGARACRLRCSVLEARDLAPKD RNGTSDPFVRVRYKGRTRETSIVKK SCYPRWNETFEFELQEGAMEALCV EAWDWDLVSRNDFLGKVVIVDQR LRVVQQUEGWFRLOPDQSKSRRHD EGNLGSLQLEVRLRDETVPSSYYQ PLVHLLCHEVKLGMOGPGQLIPLIE ETTSTECRQDVATNLLKFLGQGLA KDFLDLLFQLELSRTSETNTLFRSNS LASKSMESFLKFALHVYLAPSWAD TAGKRCKGGCREKVGWSWGTGGD RINVTCCGGPQVAGMQYLHGVLGPII NKVFEEKKYVELDPSKVEVKDVC SGLHRPQTEAEVLEQSAQTLRAHLG ALLSALSRSVRACPAVVRATFRQLF RRVRERFPGAQHENVPIA VTSFLC LRFFSPAIMSPKLFHLRERHADARTS RTL LLLAKAVQNVGNMDTPASRAK EAWMEPLQPTVRQGV AQLKDFITK LVDIEEKDELDLQRTL SLQAPPVKE GPLFIHRTKGKGPLMSSSFKKLYFSL TTEALSFAKTPSSKKSALIKLANIRA AEKVEEKSFGGSHVMQVIYTDAG RPQTAYLQCKCVNELNQWLSALRK VSINNTGLLGSYHPGVFRGDKWSC CHQI*INTGQG\CDKTRVTG*PCREW NDLLDRDLESQLIYRHLLGVEAML WERHRELSGGAEAGTVPTKPLAKV PEDSLARLAPGCLQDLREAHSSSPA GSPSEPNLASLEAADVRPALRSPC
4040	9537	A	4324	69	194	
4041	9538	A	4325	1350	2203	TWRLDPQIISSPKPQPGGTYTLEV KSSKSKKVLSPHP*WPPLRLWQRIG GSPEGGTQAPDGLPPPPRPKSERV GSPKLSGGKR/EGSHPGGPPHITHP/ DGEKAKSSWFGLEAKDPTQKPS PHPVKPLSAAPVEGSPDRKQSRSSL SIALSSGLEKLKTVTSGSIQPVTPAP QAGQMVDTKRLKDSAVLDQSAKY YHLTHDELISLLLQRERELQSQRDEH VQELESYIDRLLVRIMETSPTLLQIPP GPPK
4042	9539	A	4326	2	761	
4043	9540	A	4327	2	410	

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4044	9541	A	4328	295	780	
4045	9542	A	4329	1	2203	
4046	9543	A	4330	1	190	RFIMLVRLVFNS*PQ/CDPPASASQS AGITGMSHRARPELSVLTQGFNRW AFRLLLQCHSPDF
4047	9544	A	4331	2	269	
4048	9545	A	4332	3	223	DFEPSLQHCSSKLCRNILRASSCHSS WGRM*FPGSV*PTWKI*REESCEWS RTAINPKYKILLHGFVVRTVWR
4049	9546	A	4333	2	366	PCSEPPTRRSGATPSHPGGCGAKL CRNILRASSCHSSWGRM*FPGSV*P TWKI*REESCEWSCCTAINPSTRSCCT VCGTNCLEETPTTCPSTRGLQCGRG LTRATGNCPRNDGLTLLSLN
4050	9547	A	4334	3	131	
4051	9548	A	4335	923	1442	GGPCLCRPSWPAVLQVRSGLPSTIPS PWPLFCLPQSILLGPLEMPG*RPLLQ RPFYRMSLRTCQRRVRCWTWSVRC RTAWHTRVFLKLPDFTTNDSTTG *AKPSALLSTGWS*WATA/CGGGA AALLATMLRAAYPAGQVLRLLPSP PAPGAKLCRNILRASSCHSSWGRM
4052	9549	A	4336	1	137	
4053	9550	A	4337	876	1012	
4054	9551	A	4338	148	278	
4055	9552	B	4339	7	673	MVEVTILMIMGLYRIYGFVAVVS MILSYNVCSEGEVVSVMFSFVVTSS SCGMHRSTLLSSVYSHLIFDSAYVIN NVADALSRGFSMHCMHCDNLKTC HTSHGSVMAETA VINHKRKNSPRI VQSNDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHVAKY AEIFGLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPWFIKX *
4056	9553	A	4340	786	1088	
4057	9554	A	4342	1	66	
4058	9555	A	4343	2	80	
4059	9556	A	4344	8	258	
4060	9557	A	4345	5	383	
4061	9558	A	4346	99	634	TTMSSKRTKTKTKKRPQRATSN VFAMFDQSQIQEFKEAFNMIDQNR DGFIDKEDLHDMLASLGK\NPTDAY LDAMMNEAPGPINFTMFLTMFGEK LNGTDPEDVIRNAFACFDEEA\GTI QEDYLRE\LLTTMGDRFTDEE\DEL YREAPY*QKGGISNYIEFTRILTGRP PKHKDD
4062	9559	A	4347	1	966	
4063	9560	A	4348	3	215	
4064	9561	A	4349	1	1416	NSGGSGGGTSGSGSSSGQGKMGQS QSGGHGPGGGKKDDEDKKKKYEP VPTRVGKKKKKTKGPDAASKLPLV TPHTQCRLLKLLKLERIKDYLLMEEE FIRNQEOMKPLEEKQEEERSKVDDL RGTPMSVGTLEEIINDNHAIVSTSVG SEHYVSILSFVDKDLLEPGCSVLLN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HKVHAVIGVLMDDTDPLVTVMKV EKAPQETYADIGGLDNQIQEIKESV ELPLTHPEYYEEMGIKPPKGVHPFG PTWPRVKTLAKAVANQTSVASFLR VVGYYELIQKYLGDGPKLVRELFRV A\EEHAPSIVFIDEIDAIGTKRY\DSN SGGE\REFHRTNVGN*LEPVGMGFD SRG\DV\KVFPWATNR\IETLADPALI RPGRI\DR\KNEFFLPDEKTKKRIFQI HTSRMTLADDVTLDDLIHGLKIDLS GA\DI\KAIC\TEAGL\MGL*GERRMK VTNEDFKKSKENVLYKKQEGTPEG LYL
4065	9562	A	4350	2	70	
4066	9563	A	4351	1	1605	
4067	9564	A	4352	3	193	
4068	9565	A	4353	3	127	LFHPCQDSQQHH*CVCCRLTGHGA A*VHGPCQAVQTYRASH
4069	9566	A	4354	2	323	
4070	9567	A	4355	3	85	
4071	9568	A	4356	49	413	
4072	9569	A	4357	3	338	
4073	9570	A	4358	1	3735	
4074	9571	A	4359	2	317	
4075	9572	B	4360	2576	2685	MDGKNSSGSKRYNRKRELSYPKNE SFNNQSRSSSQKSKTFNMPPQRG GGSSKLFSSSFNGGRRDEVAEAQRA EFSPAQFSGPKKINLNHLLNFTFEPR GQTGHFEGSGHGSWGKRKNWGHK PFNKELFLQANCQFVVSSEDQDYTA HFADPDTLVNWDVFVEQVRICSEV PSPICLYPPTAAKITRCGHIFCWAC ILHYLSLSEKTWSKCPICYSSVHKK DLKSVVATESHQYVVGDTITMQLM KREKGV LVALPKSKWMNVDPHPIHL GDEQHSQYSKLLLASKEQVLHRVV LEEKVALEQQLAEEKHTPESCFIEA AIQELKTREEALSGLAGSRREVTGV VAALEQLVLMAPLAKESVFQPRKG VLEYLSAFDEETTEVCSLDTPSRPLA LPLVEEEEA VSEPEPEGLPEACDDLE LADDNLKEGTICTESSQEPITKSGF TRLSSSPCYFYQAEDGQHMFLHP VNVRC LVREYGS LERSPEKISATVV EIAGYSMSEDVRQRHRYLSHLPLTC EFSICELALQPPVVSKE TLEMFSDDI EKRRQRQKKAREERRRERRIEIEE NKKQGGKCEVHIPLNLQQFPAFKF LYLLLFEKPRKETGKNVAMKAENR CRRRPPPALNAMS LGPRRARSAPTA VAAEAPVDAAELPQRRRHRLRHGQ EQRLQQLLR LFGQQQRATAAPLRL GGASRRV*
4076	9573	A	4361	3	93	
4077	9574	A	4362	1	289	VGNPQQEVQNIFKAKHPMDTEVTK AKIIGFGSALLEEVDPNPANFVGAGI IHTKTTQIGCLVRLEPNLQAQMYRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						T/LRTSKEAVSQRLCELLSAQF
4078	9575	A	4363	1	275	
4079	9576	A	4364	2	2803	RGLAVFISDIRNCKSKEAEIKRINKE LANIRSKFKGDKALDGYSKKKYVC KLLFIFLLGHDIDFGHMEAVNLLSS NRYTEKQIGYLFISVLVNSNSELIRLI NNAIKNDLASRNPTFMGLALHCIAS VGSREMAEAFAGEIPKVLVAGDTM DSVKQSAALCLRLYRTSPDLVPM GDWTSRVVHLLNDQHLGVVTAAT SLITTLAQKNPEEFKTSVSLAVSRLS RIVTSASTDLQDYTYFVPAPWLSV KLLRLLQCYPPPDPAVRGRLTECLE TILNKAQEPPKSKKVQHSNAKNAV LFEAISLIHHDSEPNNLVRACNQLG QFLQHRETNLRYLALESMTLASSE FSHEAVKTHIETVINALKTERDVS RQRAVDLLYAMCDRSNAPQIVAEM LSYLETADYSIREEIVLKVAILAEKY AVDYTWYVDLILNLIRIAGDYVSEE VWYRVIQIVINRDDVQGYAAKTVF EALQAPACHENLVKVGYYILGEFG NLIAGDPRSSPLIQFHLLHSKFHLC VPTRALLLSTYIKFVNLFPVKPTIQ DVLRSDSLRLNADVELQQRAVEYL RLSTVASTDILATVLEEMPPPERES SILAKLKKKKGPSTVTDLEDTKRDR SVDVNGGPEPAPASTSAVSTPSPSA DLLGLGAAPPAPAGPPSSGGSGLL VDVFSDSASVVAPLAPGSEDNFARF VCKNNGVLFENQLLQIGLKSEFRQN LGRMFIFYGNKTSTQFLNFTPTLICS DDLQPNLNLQTKPVDPTVEGGAQV QQVVNIECVSDFTEAPVLNIQVHGS GGTFQNVSLQLPITLNKFFQPTNEK FCQDFQRWKQTSNPQQEVHNIFK AKHPMDTEFTKAKIIGVFGSELLAE VDPNPANFVGAGNIHTKTTQIGCP LRL*PNLQAQMYRLTLRTSKEAVS\ QRLCELLSAQF
4080	9577	A	4365	2	231	
4081	9578	A	4366	1	224	
4082	9579	A	4373	131	381	
4083	9580	A	4374	93	449	
4084	9581	A	4375	11	594	
4085	9582	A	4376	1	1410	
4086	9583	A	4377	1	66	
4087	9584	A	4378	1	553	RRGPLSQNGSFGPSPVSGGECSPPLT VEPPVRPLSATLNRDMPRSEFGSV DGPLPHPRWSAEASGKPSPPDPSG TATMMNS\SS*GSSPTRVLDEGMQT VLQEPEVPSVPSITSLAERPVAVNM APKGPPFPFPGVPLMSTPMGGPVPPPI RYGPPQQLCGPFGPRALPPFPGPM RPPLCLRE
4088	9585	A	4379	1	3589	AFLSKVEEDDYPSEELLEDENAINA KRSKEKNPGNQGRQFDVNLQVPDR

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						AVLGTIHPDPEIEESKQETSMILDSE KTSETAAKGVNTGGREPNTMVEKE RPLADKKAQRPFERSDFSDSIKIQT ELGEVFNKDSYDLKNDNPEEHLK TSGLAGEPGELSKEHDHGNTKYM GTESQGSAAAEPEDDSFHWTPHTSV EPGHSDKREDLLISSFFKEQQLQR FQKYFNVHELEALLQEMSSKLKSA QQESLPYNMEKVLDKVFRASESQIL SIAEKMLDTRVAENRDLGMNENNI FEEAAVLDDIQDLIYFVRYKHSTAE ETATLVMAPPLEEGLGGAMEEMQP LHEDNFSREKTAELNVQVPEEPHLL DQRVIGDTHASEVSQKPNTKDLDP GPVTTEPTMDAIDANKQPETAEE PASVTPLENAILLIYSFMFYLTSLV ATLPDDVQPGPDFYGLPWKPVFITA FLGASFAIFLWRTVLVVKDRVYQV TEQQISEKLKTIMKENTELVQKLSN YEQKIKESKKHVQETRKQNMILSDE AIKYKDKIKTLEKNQEILDDTAKNL RVMLESEREQNVKNQDLISENKKSI EKLKDVISMNASEFSEVQIALNEAK LSEKVKSECHRVQEENARLKKKK EQLQOEIEDWSKLHAESEIQKSFE KSQKDLEVALTHKDDNINALTNCIT QLNLLCESESESGQNKGGNDSDEL ANGEVGGDRNEKMKNQIKQMMDV SRTQTAISVVEEDLKLQLKLRSV STKCNLEDQVKKLEDDRNSLQAAK AGLEDECKTLRQKVEILNELYQQKE MALQKKLSQEYERQEREHRLSAA DEKAVSAAEEVKTYKRRIEMEDE LQKTERSFKNQIATHEKKAHENWL KARAAERAIAEEKREAANLRHKLL ELTQKMAMLQEEPVIVKPMGKPN TQNPPRRGPLSQNGSFGPSPVSGGE CSPPLTVEPPVRPLSATLNRRDMPR SEFGSDGPLPHPRWSAEASGKPS SDPGSGTATMMNSSSRGSSPTRVL DEGK\VNMGPK\GAPSPKEFPLMS TPMGGPV\PPPIRYGPPQLCGPFGP RHLPPFGPGMRPPLGLREFAPGVP PGRDLPLHPRGFLPGHAPFRPLGS LGPREYFIPGTRLPPPTHGPEYPPP PAVRDLLPSGSRDEPPASQSTSQD CSQALKQSP
4089	9586	A	4380	3	148	
4090	9587	A	4381	1885	2826	CLQEAIMDGTEIAVSPRSLHSELMC PICLDMLKNTIGSA*ASVPLTDHSG L PFSYPRNKECPTCRKKLVSKRSLRP DPNFDALISKIYPSREEYEAHQDRV LIRLSRLDRGGTLGGGTGPPSPPGA PSPPEPGDPYLQSSSEALWL*ACPP SHSRYVKTGNATVDHLSKYLALRI ALERRQQQEAGEPGGPGGGASDTG GPDGCGGEGGGAGGGDGPEEPALP SLFHLLQLSSLFSPLSLLPPPQTLNGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LTLELVNSPRRPLPRQGLTLRALSLP GSPQHPPGKLLTGGCALGFSTPATLH TGKQPYVCAT
4091	9588	A	4382	2	456	DRGGTLGGGTGPPSPPGAPSPPEP GGDPYLQSSSEALWL*ACPPSHSR VKTTGNATVDHLSKYLALRIALERR QQQEAGEPGGGGGASDTGGPDGC GGEGGGAGGGDGPEEPALPSLFHLL QLSSLFSPLSLLPPPQTLNGSLTLEL V
4092	9589	A	4383	58	1262	CLQEAIMDGTEIAVSPRSLHSELMC PICLDMKNTMTTKECLHRFCSDCI VTALRSGNKECPTCRKKLVSKRSLR PDPNFDALISKIYPSREEYEAHQDRV LIRLSRLHNQALSSSIEGLRMQA MHRAQVRRRPIPGSDQTTMSGGE GEPGEGEGDGEDVSSDSAPDSAPGP APKRPRGGGAGGSSVGTGGGGTGG VGGGAGSEDSGDRGGTLGGGTGPG PSPPGAPSPPEPGGEIELVFRPHLLV EKGEYCQTRYVKTTGNATVDHLSK YLALRIALERRQQQEAGEPGGGGG GASINTEELNVC GGEGGGAGGGDG\ PKEPALPSLEGVSEKQYTIYIAPGG GAFTTLNGSLTLELVNEKFWKVS RPLELCYAPHPRIQSDPHPGDKPEE RGPLG
4093	9590	A	4384	3	221	
4094	9591	A	4386	2	271	
4095	9592	A	4387	54	990	HSIMMKIPWGSIPVLMLLLLGLIDI SQAQLSCTGPPAIPGIPGTPGPDG QPGTPGIKGEKGLPGLAGDHGEFGE KGDPWIPGNPGKVGPKGPMGPKGG PGAPGAPGPKG\DSGDYKATQKIAF SATRTINVP/LLRRSQTNFRPRCITN MNTN\YE\PRSGKFTLQGCPLY*FN LSTPSSRG\NLCVN\LMRGRERAQE/ VWVTFCDYCLTN\TFPGSPQGGNGP QLKKAPKGGGGGEKKTVLPAGPPN KNFTYWGMGGCPTAIFSGFLAFFQI WEGLTCGLASHPTAPPAQQRSLYP QQQPYDQAKCTQ
4096	9593	A	4388	3	493	
4097	9594	B	4389	272	2158	MGPLMVLFCLLFLYPGLADSAPSCP QNVNISGGTFTLSHGWAQSLTYS CPQGLYPSPASRLCKSSGQWQTPGA TRSLSKAVCKPVRCPAPVSFENGII TPRLGSYPVGGNVSFECEDGFILRG SPVRQCRPNMWDGETAVCDNGA GHCPNPGISLGAVRTGFRFGHGDKV RYRCSSNLVLTGSSERECQNGNVW SGTEPICRQPYSYDFPEDVAPALGTS FSHMLGATNPTQKTESLGRKIQIQ RSGHLNLYLLDCSQSVSENDFLIF KESASLMVDRIFSFEINVSAIITFAS EPKVLMSVLNDNSRDMTEVISSLEN ANYKDHENGTGTNTYAALNSVYL MMNNQMRLLGMETMAWQEIRHAI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ILLTDGKSNMGGSPKTAVDHIREIL NINQKRNDYLDIYAIGVGKLDVDW RELNELGSKKDGERHAFILQDTKAL HQVFEHMLDVSKLTDITICGVGNMS ANASDQERTPWVHTIKPKSQETCR GALISDQWVLTAAHCFRDGNDHSL WRVNVGDPKSQWGKEFLIEKAAIS PGFDVFAKKNQGILEFYGDDIALLK LAQVKMSTHARPICLPCTMEANL ALRRPQGSTCRDHENELLNKQSVL CTFWSPLNKSKPKI*
4098	9595	A	4390	2	201	
4099	9596	A	4391	1	130	
4100	9597	A	4392	2	215	
4101	9598	A	4393	3	300	
4102	9599	A	4394	3	310	
4103	9600	A	4395	2	228	
4104	9601	A	4396	2	448	PRVRKDAVRDGLRAVKNAIDGCV V/PGAGAVEVAMAEALNKYKLSVK GKAQLGVQAFADALLVIPKVLAQN SGFDLQETLVKI*AEHSESGQLVGV DLNTGEPVVAEEAGI\WDNDCVKK QLLHSCVTIATNILLVDEIMRAGMS SLKG
4105	9602	A	4397	2	100	
4106	9603	A	4398	3	174	
4107	9604	A	4399	1	147	
4108	9605	A	4400	1	104	
4109	9606	A	4401	153	480	TTLKQQFSFMSYKAVKLKVFLIMSC YPRNPSHFP*CGA/WVMCPLRVGSE RRLCPFMATS\QSLSNKFHNRKIFMS REIKFRNLLKKNETQLMYLQIFRW YTKQRLFLF
4110	9607	A	4402	1	186	
4111	9608	A	4403	3	478	
4112	9609	B	4404	56	390	XAAYVQPFLDKSGLEKYLYPASAA APFLLYPGIPAAAAFFCLSSVLSP PPEKAGAAAATLLPHEVAPLGAPHP QHPHGRTHLPFAGPREPGNPRESSAQ EDPSQPGKEAP*
4113	9610	A	4405	2	485	
4114	9611	A	4406	105	183	
4115	9612	A	4407	1	1560	MLRKKEKANYRLLAERTRKRPRKA SAELQRKHYPMLRGHLRLFLPGRL RPLPSNPRLAFPAAERGGGHCGRMR HFPVSTQERGADPVHPASPLPPNQ APNAGHSPPTPRSPNTSSPRRRRRR PESGWGRPGGGFTSILRPDSPLPTRV QYGTERKRRGQSSRDAPSARRQSV GGANWEGGGAKRARRGTGPAG WRAEGGGAACRGSARASPAFRGRG PLPPFASGRVPGRQCGLRQWLQEK LLGPSDHLSCFQMPGTSVCDCAACL RACTEKPDCSNMWDSQAPWTGLK TRLTYRIFTINDLRQDWWRDYFEK YGKIETIEVMEDRQSGKKRGFAFVT FDDHDTVDKIVGRGGGSGNFMGRG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GNFGGGGGNFGRGGNFGGRGGYG GGGGGSRGSYGGGDGGYNGFGGD GGNYGGGPGYSSRGGYGGGGPGY GNQGGGYGG/G/GGGYDGYNEGNN FGGGNYGGGGNYNDF\GNYSG\QQ QS\NYGPMKGGSLGG\RSSGSPYGG GYGSG\G\GSGGYGSRRF
4116	9613	A	4408	2	370	
4117	9614	A	4409	1	159	
4118	9615	A	4410	3	261	
4119	9616	A	4411	1	8748	
4120	9617	A	4412	1	2176	
4121	9618	A	4413	37	441	
4122	9619	A	4414	1	1940	PVLRHAVWLKSEKSSFGLCAPLR KGSFLQKSWIFFRPVMAKDLTRIAI VNHDKCKPKKCRQECKKSCPVR MGKLCIEVTPQSKIAWISLTCIGCG ICIKKCPFGALSIVNLPSNLEKETH RYCANAFKLHRLPIPRPGEVLGLVG TNGIGKSAALKILAGKQKPNLGKY DDPPDWQEILTYFRGSELQNYFTKI LEDDLKAIKPQYVDQIPKAAKGTV GSILDRKDETKTQAIVCQQLDLTHL KERNVEDLSGGELQRFACAVVCIQ KADIFMFDEPSSYLDVKQRLKAAITI RSLINPDRIIVVEHDLVDYLSDFI CCLYGVPSAYGVVTMPFSVREGINI FLDGYVPTENLRFDRASLVFKAET ANEEEVKKMCMYKYPGMKKKMG EFELAIVAGEFTDSEIMVMMLGENG MGKTTFIRMLAGRLEPDEEGEVPVL NVSYKLQKISPKSTGSRVQLLREKIR DAYTHPQFVTNVMKPLQIENIIDQE VQTLSSGGELQRVTLAL*LGQNLDP VYL\DEPPA\YLDSEQRMAARVV KRFIPHAKKTA\FVVGTVTFIMATY LAADRVIVFD\GVPSTKNTVANSPQT LLAGMNKFLSQLEITFRDPNNYRP RINKLNSIKDVEQKSGN\YFFLDD
4123	9620	A	4415	1	122	
4124	9621	A	4416	2	1382	
4125	9622	A	4417	135	282	
4126	9623	A	4418	2	1652	
4127	9624	A	4419	3	279	
4128	9625	A	4420	8	353	
4129	9626	A	4421	1	1542	
4130	9627	A	4422	1	496	
4131	9628	A	4423	70	365	
4132	9629	A	4424	1	3771	
4133	9630	A	4425	2	285	
4134	9631	A	4426	1	724	
4135	9632	A	4427	58	197	
4136	9633	A	4428	640	813	
4137	9634	A	4429	3	268	
4138	9635	A	4430	1	1512	
4139	9636	A	4431	3	1625	
4140	9637	A	4432	1	330	GKTITLEVEPSDTIENVKAKIQDKEG

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						IPPDQQLIFAGKQLEDGRTLSDYNI QKESTLHLVLRRLRGGIKYNCDKMI CRKCYARLHPRAVNCRKKKCGHT NNLRPKKKVK
4141	9638	A	4433	2	544	DPRLQFFFFLSSLLQRGDRAGWW RRFFGTQTCRVFVKLT\TGKNLHPL RYETQ*HPLKNVQKPKISRTKEGIP\ PDQAAS**FAGK\QLE\DGRTLSDY\ NIQKESTRAPWLLRL\GGIIEPFSP GLPKKYN\CDKMI\CRKCYAR/LFHP RCLSTCRK\KKCGSHQTTLRPQRRR SNKGGFFP
4142	9639	A	4434	385	499	
4143	9640	A	4435	2	127	
4144	9641	A	4436	3	424	
4145	9642	A	4437	1	110	
4146	9643	A	4438	1	110	
4147	9644	A	4439	1	110	
4148	9645	A	4440	1	110	
4149	9646	A	4441	1	108	
4150	9647	A	4442	3429	7466	
4151	9648	A	4443	4048	4181	
4152	9649	A	4444	682	829	
4153	9650	A	4445	163	320	EFEGFNPLKLGEAGWARWLTVPVIPA L*ETEAGGSRGQEIETILANTVKPHL Y
4154	9651	A	4446	1122	1446	
4155	9652	B	4447	124	27844	XRSTVPPRISAYERPVWPGEWNDP RGPGRRASAVVSPREGNWGVLRDP RLQARKPRMVRSRQMCNTNMSVP TDGAVTTSQIPASEQETLVRPKPLLL KLLKSVGAQKDTYTMKEVLFYLGQ YIMTKRLYDEKQQHIVYCSNDLLG DLFGVPSFSVKEHRKIYTMIRNLV VVNQQESSDSGTSVSENCHLEGGS DQKDLVQELQEEKPSSSHLVSRPST SSRRRAISETEENSDELSGERQKRKH KSDSISLSFDESLALCVIREICCERSS SSESTGTSPNPDLDAGVSEHSGDWL DQDSVSDQFSVEFEVESLDSSEYSL SEEGQELSDDEDEVYQVTVYQAGE SDTDSFEEDPEISLADYWKCTSCNE MNPPLPSHCNRCWALRENWLPEDK GKDKGEISEKAKLENSTQAEFGDV PDCKKTIVNDSRESCVEENDDKITQ ASQSQESSEDYSQPSTSSSIYSSQEDV KEFEREETQDKEESVESSLPLNAIEP CVICQGRPKNGCIVHGKTGHLMAC FTCAKKLKKRNKPCPVLTGHIRTEQ PIIILPKKHKKKKERKSLPEEDVAVS SNVDFDTLTKKKVYLNKLNKERSV FKGFQGMGQHWTFINLDKPSNPS SHEVVAWIRRLRVEKTGHSQTLDP KVTGCLIVCIERATRLVKSQSAGK EYVGIVRLHNAIEGGTQLSRALET TGALFQRPPLIAAVKRQLRVRTIYES KMIEYDPERRLGIFWVSCEADTYSR

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						TLCVHLGLLLGVGGMQELRRVRS GVMSEKDHMTMHDVLDQWLY DNHKDESYLRRVVYPLEKLLTSHK RLVMKDSAVNAICYGAKIMLPGLVI RYEDGIEVNQEIVVITTKGEAICMV EHDKEFFHPRYHHREFRFDLSKIPE GEAVTAAEFRIYKDYIRERFDNETF RISVYQGIGSLPARQPYLWASEEGW LVFDITATSNHWVVPNRHNLGLQL SVETLDGQTINPKLAGLGRHGPQN KQPFMVAFFKATEVHFRSIRSTGSK QRSQNRSKTPKNQEALGWPTMCTD ELSFGLDVLTLQSLFEKRTAAGTRG RPCKKHELYVSFRDLGWQDWIAPAE GYARYYCEGECAFLNSYMNATNH AIVQTLVHFINPETVVPKPCCAPTQLN AISVLYFDDSSNVILKKYRNMVVRA CGCH*
4156	9653	A	4448	2	129	
4157	9654	B	4449	1	462	MSQQYYVRLCQIQSPSPRSVGRENL VLVGDFPDPTTELKRVKGRGCAHCG LTDLPEPTAQVLVEQQQDEALWFH NVISEEFGVGVNIFWKHLPSECYDK TDTYGNKDPTAASRAAQILDRALK TLAELPEEYRDFYARRMVLHIQDK AYSKNSE*
4158	9655	A	4450	3	366	
4159	9656	A	4451	1	167	
4160	9657	A	4452	2	382	TMVLSPADKTNVKA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKL RVD PVNFKLLSHCLLV LAAHLPAEFTPAVHASLDFLASVS TVLTSKYR
4161	9658	A	4453	2	252	
4162	9659	B	4454	31	449	MVLSPADKTNVKA/WGKTYFPHF DLSPGSAQVKGHGKKVADALTNA VAHVDDNAQRAVRPKRPCTRTSFG WTRSNFKLLSHCLLVTLAAHLPAEF NPCGARLPQGVPFGCYAPC*
4163	9660	A	4455	2	81	
4164	9661	A	4456	2	81	
4165	9662	A	4457	3	452	
4166	9663	A	4458	1	493	RPRIRHEHRLRENPPWFLFPAAKTN VKAGLG*G*GSHPPSNVAKTLERIM FLSFPTTKTYFPQLRTL SHGFISQV* GPRSRRLPDALTKRPWRHVDDHAQ TRCPALSDLVAHKL RVD PVNFKLL SHCLLVTLAAHLPAEFTPAVHAYL DKFLASVSTVLTSKYR
4167	9664	B	4459	208	420	MGNPKVKAHGKKVLTSLGDAIKHL DDLKGTFAQLSELHCDKLHVDPEN FKLLGNVLVTS LAIHFGIEFTPE*
4168	9665	A	4460	40	534	SRRHGSVSHREAKATIASLWGKVN VEDAGGETMIRLALVYPWPQRSF ASF\SSLFSASAIMGNPKVKA\HGKK VLTSLGDAIKHLDDLKGTFAQLSEL

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						HCDKLHVDPENFKLLGNVLVTVLA IHF\GKEFTPEVQASWQKM\VTGV ANA\LSSTYHLNSLPMMQNf
4169	9666	A	4461	2	171	
4170	9667	B	4462	10	351	MAPRTLVL LLSGALALTQTWAGSH SMRYFYTSVSRPGRGEPRFIAVGYY DDTQFVRFDSDAASQRMEPRAPWI EQEGPEYWDNRNTRNVKAHSQTDR VDLGTLRGYYRCVSHSL*
4171	9668	A	4463	1	986	
4172	9669	A	4464	3	1282	
4173	9670	A	4465	1	1004	MAVMAPRTLLLLL LGALALTQTWA GSHSMRYFTTSVSRPGRGEPRFIAV GYVDDTQFVRFDSDAASQRMEPRA PWIEQGPEYWDNRNTRNVKAHSQI DRVLDGLTRLGYYNQSEAGSHTIQM MYGCDVGSDGRFLRGYQQDAYDG KDYIALNEDLRSWTAADMAAQITQ RKWEAAARVAEQLRAYLEGTCVEW LRRHLENGKETLQRTDPPRTHMTH HAVSDHEATLRCWALSFP AEITLT WQRDGEDQT\HTCHVQHEGLPKPL TLRWEPSSOPTIPIVGIAGLVLF GAV ITGAVVAAMWRRKSSDRKGGSYS QAASSDSAQGS DVSLTACKV
4174	9671	A	4466	1090	2175	
4175	9672	A	4467	1	780	
4176	9673	A	4468	59	169	
4177	9674	A	4469	89	134	
4178	9675	A	4470	864	1885	
4179	9676	A	4471	89	176	
4180	9677	A	4472	1	1127	
4181	9678	A	4473	1	405	
4182	9679	A	4474	3	199	
4183	9680	A	4475	3	607	
4184	9681	A	4476	1017	2029	
4185	9682	A	4477	844	1572	
4186	9683	A	4478	1	846	
4187	9684	A	4479	452	1220	
4188	9685	A	4480	1	1254	
4189	9686	A	4481	1	1383	
4190	9687	A	4482	1	1290	
4191	9688	A	4483	666	1606	
4192	9689	A	4484	1	1236	
4193	9690	A	4485	1	1269	
4194	9691	A	4486	719	1175	
4195	9692	A	4487	1	1182	
4196	9693	A	4488	1	1377	
4197	9694	A	4489	1	1335	
4198	9695	A	4490	1	2456	
4199	9696	A	4491	1	1827	
4200	9697	A	4492	1	1011	
4201	9698	A	4493	452	950	
4202	9699	A	4494	1	1433	
4203	9700	A	4495	1	1933	
4204	9701	A	4496	641	2107	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4205	9702	A	4497	1	2582	
4206	9703	A	4498	1	1095	
4207	9704	A	4499	1544	525	
4208	9705	A	4500	2	161	
4209	9706	A	4501	3	452	
4210	9707	A	4502	25	622	EFHRLRENPPWFLFPAAKTNVRAIA WG*RS GAHAGÆYGAELERIMVLF PPPTPKPYFPELRT*AHGFCPKVKGP TAKKVAERA*PNAVAHVVDGHAPN GAVPP*ADLQRRTSFRVDPVNFQAP *ATCLLVTLAAHLPAEFTPAV\HA SLGQVPGLSVSTVLTSTKIPVKLEPSV GHAFLPLWAFPPAPPPLSCTRTPVG L
4211	9708	A	4505	2	213	
4212	9709	A	4506	2	382	TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAAHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR
4213	9710	A	4507	2	252	
4214	9711	A	4508	1	466	WSPQTQREPTMVLSPADKTNVKAA WGKVG AHAGEYGAELGRIFLSFP PTKTYFPHFDLSPGSAQVKGHGKK VADALTNAGAHVDDMPNALSSPE ATLHAHKLRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASV STVLT SKYR
4215	9712	A	4509	256	391	NELHAENLKNEDD VDTGLLGFWTL LIISLTAGFSCCSFSWTVTYFDSFEP GMFPPTPLSPARFKK*R*CRHWTIRI LDSTYNIPNCWILLQLFLDSDL
4216	9713	A	4510	2	490	
4217	9714	A	4511	1	160	
4218	9715	A	4512	1	150	
4219	9716	A	4513	1	73	
4220	9717	A	4514	2	213	ISPFYHLCQMLKTADVLR RMALWR CRDALLS*GGSSIEIPLFLLYGSREL LGFCFTGMNHCAQSIYNRF
4221	9718	C	4515	186	365	MFQLLYDSLXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXIYNRF*
4222	9719	A	4516	251	454	GGSSIEIPLFLLYGSRARTWILF*EM AAGRVQWLTSVIPALWEAEAGGSR GQEFKTS LAKRVKPHLY
4223	9720	A	4517	3	192	
4224	9721	A	4518	1	129	
4225	9722	A	4519	23	115	
4226	9723	A	4520	1	1582	GRGWRAVLGWSRRRSGLEPATVGS SMALLFLLPLVMHGVSR AEMGTAD LGPSSVPTPTNVTIESYNMNPVYW EYQIMPQVPVFTVEVKNYGVKNSE WIDACINISHHYCNISDHVGDPSNSL WVRVKARVGQKESAYAKSEFAV CRDGKIGPPKLDIRKEEKQIMIDIFH PSVFNVDGEQVDYDPETTCYIRVY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NVYVRMNGSEIQYKILTQKEDDCD EIQCQLAIPVSSLNSQYCVSAEGL HVWGVVTEKSKEVCITIFNSSIKGSL WIPVVAALLFLVLSLVFICFYIKKI NPLKEKSIILPKSLISVVRSALETKP ESKYVSLITSYQPFSLKEVVCCEPL SPATVPGMHTEPNPGKVEHTEELSS ITEVVTTEENIPDVVPGSHLTPIERE SSSPLSSNQSEPGSIALNSYHSRNC ESDHSRNGFDTSSCLESSESLSDSE FPPNNKGEIKTEGQELITVIKSPPSF CYDKPAHVLVDLLVDDSGKESLIG YRPTNEDSQRNFEISLSCTQL
4227	9724	A	4521	1	408	
4228	9725	A	4522	2	377	
4229	9726	A	4523	50	326	
4230	9727	A	4524	3	1948	AAAAAAVPASFGLCSRDPAAPPQ ASMSGIKKQKTENQKSTNVVYQA HHVSRNKRQVVGTRGGFRGCTV WLTGLSGAGKTTISFALEEYLVSHA IPCYSLDGDNVHRHGLNRNLGFSPGD REENIRRIA EVAKL FADAGLVCITSF ISPFADRENARKIHESAGLPFEIFV DAPLNICESRDVKGLYKRARAGEIK GFTGIDSDYEKPEPTEPVLTNLST VSDCVHQVVELLQEQNIVPYTHKDI HELFVPENKLDHVRAEAETLPSLSIT KLDLQWVQVLESEGWATPLKGFM EKEYLQVMHFDTL DGMALPDGVI NMSIPIVLPVSAEDKTRLEGCSKFVL AHGGRRVAYLTETA EF/HTEHRKE ERCS/RVFWGTTCTKHPHIK/MVME SGDWLVGGDLQVLEKIRWNDGLD QYRLTPELEKQCKEMNADAVFAF QLRNPVHNGHALLMQDTRRRLLER GYKHPVLLHPLGGWTKDDDVPLD WRMKQHAAVLEEGVLPKSTIVAI FPSPMLYAGPTEVQWHCSRMIAG ANFYIVGRDPAGMPHPETKKDLYE PTHGGKVLSPAGLTSVEIIPFRVA AYNKAKKAMDFYDLARHNEFDIS GTRMRKLAREGENPPDGFMAPKA WKVLTDYYSLEKN
4231	9728	A	4525	1	626	
4232	9729	A	4526	66	409	LGLLQVTTNPPSPNTYLLKMLFK LRTPPFISHHSFILKNYDIQYFSMRDI DRLGIQKVMERTFDLLIGKRORPIH LSFDIDAFDPTLAPATGTPVVGGLT YREGMYIAEEIH
4233	9730	A	4527	1	1257	
4234	9731	A	4528	3	1086	FSVLRIMSLRGSLSRLLQTRVHSILK KSVHSAVIGAPFSQGGQKRKGVEH GPAAIREAGLMKRLSSLGCHLKDFG DLSFTVPKDDLNNLIVNPRSVGL ANQELAEVVSRAVSDGYSCVTLGG DHSLAIGTISGHARHCPDLCVWV DAHADINTPLTTSSGNLHGQPVSL LRELQDKVPQLPGFSWIKPCISSASI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VYIGLRDVPPEHFILKNYDIQ\YFP MKDIDRLGIQKVMERTFDLLIGKRQ RPIHLSFDIDAFDPTLAPATGTPVVG GLTYREGMYIAEEIH\NTGLLSALDL VEVNTQLATSNEEAKTTADLAVDV IASSFGQTREGGHIVYDQLPTPSSPD ESENQARVRI
4235	9732	A	4529	1	128	
4236	9733	A	4530	3	126	
4237	9734	A	4531	1	79	
4238	9735	B	4532	214	268	XELEKLQVVRQLEAEPGLPPVQPV FITVDPERDDVEAMARYVQDFHPR LLGLTGSTKQDEDQDIYVDHSIAIY LLNSDGLFTDYYGRSRSAEQISDSV RRHMAAFRSVLS*
4239	9736	A	4533	23	257	AYLIDDTEAQSRSQAKATPLEGLR TQPSSRPLGGIKLV*YEVLCLLMTA LKAI/TQIQLPATSHSAARLRGVLP AIR
4240	9737	A	4534	3	229	
4241	9738	A	4535	1	297	
4242	9739	A	4536	67	552	GPWRFCFSEAVSEPTTVAFDVVRPGG VVHSFSHNVGPGDKYTCMFTYASQ GGTNEQWQMSLGTSEDHGHFTCT IWRPPRGKSYL\YFTQFKAEVAGRL RFEYRHGLTFKARILKGESDVPLEN LRNFEVTKTAVGSQGPAPKLT PKLVIVAKASRTEL
4243	9740	A	4537	2	232	RDGTVHARAANKNRVISVLLPSDLV H*LWEP*PDED*DA*SETGDIDHRV TEESHE*PAFHNFMQESMAQYWK NNK
4244	9741	A	4538	2	1094	RHPVCLLVLMAGSGKTTFFVQRLT GHLHAQGTPPYVINLDPVHEVPFP ANIDIRDTVKYKEVMKQYGLGPNG GIVTSLNLFATRFDQVMKFIEKAQN MSKYVLIDTPGQIEVFTWSASGTIT EALASSFPTVVIYVMDTSRSTNPVT FMSNMLYACSIKYTKLPFIVVMNK TDIHDHSFAVEWMQDFEAFQDALN QETTYVSNLTRMSLVLDEFYSSLR VVGVS AVLGTGLDEL FVQVTSAAE EYEREYRPEYERLKKSLANAES\QQ EREQLERLRKDMGSVALDAGTAKG VFTVDSLSPVLHPSDLILTRGTLDEE DEEADSDTDDIDHRVTEESHEEP AFQNFMQESMAQYWKNNK
4245	9742	A	4539	710	1053	
4246	9743	A	4540	3	281	
4247	9744	A	4541	30	320	
4248	9745	A	4542	3	115	
4249	9746	A	4543	1	137	
4250	9747	A	4544	3	32	
4251	9748	A	4545	1	135	
4252	9749	A	4546	1	2694	
4253	9750	A	4547	3	544	
4254	9751	A	4548	2	323	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
4255	9752	A	4549	1	384	
4256	9753	A	4550	1	1299	MASPVAQAQAGKLLRALALRPRFLA AGSQAVQLTSRRWLNLOEYQSKKL MSDNGVRVQRFFVADTANEALEAA KRLNAKEIVLKAQILAGGRGKGVF NSGLKGGVHLTKDPNVVGQLAKQ MIGYNLATKQTPKEGVKVNKVMV AEALDISRETYLAILMDRSCNGPVL VGQPQGGVDIEEVAASNPELIFKEQI DIFEGIKDSQAQRMAENLGFVGPLK SQAADQITKLYNLFLKIDATQVEVN PFGETPEGQVVCFDAKINFDDNAEF RQKDIFAMDDKSENEPIENEAAKYD LKYIGLDGNIACFVNGAGLAMATC DIIFLNGGKPANFLDLGGGVKEAQV YQAFKLLTADPKVEAILVNIFGGIV NCAIIANGITKACRELELKVPLVVR EGANVQEAQKILNNSGLPITSAIDL EDAAKKAVASVAMK
4257	9754	A	4551	1	590	RVRTKDPNVVGQLAKQMIGYNLAT KQTPKEGVKVNKVMVAEALDISRE TYLAILMDRSCNGPVLVGSPQGGV DIEEVAASNPELIFKEQIDIFEGIKDS QAQRMAENLGFVGPLKSQVEAILV NIFGGIVNCAIIANGIPKACRELELK VPLVVRLEGTNVQEAQKILNNSGLP ITSAIDLEDA\AKKAVA\SVAKK
4258	9755	A	4552	3	168	
4259	9756	A	4553	3	95	
4260	9757	A	4554	3	354	
4261	9758	A	4556	1	95	
4262	9759	A	4557	156	364	GPVE*KPVEEESRGLLD*GLPGMD WGWWFGKGGDPPLAQLNCPSTV SEIIGRDLSGFPAPPGEPPA
4263	9760	A	4558	1	2523	
4264	9761	A	4559	3	469	
4265	9762	A	4560	3	132	
4266	9763	A	4561	1	2961	MGAASCEDEEFLKLVFGEEKEAPP LGAGGLGEELDSEDAPPCCRLALGE PPPYGAAPIGIPRPPPRPGMHSPPPR PAPSPGTWESQPARSVRLGGPGGG AGGAGGGRVLECPISIRITSISPTPEPP AALEDNPDAWGDGSPRDYPPPEGF GGYREAGAQQGGAFFSPSPGSSSL SWSFFSDASDEAALYAACDEVESEL NEAASRFLGSLPLSPRASRPWPTE DPWSLYGPSPGGRGPEDSWLLLSAP GTPASPRPASPCGKRRYSSSGTPSS ASPALSRRGSLGEEGSEPPPPPLPL ARDPGSPGPFDYVGAPPAESIPQKT RTTSSEQAVALPRSEEPASCNGKLP LGAEESVAPPGGRKEVAGMDYLA VPSPLAWSKARIGGHSPIFRTSALPP LDWPLPSQYEQLRIEVQPRAHHR AHYETEGSRGAVKAAPGGHPVVKL LGYSEKPLTLQMFIGTADERNLRPH AFYQVHRITGKMVATASYEAVVSG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TKVLEMTLLPENNMAANIDCAGIL KLRNSDIELRKGETDIGRKNTRVRL VFRVHVPQGGGKVSVQAASVPIE CSQRSAQELPQVEAYSPSACSVRGG EELVLTGSNFLPDSKVVFIERGPDG KLQWEEEA TVNRLQSNEVTLT TV PEYSNKRVS RPVQVYFVVSNGRRK RSPTQSFRLPVICKEEPLDSSLRGF PSASATPFGTDMDFSPRPYPSPYH EDPACETPYLSEGFGYGMPLYPQT GPPPSYRPLRMFPETRTGTGCAQP PAVSFLPRFPSPDPYGGRGSSFLGL PFSPAPFRPPPLPASPPLEGFPQS DVHPLPAEG\YNKVGPGYGPGE GAP EQEKS RGGYSSGFRDSVPIQGITLEE VSEIIGRDL\SGFPETSLEKKPPALKP RETVITLATPAPASALPPFPFLELV ATEAWGQPLAPLSPSFCLSHCLPLPS PSLGCGPQAWLA ALEGLGGKECVE EGGG
4267	9764	A	4562	19	387	
4268	9765	A	4563	1	373	
4269	9766	A	4564	2	343	
4270	9767	B	4565	19	507	MEANGLGPQGFPPELKNDTFLRAAW GEETDYTPVWCMRQAGRYLPEFRE TRAAQDFFSTCRSPEACCELTLQPL RRFPLDAAIIFSDILVVPQALGMEVT MVPSKGPSFPEPLREEQDLEALRDP EVEASKLGYGFQAITPYPTTTGWDV CRLIGFCWC PHGP*
4271	9768	A	4566	3	339	
4272	9769	A	4567	3	679	
4273	9770	A	4568	1	139	
4274	9771	A	4569	1	526	HERFETTYFKKFPAGYYVTGDGCQR DQDGYWITGRIDDMNLNVSGHLLS TAEVESALVEH*RLQEA\AVVGHP HPCEGVNASYCFVTLCDGHTFSPKL TEELKKA\VMRKRLAPFATPDYIQN APGLPKTRSGKIMRRVLRKICS/VT DHDLDGDMSTVADPS\VISHLFSHRC LTIQ
4275	9772	A	4570	537	2357	GVCHQRRLAPQAWPGAGTDSLILA TRWATGAPGHCCWHLPARHTCGSP GLSPVPQPASAGPPGGLWERHSRE YIKTWRPR/YFLKSDGSFIGYKERP/ EAPDQTLPLNNSVAGCLGMS\EC QLMKTERPRPNT/FVIRCLQWTTVIE RTFH/VDSPDE/REEWMRAIQMVAN SLKQ/RAPGEDPMDYKCGSPSD/SST TEEMEVAVSKARA/KVGTFGKVILV REKAT/GRYYAMKILRKEVIIA/KVR APGIALASLCGGCVCLQDEVAHTV/ TESRVLQNTRHPFLTALKYAFQTHD RL/CFVMEYANGAVFHLSRERVFT ERAR/FYGAEIVSALEYLHSRD/VVY RDIKLCAQEKGDTHSP*KVSPSLSSR ITLAPTGTQVSTVRGTSDP/AVECS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HSGTPHSSWNEQLHTTVWTRLIG YVEGKPHRGAVPRYMGVGQRVLE DN/DYGRAVDWWGLGVVMYE/MM CGRLPFYNQDHERLF/ELILMEEIRF PRTLSP/EAKSLLAGLLKKDPKQ/RL LP/PFKPQVTSEVDTRYFDD/EFTAQ SITITPPDRCECWGPRAESRCLPHAE PSSAAVPDGFAPAGPLSPQDAWRGR RGWRRRERAGAAGRTRVRRGHLPE VMPAFLAS
4276	9773	A	4571	64	1537	VTAYHAATMNEVSVIKEGWLHKR GEYIKTWRPRYFLLKSDGSFIGYKE RPEAPDQTLPLNNSVAECQLMKT ERPRPNTFVIRCLQWTTVIERTFHV DSPDEREEWMRAIQMVANSCLKQRA PGEDPMDYKCGSPSDSSTTEEMEV AVSKARAKVTMNDFDYLKLLGKG TFGKVILVREKATGRYYAMKILRKE VIIAKDEVAHTVTSRVLQNTRHPF LTALKYAFQTHDRLCFVMEYANGG ELFFHLSRERVFTTEERARFYGAEIVS ALEYLHSRDVVYRDIKLENLMLDK DGHKITDFGLCKEGISDGATMKT CGTPEYLAPEVLEDNDYGRAVDW WGLGVVMYEMMCGRLPFYNQDHE RLFELILMEEIRFPRTLSPKASLLA GLL\KKDPKQRLG\GGPSDAKEVME HRFFLSINWQDVVQKLLPPFKPQV TSEVDTRYFDDEFTAQSITITPPDRY DSLGLLE\LDQRT\HFP\QFSYSASIRE
4277	9774	A	4572	2	423	
4278	9775	A	4573	1	106	
4279	9776	A	4574	3	58	
4280	9777	A	4575	1	191	
4281	9778	A	4576	3	325	
4282	9779	A	4577	3	277	
4283	9780	C	4578	77	292	MVDFCPCPSICFXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXHWSIC IS*
4284	9781	A	4579	645	849	
4285	9782	A	4580	3	140	EANKENREAQMAAKLERLPEKD*A /HLEEVKKNK\ESKDPADETead
4286	9783	A	4581	49	605	NSARGLSLSQLIVQNTLPVACLFT MASSDIQVKELEKRASGQAFELILSP RSKESVPEFPLSPPKEEGFFPGKFR EN*EAAEERRQSP*SCSS*RQLAEKR EVHGKEVLQKAIEENNNFQ*NGQK RKLTPHKMEA**RDPREATNGLPKL EPFAEEKDKAH*KKCRKNKESQRP CPRDLKPD
4287	9784	A	4582	1	567	VVREPAFSLA/EAQFTARYFSTSSIP NV\NKAPV\IRRSKHM*QGVTLPI EHYHEGTDSL*TALV*ARVGNQLA KLKR\NYAKAVELLVQLASLQTSFV TLDEAIKITNRRVNAIEHVIIPIERT LAYIITELDEREREFEYRLKKIQEKK

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						KILKEKSEKDLEQORRAAGEVLEPAN LLAEKDEDLLFE
4288	9785	A	4583	1	748	MSGKDRIEIFPSRMAQTIMKARLKG AQTGRNLLKKKSDALTFRQILKK IETKMLMGEVMREAAFS LAEAKFT AGDFSTTVIQNVNKAQVKIRAKKD NVAGVTLVPFEHYHEGTDSEYELTG LARGGE\QLAKLKRNYAKAVELLV ELASLQTSFVTLDEAIKITNRRVNAI EHVPIPRIERTLAYIITELDERVREEF YRLKKIQEKKKILKEKSEKDLEQRR AAGEVLEP\ANLLAEKDEDLLFE
4289	9786	A	4584	166	238	
4290	9787	A	4585	53	203	
4291	9788	A	4586	357	498	
4292	9789	A	4587	262	397	
4293	9790	A	4588	68	422	
4294	9791	A	4589	70	361	
4295	9792	A	4590	259	2603	
4296	9793	A	4591	246	667	
4297	9794	A	4592	25	471	
4298	9795	A	4593	2	3788	
4299	9796	A	4594	1	700	
4300	9797	A	4595	604	1047	SNNRTDNPTSVAYLSKETDVVAKG WPHCLWVVAVAILVLEAIKIIQGGK DFTVWTS HDVNGILGAKGNSWLS D KRLRYQALLLEGPVLQIHTCVALN PAIFLPEDGEPIKHDYQQIVAQTYVT *EDLLEVPLANPDNLNLYTNGSSFV
4301	9798	A	4596	1	1410	
4302	9799	A	4597	510	755	
4303	9800	A	4598	59	411	SWPSDKQTLVVQRGQKMEQANHP DPTDHMSQLMWT/VLPQGFRDSPH LFGQALAQDLGHFSSPGTLVLQYV DDLLATSSEASCQATLALLNFLA NQGYK/LSRSKAQLCLQQVKYLCL
4304	9801	A	4599	1	565	
4305	9802	A	4600	126	492	CNNSMTSLQVRLKVCPRPCRTSM/L PIRII*KLPQVCLDLL*IREGEWDMY PCWAKFPCPYSLKGT*PIAWGILWS FGDFFAY/IPLMQQQKH*FSSQNTRR NEEGQI*WPLLMHSQKPAPLPVV
4306	9803	A	4601	1	342	
4307	9804	A	4602	55	219	LGNKHLLGSIDPRGSWVTGEYIFLR PIIAA*GRQ*DFLPFELWWTSLNNS WAFS
4308	9805	A	4603	339	1371	ASHPLRGLLCGPSLPNEPCPLLHGT QSHRPLKG*GVRAHSTGLAGSSTCR PLRDPLGEASWAPESAQGL*IHQSA LCI*LKLKPAGQRAKLGDRLDIPDR RKSSTILGRAGDLQPAMPEPTLSV GSCAAQASPMNPAPCSTAPSPIDHS RAEECGRIARDWQAAPPAGPCGIH WVKPAGLLSLLRDCKYTNRHSVSS SRFANTNQHPASSSGFVNAPIDTLY LANLVGTWRTFVASSGIVNAPISTL SKQTTWLYQSAGCGKESTQASGAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TGGTSFKSLETTGSISEASSAKHCTE LFSRFTTFNPDSVPSDGVVGDTAGT VWPGVLKGEPCHLGTCTYRCVLDPH PTPSESDTIQGIHVQVCYMSTLHDA DVCDTNDPVTHTNKKYIYSTEFTS NNPELRSEDETVFRALEKWKTSQET IGEMDFYICNDPHPDALYQNGLSK MQDTVSLSVFSPSVAA
4309	9806	A	4604	749	1002	QLKKGTSNLLVSKPSPVWIPTGTLT QIMGTGVANIC*PVF*KD*GELGKM NYAMMSTITQGKEENPAFLKWLWE ALRKYTPLSP
4310	9807	A	4605	1	1632	
4311	9808	A	4606	307	543	
4312	9809	A	4607	1	1149	
4313	9810	A	4608	119	409	GDICHLGLTPVGSLSLSCSR*QV A*VGAVTAATIGTGILLQQLAFLVC NWLLLSGSSNFPRSALICFKSREK GTCIQVGPNSPPPTACKGHN
4314	9811	A	4609	1	2433	
4315	9812	B	4610	97	1065	MHAVHTSLLVERTILTTTKERGSTL QYPLRPGAHKGLQDIVKRFKAQALI RKCSSPCNTPILGVQKPNGQWRLV QDLRLINEAVIPLYPVVPNPYNLLSQ IPEEAWEFTVLDLKDAPFCIPLHSDS QFLFAFEDPTDHTSQTWTVPVPPGF RDSPPFLGQALAQDLGHFSSPGTLV LQYVDDLLLATSSEASCQQAATDLL NFLANQGYKTHSRSDAPVGFTRDR HLVATEKIPRGREPLSSLA VYTRGR PTRTGARRTIVSRIRDRFRFFRYLA QREPLYQQSLLIHLQLDSQPALS VIGKVPNVVELTPNFGTAAQV*
4316	9813	A	4611	1	2403	
4317	9814	A	4612	1	2838	
4318	9815	A	4613	1908	4698	SNDRTEDDCGKHPFMSSPP/TEPWV CLIEGQEIDFLDTGTTFSVLIPCLG RLSSRSVTIQILGQPVTTRYFSHLLS CNWETLLFSHAFLVMPESTPLLGR DILAKAGAIISMKTGNKLPICCPLE GINPEVWALEGQFGRAKNAHPLQIR LKDPISFPYQRQYPLRPEAHKGLQDI VKHLKAQDSVRKCSSPCNTPILGVQ KLNSQWRLVQDLRLINEAVIPLYPV VRNPYTLLSQVPPEAEWFTVLDLK DAFFCIPLHSDSQFLFAFEDPTDHTS QLMWMVLPQRFRDSPHLFGQAQA QDLGHFSSPGTLVLQYSEIAKTLTY LIKEMERANTHLVEWEPEAETAFET LKQALVQAPALSLPTGQNFALYVIE RAGIALGVLTQTHRTTPQPVAYLSK EIDVVAKGWPHCLRTVAVAVLVLS EAIKIIQKGKDFTVWTTTHDVNGILGA KGGLWPSDNCLLRYQALLLEPVL QIHMCIAINPATFLPEDGEPIKHDCQ QIIVQTYATQDDLLEVPLANPDFNL YNSGSSFVENGIQRAGYAIIVSDVT

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LGSKPLSPGTSTQLAELVALTRALE LGKGKRINVYTD SKYAYLILHAHA AIWKEREFLTSGGTPIKYHKEIMELL HTVQKPKEVAVLHCQSHQKGSARR IFCLTRIPGTRVCKNPHVSLSGISEW PLRDHTPLCFRPKALLA WVHEEICS MGCKDPGWNSLKVSEEDRKMQUES LETSRDLLNGFDQNVNDMDMSKVQ AEGASDGDEELIGKWRKGLSMLW KILSIENMMNVWKDGTIKDAIIVIEK AVKAIKPETINSCQRNLCPDVVHDF TRFTTEPIKDIKEIGDLAIKLGIFESS NSTQFLNQFVPDDRSLPHNKLKLFY KPEFYSSYPLVSCLDHYVDQVGARI SMSFCVTTVTASGSGSWTCGVSQ LKLSYAD
4319	9816	A	4614	1529	2945	
4320	9817	A	4615	3	374	
4321	9818	A	4617	3	112	
4322	9819	A	4618	359	465	
4323	9820	A	4619	3	381	MRILMVGLDAAGKTTILYKLLGEI VTTIPTIGFIFVVD SDRERIQEVAD ELQKMLLVDEL RDAVLLL FANKQD LPNAMAISEMTDKLGLQSLRNRTW YVQATCATQGTGLYEGLDWLSNEL SKR
4324	9821	A	4620	395	552	
4325	9822	B	4621	1289	1603	MVVTISP NFSLYRMVVLPAASNPTI KMRICFLPNSREKREEIVRPM AVVA LVMGRSRRGLGRPRAFSFQAPROT KREGREAAEEERGRQKRLSGPCAD EDPAQE*
4326	9823	A	4622	2	116	
4327	9824	A	4623	156	403	
4328	9825	A	4624	8	2648	WIQYSSTTLPNDWNKRKKKEKKA MLSARAKTPRKPTV/KKGSQTNLKD PVG\YCRVRLGFPDQECCIEVINNTT VQLHTPEGYRLNRNGDYKETQYSF KQVFGTHTTQKELFDVVANPLVND LIHGKNGLLFTYGV TSGKTHMT GSPGEGGLLPRCLDMIFNSIGSFQAK RYVFKSNDNRNSMDIQCEVDALLER QKREAMPNPKTSSSKRQVDPEFAD MITVQEFCKAAEEVDEDSVYG VFS YIEIYNNYIYDLLEVPFDP/IKPKPP QSKLLRED\KNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRIANTHL NRESSRSHSVFNIKLVQAPLDADGD NVLQEKEQITISQLSLVDLAGSERTN RTRAEGNRLREAGNINQSLMTLRTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAICGLTPGRRYRNQPRGPVGN EPLVTDVVLQSFPLPSCEILDINDE QTLPRLIEALEKRHNLRQMMIDEFN QQSNAFKALLQEFDNAVLSKENHM

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						QGKLNEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIYEEDKRNLLQ ELETQNQKLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLWVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFPDQONAPPRLRHRRSRASG DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKGDYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAESIEWTDVETRCVSGC GR*GAGSQLGPGYQHHAQPKRKK P
4329	9826	A	4625	1	331	
4330	9827	A	4626	142	461	
4331	9828	B	4627	136	906	XPELKPVDKESVVMKFPDGFEEKFS PPILQLDEVDFYYDLKHVIFSRLSVS ADLESRICVVGENGAGKSTMLKLL LGD LAPVRGIRHAHRNLKIGYFSQH HVEQLDLNVSACGTAGHASFLGRP EEEYXGWCDSGVPRMKRFKAGVP GSCGYAKEGGVTRVERKDFDQYRA LLQGTVSAAKAFL*
4332	9829	A	4628	1	233	
4333	9830	A	4629	1	312	
4334	9831	A	4630	2	119	
4335	9832	A	4631	1	145	
4336	9833	B	4632	78	236	MSYIPGQPVTAVVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFSDKT DK*
4337	9834	A	4633	102	583	IRVEMSYIPGQPGTAVVQRGEIHKL RQGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIALQ IGDKIMQVNGWDMTMVTHDQAR KRLHQALRRRLVRL\VTRQS\LQK\ AVQQSMPVLAATTILRLPAASLYS NATSTLWSPSGFC
4338	9835	A	4634	1	373	
4339	9836	A	4635	3	86	
4340	9837	A	4636	1	204	
4341	9838	A	4637	1	767	
4342	9839	A	4638	20	515	
4343	9840	A	4639	3	391	HEESRSVSQAGVQWRYLGSLQRP PRFKRFSCLSPSSWDHRCCTTS*LAN F*YL VETGFHHVELLTSSDLPTSAS QSAGITGVSHHAWPWFALNVFKDG CESPWP HNKLEFYTAYYNNFTGT LRPPL
4344	9841	C	4640	201	368	MGKSKXAFRXKSXGIVFIQGTFPXE YNXXPRGIKVSQEXNXXXXXCXKI GGEDVX*
4345	9842	A	4641	1	307	RLFFFFETVSHSVTQARVHLSHLGS LQPLLPTFKQFSLSLPGS*DYRRLL LHPANF*FSVETGFHHVGOAGLEL LTSGDPPTSASQSAGITGVSHRAWP ST

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4346	9843	A	4642	1	310	
4347	9844	A	4643	49	360	DRVSVTQAGVQWCNLSLQPLPPR FR*FSCLSLSSWDYRRPPRPANF* FLVETGFHHVGQAGLKLLTSSDPPT SASQSAEITGVSHRAWPVLSSPQPF FF
4348	9845	A	4644	2	119	
4349	9846	A	4645	1	276	FFFFFFFFLTQSLTHSVTRLECSGVI SAHCNLCLLGSSS*LASAS*VAGTT GANHYAQLIFVFLVEMGFHHVGRA GLKL/HDLK*SKVLGLQA
4350	9847	A	4646	2	273	LRQFSLLLPRVECSGAISAHCNLCLL GSSDSPASASRVSGITGTHQTLWT FFVFLVEMGFHHVGQAGLQLLT*V IRPPRPVKVLGLQA
4351	9848	A	4647	1	106	
4352	9849	A	4648	1	485	SSIDTLGRRVGQPAPGSPGASNHLC CESYPWQLLQPCPVQAGARAELVP VPAHHPGDPVKTEP*RGQGASSGSC TCWGCPTAQAQAQ\PSSPAAPMRK EGPPSL*SERTGRPSRGVTSAGSDG AQPGSA*HSPWPGIVLLSVRYLQETI NHRPGGRPTGFSS
4353	9850	A	4649	1	623	CDLNSQPRSTDGTFDLTVLSNDGVH STVTSNIRVFFAGFSNATVDNSILLR LGVPTVKDFLTNHYLHFLRIASSQL TGLGTAVQLYSAYE/GEQ*NVSFGQ L*SENHNQYVNPSSGRSHLLERHSK RSF/FROSGVKVESVDHDCVHGPC QNGGSCLRRLAVSSVLKSRESLPVII VANEPLQPFLCKCLPGYAGSWCEID IDECLPSP
4354	9851	A	4650	1	446	LMLRPRLKLQEPVPHHHLGFQCPSS PLLPP\GPPPHKV*PLGFQEGGQHS SSLNFVAHSTPAKP/PPGCVCPSLPA SHAHCLSRVIGGVGLRNCTVVPTRG GGSQLPALLPSLIVPLIVHQSPVSS LQPIRHDLPAPGDGTHSSAYC
4355	9852	A	4651	2	388	SHGSYVMYHDQVEFISGMKHW/FN TKIQTIIY*KNEEKNMIISTNAENG HDKILLPFMIKTHITLGI*GNVLILIT GIHKQFFWQQGQGWGACGGGRVL LFPQAGVQWWDHSSLQPQPSLNSF SNSSL
4356	9853	A	4652	115	413	LHIYSQPKFRKGTKKIH*W*KDSVFH SSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSPMQLIQENTG/IMLQDI GFGKDYLSKTSKAQATKQK*TRKH WEMLQDIGFGKDYLSKTSKAQATK QK
4357	9854	A	4653	3	129	NTLLKKTVSFHQCCWKNWISICRKI KLDSYLSPTYTKIKSKLIKLNKVRPET MQLIQENTG/IMLQDIGFGKDYLSK TSKAQATKPK*TRLLSLTIYKNQVK VD
4358	9855	A	4654	1	405	LTLKPNSGFRFPFQVATR*IKYPGIH PAKEVKDLYRKT*KTLKGITDGN

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						Q*KTIRGSWIGRINITEMAILPKAIYR FNTTPIKLPMFAITQLEKTIQKFIWN QKGAQIAKRILSKKTNSTSHITVL QTIRI
4359	9856	A	4655	3	448	FFFFFAFLLLGLLHQIPDVSPTGKYT TLLPLMIILMISGIKEVIYIINDMADK IVKEHKTVMTRLWDTFKWKEVKC GLNTVKALEMGELPSLQDTPDVFI *QHSNPG*RDCKKTRQGFDREQLLY QCRDILPPROQAFKLOSLRAQP
4360	9857	A	4656	2	502	KKKKERKRKRTPIKKWAKDDRHF TGDKIKMVNKNIKICSISLVIS*MQI KAITIHPTRLAKVKCLPRMGR/KGIL FYCW WARKLEQ/SFRKIFIP*NPGVR LLSTNPRKICAPFAKNTRASETWTK LLLAALCVVTPN*KQTNC PSTAGMS NLLASMDHTGRTVSGHA
4361	9858	A	4657	61	364	KTVWF CARVEGQGNLG*WKPRLP GLKHFPGLSSQ/WNRKLPDGPTNPG *FWNFKKKGGFPLWPKRI*IFGPGD PPSRASKRAGITGITHGAGPRFNFKK WR
4362	9859	A	4658	2	436	KLIIFLYTSNEQREFEIKNTIPFTLAPP KIK*LGTNLT/KWIQELYEKIYKSVM KNIKELNKWRSSYGK GKSSSSSSSS SSSLDIACSWLRLKIVKISGLHNLI YRFNIVPIEIPETYLV DVNKLIPQFIW RGRHRIVNKIVE
4363	9860	A	4659	3	480	GSHDFFDKLILKFIWNSRPRIAKTIL KKKNKVGGTLCDFKTYRATV*I KTVWYWD/QIRHI/DQWSRITSPEIN PYIYCQLIFNRYTKTIQ/YGNNRLFN K*C*DMRRVKSDPFLTY/PYIIN*K MIIDVKAMIMKL/LEGNTGMSLSDF GLRKALDVTTKV
4364	9861	A	4660	362	408	CQVISVLW FYSSVLGWL VWIFCFSL KF*/WKSRSRQANPILKNKTRVLIL PDIKTYPK\AGVIKPVW*QCS*KVW GEKVWY WQKMTQIVQWDRTESPQ IDN*SLTKEIQWRKDSL FNKW*GNN WTAPFSS/RSLNLNKDLTAVTKIKSK WVTDLNVKHKTINLL
4365	9862	A	4661	93	367	KVWGEKVWY WQKMTQIVQWDRTE SPQIDN*SLTKEIQWRKDSL FNKR* GNNWTAPFSS/RSLNLNKDLTAVTK IKSKWVTDLNVKHKTIKLL
4366	9863	A	4662	123	397	KVWGEKVWY WQKMTQIVQWDRTE SPQIGH*SLAKEIQWRKNSL FNKW *GDHWAAAFSSSSSI*TKTLQ/CTKI KSKWVTDLNVKRKTIQLL
4367	9864	A	4663	2	433	ETADFGPLVLDSD/DDSVD RDIAEAI REYLKAKSGAAQTGAGRGQPGAA QPSRAAGSGSRCKPELSHGSAPTSV CPPKLVPGSGGGPGSQVRSSED*GS AFPVRASSNDSFEQSIKAEIEQLLNE KR*HATPKCDG\SIDKKPDP
4368	9865	A	4664	94	445	HHQLTLESLGKSKNSPRLSPSLGAC

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						LSCIIWQPAKGQG\SGDGGNWQRG KTAETE/SAAIGGETEWTAKCP*YSC L/GVGPTALTSQPPT/PEAEHPQA/GG TYRDLHPDPTWKTGWCHFVFC
4369	9866	A	4665	52	119	
4370	9867	A	4666	987	1324	VSNTPSARNQGRASSPGNSSPE/SSS ESAPAAATANGCDEAHLIPGGKFREP LKQGRGPELGPRPRALGGPRGSI/RP GSGGSFRG*LGGQMLLEPAASPGTQ PSGHLPALCGLSN
4371	9868	B	4667	3888	8771	MRLWSWVLHLGLLSAALGCGLAE RPRRARRDPGRAPPRPAAGPATCA TRGPRPPRLAAAAAAGRAWAEVR VPRRRQREARGATEEPSPPSRALY FSGRGEQLRVLRADLELPRDAFTLQ VWLRAEGGQRSPAVITGLYDKCSYI SRDRGWVVGIHTISDQDNKDPRYFF SLKTDRARQVTTINAHRSYLPQW VYLAATYDQGFMKLYVNGAQVAT SGEQVGGIFSPLTQCKVLMLGGA LNHNRYRGYIEHFSWKVARTQREIL SDMETHGAHTALPQLLLQENWDN VKHAWSPMKDGSSPKVEFSNAHGF LLDTSLEPPLCGQTLCNDTEVIASY NQLSSFRQPKVVRYRVVNLYEDDH KNPTVTREQVDFQHHQLAEAFKQY NISWELDVLEVSNSSLRRRLILANC DISKIGDENCDECNHTLTGHDGGD CRHLRHPAFVKKQHNGVCDMDCN YERFNFDDGGECCDPEITNVTQTCFD PDSPHRA YLDVNELKNILKLDGSTH LNIFFAKSSEEELAGVATWPDKE ALMHLGGIVLNPSFYGMPGHTHTM IHEIGHSLGLYHVFRGISEIQSCSDPC METEPSFETGDLCDNTNPAPKHKSC GDPGPGNDTCGFHSFFNTPYNNFMS YADDDCTDSFTPNQVARMHCYLDL VYQGWQPSRKPAVALAPQVLGHT TDSVTLEWFPIDGHFFERELGSAC HLCLEGRILVQYASNASSPMPCSPS GHWSPREAEGHPDVEQPCKSSVRT WSPNSAVNPHTVPPACPEPQGCYLE LEFLYPLVPESLTIWVTFVSTDWDS SGAVNDIKLLAVSGKNISLGPQNVF CDVPLTIRLWDVGEEVYGIQIYTL EHLEIDAAMLTSTADTPLCLQCKPL KYKVVRDPPLQMDVASILHLNRKF VDMDLNLGSVYQYVWITISGTEESE PSPAVTYIHGRGYCGDGIIQKDQGE QCDDMNKINGDGCSLFCRQEVSN CIDEPSRCYFHDGDGVCEEFEQKTSI KDCGVYTPQGFLDQWASNASVSHQ DQQCPGWVIGQPAASQVCRTKVID LSEGISQHA WYPCTISYPYSQLAQT TFWLRAYFSQPMVAAVIVHLVTD GTYYGDKQKETISVQLLDTKDQSH DLGLHVLSCRNNPLIIPVVHDLSPF YHSQAVRVSFSSPLVAISGVALRSF

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						DNFDPVTLSSCQRGETYSPAEQSCV HFACEKTDCELA VENASLNCSSSD RYHGAQCTVSCRTGYVLQIRRDDE LIKSGTGPSVTVTCTEGKWNKQVA CEPVDCSI PDHHQVYAASFSCPEGT TFGSQCSFQCRHPAQLKGNNLLTC MEDGLWSFPEALCELMCLAPPPVP NADLQTARCRENKHKVGSFCKYKC KPGYHVP GSSRKS KKR AFKTQCTQ DGSWQEGACVPVTC DPPP KFHGL YQCTNGFQFNSECRKCEDSDASQG LGSNVIHCRKDG TWNGSFHVCQEM QGQCSVPNELNSNLKLQCPDGYAIG SECATSLDHNSESIILPMNVTVRDI PHWLNPT RVERVVCTAGLKWYPHP ALIHCVKGCEPFMGDNYCDAINNRR AFCNYDGGDCCTSTVKT KKVTPFP MSCDLQGDCA CRDPQAQEH SRKDL RGYSHG*
4372	9869	A	4668	1	183	GRDGVLPCCPGWP*SP ELKQSA/CL GLPKCWDY/RARATAPGLLFFSYAK ICPCLTSCQYSKC
4373	9870	A	4669	3	462	TYQSFSPSHMLPLRGYDVW*TTLFQN P*HG*PGLQRFPLANMLCGPSGSHL VLLKL*RSVTLNHREALICLPPE*YV EPSGK\CIAGWGETKGTGNDTVLN VSLNDISNQE*NNQHRGHVR*S*M STDGLQASVGAL***YGGPHSWFIH HRG
4374	9871	A	4670	1	360	ARGPQRSERSSRRPAPPSRSSGS*RC SCIPWPTLLLRGPR*RPL*NARYMKI LASPFQLSHPRKGPRRW/AGVLS PPAAPPSSSSVPEAGGPPKKQKAD VTL SALNDSDAHS DVVDM
4375	9872	A	4671	70	631	RQRPQRSERYYWRAAPS*GDKVG PQMASQOPSASLYPYPSTSHITAGS RLGEFHEL GWLEVRWFVVDPLAC RENCETGVWAMGLSVFLSVIHS LT QRSFINTDSVLCHAQRETNVCPCAR EGPCL*PSPSARSQRPRSPGSRTPQ EKS RPRDAAASSAPRAS*RRRRPPII PLRPLWTLTSWPRAPPHGDAAAAA TREPEFHL
4376	9873	A	4672	93	338	
4377	9874	A	4673	1	660	FRRFRWRRRLH*AGPASSAGGSPGE ASGTMSGELPPNINIKEPRWDQSTFI GRANHFFTVDPRNILLTNEQLESA RKIVHDYRQGIVPPG\LTENELWRA KYIYDSAFHPDTGE\KMILIGKNGQ AQGF PWNMTITGCM DGRFTGTP AVLFWQWINQSFNAV VNYTNRSGD APLTVNELGTAYVSATTGAVATAL GLNALTKHVSPLIGPF GPFA CVA
4378	9875	A	4674	1	387	FFF*RWVSHSVAQAAVRWRNHGSL *PKTLGPK*SSH/CQSP*RAWDS*AH AHYHPA*FLNFFL*RQGPLSMF PK MVLNSRPQAVPPT*ASQSDGITGVS HHTLALKV/CLFKMKYFE**TEKGI

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						HFKRTK
4379	9876	A	4675	3	383	GQLQARPPAPAAADCPPWTLRGSA LVPWLVPWRKASPQLSPGSPEC* PSARPQDPPRPAGQIQDRASEHAAR GGPCGVLRADGALPALPPDRARPQ VCGRGEVAARARW*RSSGRRGTR RNGE
4380	9877	A	4676	490	1013	WASCSSESREYQCCFQTVPPGFSRVM KFFTFPGSCKHFPAPL/PAPQACTSF GLAGLPPNALPLILVPAPPA/SSLAN PQLVQPPVPGLVPRPSRSCSA/RP SA/RLARPPETPAR/PRAPSSAPRTRT PS*GRARSGGSAGNAPSARRTPQGP TRAACSLARILDLAGSWRVLRP
4381	9878	A	4677	1	447	KKFVIPDFEFTGHVDRIEDVKELT GGKVAAYIPQLAKSNPDLWGVSCL TVDGQRHSEGHTKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAIVVS SLIKMDCNKA*KFDFVLQYLNKMA
4382	9879	A	4678	3	284	QLGQYGETPSLLK/IKIRIQKVAGHG GRHL*SQLRLSLRQKNLLNP/GRS CSEPLRHCTPAWVTERDSVSKKK KKKKEKERKKKKAGCGGSRL
4383	9880	A	4679	122	196	CWFENVNSKSGFWVLF*FKAKLVN
4384	9881	A	4680	2575	2786	ADTESITL*FYHFFFFLRL/DSVAQA GVQWCDLGLLQV/LPPGFTPFSCLS LPSSWDYR/RPVITPS*FFVFLVEM/G FTALARMVLIS*PCDPPVSASQSAGI TGVSHCAOPTFIK
4385	9882	A	4681	3	512	YNQKVDLFSLGIIFFEMSYPHMTA SERIFVLNQLRDPTSPKFPEDFDDGE HAKQKSFISWLLNHDPKRPTATEL IKSEL/LPPPQMESE/LHEVL/HHTL/ ANVDGEGPYRTIDGPRSFQRISPAI DYTYDQRHS*KGTSSIRAKLLHL VRETMIRICTRHGACQT
4386	9883	A	4682	1	382	EESILGEVGEALTSAGEELKIDRFF*I VEGLRHNSQLNVTSMQLINALDTS PDDLDFRLHIINEFMRCGLKEILPHL *GIKNDGLDMQLKDFDEHNEEDLL ECNHRLEDIRAELDESVDVHMLW S
4387	9884	A	4683	1	472	GIMLPDLKLYDIAMVAKSAWYWH KNGHKVLWNKMAQN/HIYGQLVF VKVPKYTQWGKSLFNEWNQE/N/ WISACRRMKLDPYVSTKINSKWIK AYTIR/PETVKLLEENIGKKLIDI/GP G**FLALAPQTQATKA*IDKWDFIK VKTFCTARETVNTEKRH
4388	9885	A	4684	182	345	RFPLCSFPPTLPCEGICFPFA/FCHDC KFPEAFPTRLPEPAEL*VNSTSSLH KL
4389	9886	A	4685	205	395	VNLGIFGKNGAPPG/PEGRGGILGHR NPPPRGLNK*PPLTFQGTGTPGSSSS S*VNLGIFGKNGAPPGGQGGPKTPG PKEWAGLAPQKGGTTGLDPLGPPK

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						KGFNNHPGGIREFPGN
4390	9887	A	4686	35	389	NLFYKVLQSAGFFSMDHEDDVDFL ARFSQLVTGKRQSLIVSWTT*IQNG DIKNAQEALAAETRMALTLR*LAP DDGTSSKI/LGFCCDYVQILKHL\DQ QKAGAAAIMSVATKELMMKT
4391	9888	A	4687	3	547	GGAGRRAWAGVGGAPGAGGGPAE AGAAAEEGAHRGDGAVRAGAGG GRRYRPRRVQDPGGPAE/G*TWPPS PSSRCSSPCVPGRG*/PSEPQDPAAV SLPTSSVPETRGAPAGPIRGAPAGL RCQP*EARPGCVYWLISGGWCSPLF PWKLPGPRRPKQL*APRAGPCRPSL PCRLATGHDF
4392	9889	A	4688	65	414	WKCADTNVAQGPRVQQVLQLRGT PIPNHCALCLLREKQRQLCPRGSGN PAERSKPRRIQPEDATPAQALPRLP KGGGPGKSPTRGKHLGWGRDLFAS LSPAKATCLPPSIDNKP
4393	9890	A	4689	75	787	HVAFASGQRCNKS LPTPKVVP RVG LFPRPRPPWAALVALGLAWHPLAGI PRGCCVPHRHNAPEEGKRLPFVSPS GHRARSTWAETRPQGPRGSLASLCP AHMDLSIWKTARGATFSFQQGPPG SWRGQT/RGPVSPLRPAPPPP*RPDK DGGGGS/PDQRAGRTRKAEVGGCL ASMRPPAPLT*TRRGR*RRPAPAP ARTAPSPRCSAPSSAAAPASAGPPP APGAPPTP/PRPRPYALRR
4394	9891	A	4690	8	382	QEYWE*LYAYTF*NRDELDEFFDRH ILPNFTQEEYTT*NNPVS VKEIEFVI/ NNISTPKKNPK*TSDDFTSKFC*T FKEELIPVLYKHFQKIVEEEVLPHLF CELSITFLLKLD RRCEVRRLHR
4395	9892	A	4691	2	389	NRKRIELTRKVL FELKHMRDVQNE HLTRFVGACTDPPNICILTEYCPRG LQDILENESITLDWMFRNSLSSDIC* GMLFIHNAA/IC*HGNLNSFN SVLIR DLSRFN*FSFSSESPVNCIQIIVIIISP
4396	9893	A	4692	2	544	TKAPKYIKQTLIDPKGEVDYNNMIIV G/DANTPLSKTDRSSIQ*INKETVEL NHILD LIGLTAIYRTFHPTATE/YFFS SAHGTL SRINYTLGPKPGCEKIVKH RNYIKYPFLNTIELEINNKRMSENT NTWKLNNMFLKD*WINEEIKKEI*K LLETNENGNTM*QNLWDMTKAVL RMKFIT
4397	9894	A	4693	1	373	MPHSVPGVLMSPGIIPPTGLTAAAAA AAAATNAAIAEAMKVKNIKLQAMS NYHASNNQHGAN SQHGDMISRVAL DLPLSILPNLYTMPLVLQHSHTYN HLTYS*LHNLQTIP*INLDQRAPSLP
4398	9895	A	4694	185	417	NSELNGKEAALQ/IMILEREIGVEKA LNVQKGRVSESLKLLANRPGMVAH ACNPSTLGGQGGWVIVIRSGVRDQP *PHG
4399	9896	A	4695	88	432	TDLFLFVCLRLS\LLSVAQAGVQWF

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						DLSSQPPPPRFKRFSCLSLLSSWNH RCTPPRLV/N/FFVFLVEMGFTMLAR MVSIS*PCDLPTSASQSAGITGINCR TQLTY*F*KFSVDSL
4400	9897	A	4696	3	390	YRIPYYVSTDCENLLKRFELELNPVK RLTLKQIMNDRWINARHEEDELKPF AEP*LADILDQKGIYIIGMGYSQEEI WESLTKMKYDEITATYLLLGRKSS HLDASDSTSSTNLSLAKGRPSTDFN NSTG
4401	9898	A	4697	289	365	SPRLGLPKCWDYRHEPPHPAAFH*G CVLFIFYFIFLKQEL/NSLTQAGVQW RDLSSLQPPPPG\FK*FSRLSLQSS*D YSCVPPRLAFCIFFW*KRGLTMLTR LVSNS*PQ/CDPPALASQSAGITGMS HHTQPHSIVL
4402	9899	A	4698	33	397	NAYNQLKVCASSPWLFCCANFSSY YFYDSHNVIQG*NMTYCT/VM*YLL ITGSLSAHLKNMSLKRIMKSYRSGA ESATEEPFTILYESQFSVGGNELDFQ VKTLSSLPEVVIVHGSQDNNATA
4403	9900	A	4699	2	371	LNTVIANGVAMASRPYQPTHVNVH IHQESTLTHLLKAGGTLKKTLEHFG DTVSSSTATIGYQLALWVTQILLGR *E/CVILECVLILGPWTALSASRCF WAESVEIVPRAGAIVHDKQPVKLA
4404	9901	A	4700	3	441	GFEDKVFYVWFDATIGYLSITANYT DQWERWWKNPEQ/ALGAEDNYTL VSHLIATEYLNIEDGKFSKSRGVGV FGDMAQDTGIPADIWRFYLLYIRPE GQDSAFSWTDLLLKNNSSELLNNG NFINRAGMFVSKFFGGYVPEMVLTP
4405	9902	A	4701	2	375	CITRDLKWGTPVPLEGFEDKVFYV WFDATIGYLSITANYTDQWERWW KNPEQVDLYQFMAKDNVPFHSLVF PCSALGAEDNYTLAKLLDLKKQLA VAEGNPLKPLKARRKSKRPWLIESH FNR
4406	9903	A	4702	1	3093	
4407	9904	A	4703	2	2717	GEMRLFVSDGVPGLPVLAAAGRA RGRAEVLSTVGPEDCVVPFLTRPK VPVLQVDSGNLYFSTSAICRYFFLLS GWEQDDL TNQWLEWEATELQPAL SAPLYYL VVQGKGEDVLGSVRRRA LTHIDHSLSRQNCPLAGETESLADI VLWGAQYPLLQDPAYLPEELSALH SWFQTLSTQEPCQRAAETVLKQQG VLALRPYLQKQPQSPAEGRAVTNE PEEEELATLSEEEIAMAVTAWEKGL ESLPLRPQQNPVLPVAGERNVLITS ALPYVNNVPHLGNIIGCVLSADVFA RYSRLRQWNTLYLCGTDEYGTATE TKALEEGLTPQEICKYHIIHADIYR WFNISFDIFGRTTTTQQTKITQDIFQ QLLKRGFVLQDTVEQLRCEHCARF LADRFVEGVCPFCGYEEARGDQCD KCGKLINAVELKKPQCKVCRSCPV VQSSQHLFLDLPKLEKRLIEWLGR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPGSDWTPNAQFITSWLDRDGLKPR CITRDLKWGTPVPLEGFEDK\VFYV WFDATIGCLS\ITANYTDQWERWW KNPEQVDLYQFMAKDNVPFHSLVF PCSALGAEDNYTLVSHLIATEYLN YEDGK\FSKSRRVGVFGDMAHDTG IPPDISR FYLLYIRPEGQDSAFSWTD LLLKNNSELLNNLGNFINRAGMFVS KFFGGYVPEMVLTPDDQRLLGHVT LELQHYHQLEKVRIRDALRSILTIS RHGNQYIQVNEPWKRIKGSEADRQ RAGTVTGLAVNIAALLSVMLQPYM PTVSATIQAQLQLPPPACSILLTNFL CTLPAGHQIGTVSPLFQKLENDQIES LRQRFGGGQAKTSPKPAVVETVTT AKPQQIQALMDEVTKQGNIVRELK AQKADKNEVAEVAKLLDLKKQL AVAEGKPPEAPKGKKKK
4408	9905	A	4704	180	490	VENGNNSLTIMNRRARQKINKEVA DL*NTMNQMDLTDIDGTFYPKAEY TFFSSKCGTF*RTDHMLGHKTS\LD KFKKIKVIQNYLFNHNGVKLEINNS KKMRKF
4409	9906	A	4705	2	405	KNLNNRLFIFP*IKEEIKRQIRK*FEW NEKEKTIYQNLWDAPKAKLKEKCI VLYVKEETSQITDLSFHLKTPEKEE HVKPKVNRRMEIIRIRAEH\AVKYRK PTETNETKSWSFENFSKIDTPLIKMI RKKKVD
4410	9907	C	4706	217	486	MDDPRGHASPVTRTQKPQASRLLV GLRAGGLSWGHWGRGKPPRGRV PAAALGAAVVAAMASPDWPAGP KQGRWADLAALLCGLRPA*
4411	9908	C	4707	13	216	MLYWDCKRYKVKDKTQAWDFAG NISVKGAELSQTRAASGPRRQAQVT FSVWRGGLQVMAEEGRVDVC*
4412	9909	A	4708	132	1424	VKHGPQGGPRRQAQGD\QVFGVGV LPGEWPEEGTQKGGPPLKTLGTGD GDKIGEPTRAP\RFRTGQPGPRDGL VGPGGELAKPWGPPRGLGPASCPP GNTPLPARPEY*HLGWVWGP*RMG QGNLGVPSK/PVFGSSGPNVGSTNC DNFGSFGLSVPMFPNGPIQALFEG DLWDLGRTGHGTTGPGQCKPLSPG PKKLQGL*TC*SSLALQG/RLSLGAQ SGGRGKQSESESPCPNP*APPVVG YGITRPVGFGRGPSQPG/LMGRPGSS ALWA*NPELPNCPGLPQPCPQEV QSFGPPGVRRGLKGGQDCHRRG EGSSKCAQGGHPAPA*WNPLVYTP ASPFPRPASGKPRS/RPSCGLRAP* HLRRPCLTPPFRPQGLLGSSPCPKP APDSGLLHSP\TSPRGLSGQCNP LHPQLNQSNRDR
4413	9910	A	4709	1	340	RHEERTTGILTSVGLASDTSLICVIE DFFDTALIISRSSSEGIQMLDSFLLS L*LLVTEETVNHL\QQEDRPCMDTL DCG/LQVAISEALRRLTTSKSRDDL

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						HIWYDDESIV
4414	9911	A	4710	12	398	TYLDLPLPGFCIYDF/VPPFSSSECFIF VFMVCFFLAFILSFSSSSSPNSFFDLF FLALPQLPTLRGLFV*ALFQILSWVV FPVKFSLGCVFYLFQFIFKQLAFFH HV*ETFSVPFLICKYWDD*TYFS
4415	9912	A	4711	111	453	YPFIIITFNTLGVAGNCL/KLTYTI** MPTANIILKKLKAFSLR*RTR/H/GCP QSI*ARRII*DIQIAKEDVKLYLFTDD MILYVENPEESTQKDLL\NKVNVKS GYNINMIIRCISM
4416	9913	A	4712	1	184	SSRDILLCTDIASRGLDSTGVELVVN YDFPPTLQDELAARRRRSLPGLASS VKEPLPQAT
4417	9914	A	4713	1	1630	MALTRPVRLFSLVTRLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRRNLP RPVLVRPGLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQEAPAVRKLSS KGSFADLGLPRVLHALQEAPEV VQPTTVQSSTIPSLLRGRHVCAAE TGSGKTL SYLLPLLQRLLGQPSLDS LPIAPRGLVLVPSRELAQQVRAVA QPLGRSLGLLVRDLEGGHGMRRIRL QLSRQPSADVLVATPGALWKALKS RLISLEQLSFLVLDEADTLLDESFLE LVDYILEKSHIAEGPADLEDPFNPK AQLVLVGATFPE\GVGQLLNKVASP DAVTTITSSKLHCIMPHVKQTFRLR KGADKVAELVHILKHRDRAERTGP SGTVLVFCNSSSTVNWLG YILDDHK IQHLRLQGQMPALMRVGIF\QSFQK SSRDILLCTDIAS\RLDSTGVIELV VNY\DFPPTLQDYIHRAG\RVG\RVG SEVPGTVISFVTHPWDVSLVQKIEP AARRRRSLPGLASSVKEPLPQAT
4418	9915	A	4714	79	410	IVYWVEVENRDHYAAYLGWEEAP YSDRAYAPQEKDLGPMDIRIGLL*K NWIPLQDDLYPVDMLHTSVG*EMEI LNNCRNQGV*RMSKDRRETLETYQ QL/L*LLQTSPLYLA
4419	9916	A	4715	185	449	TTILAWGDYLSLENSRSGPN*L*LLS GCTVQSFGLDWNGLLK*DSLTRLP ALCSLQLGRK\VETITHYDCEGLGL KHLWKPAVEAYG
4420	9917	A	4716	154	364	MWRWFSLPPFSLAGVELAPPVSRR SPRGP/TPYGLPRVPLWPLHSTALYC P\PSRPTSAPFTPHPLPKLRG
4421	9918	A	4717	9	1805	SPATSP*ETAGPVKRSRNGSSPAADP EALSPPTARLQRVTVPPI*LNQQLSS PLHFAAGGGHAEIVQILLNHPETDR HITDQQGRSPLNICEENKQNNWEEA AKLLKEAINKPIEDPLAILILFDEAR YNLLKGFYTAPDAKLITLASLLLQI VYGNYESKKHKQGFLNEENLKSIVP VTKLKSAPHWTNRILHEYKNLSTS EGVSKEMHHLQRMFLQNCWEIPTY GAFFTGQIFTKASPSNHKVIPVYV

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						GVNIKGLHLLNMETKDFQYFYV D
4422	9919	A	4718	200	529	EDVSKPVPWTLNGSCTSPLISHSDN QKCPYPFVIPAMGNPENIEDAYVA VIRPKNTASLNSREYRAKSYEILLHE VPIEGQKKRERKFYWKRNFKATV K*HKAYWIT
4423	9920	A	4719	177	321	QTCSMDTKWQLYISPHQS**QPEMP SIFSSDPSLQCVLIICKRLLS
4424	9921	A	4720	166	627	MWRWFSLPFSLAGVELAPPVS/S KDTERSHPYGLPRVPLWPLHSTKW VGQSPGEGGQGPSLSHSSFPFPRHS SPAQLPVAEKPSVAKRKPS*GFPR PTRAPKAQVSGVGDPPAHLFTVLP SPRTSAPFTPHPLPKLRGPRSSKALA FHSA
4425	9922	A	4721	3	610	STFNNEP*PEKQEQNKHKIRRKQI IRA*INKIE/TKNQCKRTMKQKVAFF QKLNKTDKPLARLRKKRQDKIRNE KDITTDTAEIQRIRGYEQLYANKL ENLEEIDNS*THTTY*DLQEEIQNL NRLITSNKVEAIKSLPVKKS LGPDG FTAIFYQTFKEELIPILLKF*KVEEE RVLPN*FYEASITLMPKPKDKDT
4426	9923	A	4722	1	454	LAHCNICLLGSSNSASVSQVAGITG GCHYTQLIFLFLVEMGFHHVGQVG LELPTSGDLPALASQSVGITAVSPLC PTRIIFFEAESCLCWPGWSPNPGLKQ SPCLGFPKCWDYQPDLTMP*FYL LELEIKFGVHVLWKSFLIKIENYYC
4427	9924	A	4723	1	318	KEECNKEEKESREKK/NEKEIE*KE EEVRKEEKSLNKDKDKKRRRKREK GEGRKKEGILKVKKDGPNPSNGHA RMPKER*LYDVVRGTPHSSDHGDT AIFQTCIL
4428	9925	A	4724	42	200	LICT*MLIVALLVIARNWKQIRC/SST /DEWLNKLW*IPMEYY*AIEKEPTIG TC
4429	9926	A	4725	50	403	VVYHVMVLLKVICHHFLTLFFS FRSLILYLFILFMISLYLSCFLYNFL FIPSSIFSICFLMIIVLI*FFFYALFIH FNPIILYLN\YLLSLFLIESLFDYYLCL ISFVIFY
4430	9927	A	4726	3	282	VQGQEPLTASMLVAA/PPQEQQQM LGERLFPLIQTMHSNLAGKITGMLL EIDNSELLHMLESPELSRSKVDEAV AVLQAHHAKKEAAQKDSKAK
4431	9928	A	4727	780	1249	LVVFMSIPLCSSTHPSILQGLKLVPL EQGQPPPLLFHIVRCSIEQALNHH QVLSFPQC*PTAFPGSQAPQPAVHV QGQEPLTAS\ML\AGAPPQEQQQML GERLFPLIQTMHSNLAGKITGMLEI DNSELLHMLESPELSRSKVSWSGSDP AASVLM
4432	9929	A	4728	510	2771	NLEPSHQDRGEVQSRGEGRIVRRAF CLRCCGRGSRPPPVSVSPSPPTPA RPRRAGATCEPARARAPAPKAPLCP

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						AAGPIRSPLAGLGVVGGGEMNAAA SSYPMASLYVGDHSDVTEAMLYE KFSPAGPVLSIRVCRDMITRRSLGY AYVNFQQPADAERALDTMNFDDVIK GKPIRIMWSQRDPSLRKSGVGNVFI KNLDKSIDNKALYDTFSAFGNLS KVVCDENGSKGYAFVHFETQEAAD KAIEKMNGMMLNDRKVFGFRKSR KEREAEKGAKAKEFTNVYIKNFGEE VDDESLKELFSQFGKTLVSVKVMRD PNGKSKGFGFVSYEKHEDANKAVE EMNGKEISGKIIFVGRAQKKVERQA ELKRKFEQLKQERISRYQGVNLYIK NLDDTIDDEKLKKEFSPFGSITS AKV MLEDGRSKGFGFVCFSSPEEATKAV TEMNGRIVGSKPLYVALAQRKEER KAHLTNQYMQRVAGMRALPANAI LNQFQPAAGGYFVPAVPQAQGRPP YYTPNQLAQMRPNPRWQQGGRPQ GFQGMPSAIRQSGPRPTLRHLAPT GSECPDRLAMDFGGAGAAQQGLTDS CQSGGVPTAVQNLAPRAAVAAAAP RAVAPYKYASSVAAALILPYS LCRH PS/PAVHVQG\QEPLTASMLAACNPP /QKQKQILGERLFPL\IPTMH PNLAG K\ITGMLLEID\NSELLH MLESPELSR SK\VDEAVA VLQA\HHAQERSCEPGR CCCCCYLLDPRKTD SKAK
4433	9930	A	4729	7	365	LYTRHPPSPSCIMTACFGSHIRY RSD *VPTPVL RPAVIRSVGGGDC SERLG LRPRPI/PELGPHTPTR PPPPWQNV QRADPVAVTPCRS REGSQAEP LPRG RGAVSSSTTR PGLPAPNRP
4434	9931	A	4730	1	1520	AEGACGPRQPKNKGAGAPPQGP ATH LPGPRSGLSSTATMTANGT AEAVQI QFGLINCGNKYLTAEAF GKVNAS ASSLKKKQIWTLQPPDE AGSAAVC LRSHLGRYLAADKDG NVTCEREVP GPDCRFLIVAHDD GRWSLQSEHR RYFGGTEDRLS CFAQTVSPA EKWS VHIAHPQV NIYSVTRKRYAHL SARPADEIA VDRDVPWGVDSLITLAFQ DQ RYSVQTADHRFLRHDGRLVARP EPATGYTLEFRSGKVAFRDCE GRYL APSGPGTLKAGKATKV GKDELFA LEQSCAQVVLQAAN ERNVSTRQGM DLSANQDE\RP TRRPSSWRSTATPKS VPSVPT RASTGR*RPPGACSPPPPAR MPAATLTSSGVTGASH*GRP MASL* PPRRMGSWPPRWRQ QGTQSSSS*SS STAPSSCSA GSMASAAARSRAPWT PTAPAM TSSSWSTMAPTTSKTPQAN TGRWAVTPRSPAAATLLWT SSSSS ATITRWPSRWAGAT
4435	9932	A	4731	131	677	PSSLS/CDIFLRSPISTPSPSPL RPTPTS TPVHVKQGTAGSVIN NPYVIMDKQ PGQVIGATTPST GSPTNKISTASQISQ GTGSPV PKIHGSSFVTSTVKVIKQE

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						PGEAPHVPATGAASQSPLPQYVTVK GGHMAVSPQKQVITPGEAIAQSAK VQPSKVL/GQIG*CLPTLARADLLYS VC
4436	9933	A	4732	131	362	PSSLS/CDIFLRSPISTPSPSPLPRTPTS TPVHVKQGTAGSVINNPYVIMDKQ PGQVIGATTPSTGVY*IHICTI*RV
4437	9934	A	4733	1	4461	
4438	9935	A	4734	2	614	STTTERENYRPIFLMNTDGRILSIILP SQI***MKKIIYHDQVGFIPGMQRWL NVHK\TMHVIHHINKMKGKNYLIIS ADAEKSLGKTYHCFMMKTLNKLGI EGTLNIRKGIYD*STANILLTGKN*K AFPLRTGIRQGCPLSPLLNTVWDIQ AKVIRQDKQIKGIENGQEEVKLSHF ADDIILYL*TEKPKDSTKLLKWVN
4439	9936	A	4735	164	613	NLNMEATGTDEVDKLLTKFISAWN NMRYSWVLKTKTYFSRNSPVLLLG KCYHFKYEDEDKTLPAESGCTIEDAT *LREM*KNFRKDSISRIWLTREEFP QIEGSALTDCGWGCTLRGTGQMLL AQGLILHFLGRAWTWPDALNIEKLE L
4440	9937	A	4736	40	359	
4441	9938	A	4737	4274	5256	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLOHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVT*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVDTT KFYTAKNMIKDILKFJETGYNLSQK FKIDKFFNVFRRYVYMMVVIDFVLV SNIILPKFNHLC\TH\TH\THLTLFST YLKNDRDKTIMCKLSLIG*LAESLEF GGSGENV\DYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV
4442	9939	A	4738	133	359	LLNFMLLFHRYYALKVSYFKSSLDL KLELLWNKYWVNTLSSSSLLTVS/ DYTCKECI*ILSKLHSRLISETLFHRK
4443	9940	A	4739	1	353	NWTL*TLKKIFSLKDAIKRIKIQSVR WKKIFAKHTSDKGVES\NIYKELS*I NKASSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSYHYTSIRVA KMKKTDYVTSW
4444	9941	A	4740	1	375	LVPKRA*YWHKNTSSSSSSSSS/PSS HLHIYSQPKFRKGTKKIHW*KDSVF HSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSPMLIQENTG/IMLQD IGFGKDYLKTSKAQATKQK*TRKH WEMLQDIGFGKDYLKTSKAQATK QK
4445	9942	A	4741	1	296	FRRSL/DSVAQAGVQRRHLGSLQAP PRGFTPFSCVSLSASWDHRSPLRPA NFFVFLVETGFHVLARMVSIS*PCD RPT\SGFQSTGNTGVSHRTWPLLL

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4446	9943	A	4742	3	380	FLEEYNPPKVSQEEITSSSSSSSSSSSS SSSSLSSDIES/VIKNTSSNNKKNP PDGFTAKFYQM*KDELISTLLKIISK/ IFHSNSFCE*QTTR*FAISITWRAKPD KDTPQKEPYRLISLINIHSC
4447	9944	A	4743	3	369	SFTLIKKT KDIIIRKANYKTMSLRKIA AVILNKILAN*IEH/RJKRIIHHNQIRF I/SGTQVWLNI*K*INVTHHNRLKK KNYMIILIYEETFDKIKHPFM/IK/V LSKLGTENFFKLIKHIWRKI
4448	9945	A	4744	70	345	KVWGEEKVWYWQKMTPIVQWDRT ESPQIGN*SLTKEIQWRKDSLFNKW *GNHWTA PFSS/RSLNLNKDLTAVT KIKSKWVTDLNVKHKTIKLL
4449	9946	A	4745	3	345	KFNNDDEMDKFADRQKL PYLAQEE RQNLN/*PYLLKNLNVQNLPISKTSA PDELICKFYETF KNEIILLCSLFQK MELSQHIHDSNLT LTQKI*K*YRTE ENYRDISLINTYAK
4450	9947	A	4746	35	355	PHPPWWSLSSSPPSQSFLPSPAYM PSPSGNSM/CYLSPSRGM*APSRQGP SSFHQ LCPKCLKG CWARHMPSK *G WNGNPFVSLNYPWARNRPSLLTH FVMWEAPRP
4451	9948	C	4747	27	416	MMKR LGMFNIQHCKKLSSWVLLM KYLGNAPPSSSCLMRGNYSTWKMN SPTISSPSSWENEDRRSASLHLPKLSI TGTYDLKS VLGST GASLKVFQQWG AGPLPGFTEGGHPXKVFGGPCIKAV LEPFDE*
4452	9949	B	4748	5	763	MPSSVSWGILLLAGLCCLVPVSLAE DPQGDA A QKTD TSHHDQDHPTFNK ITPNLA EFAFSLYRQLAHQS NSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNL TEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEAFTVNFGDTEE AKKQINANGTRPFEVKDTEEDFP PGGDHREGAYDEAFRHV*
4453	9950	A	4749	11	368	GLKSLIN*LLAVYPREQTTLEEV MR DPWVNS/GSGVA FDN/TE*QILDHLN PETTQLLVAMGFQADNLSVAVREQ LFSYAMATYLDLEHTLLKKRSTIRS QTLPPGDPTWPLYIEVCTFR LS
4454	9951	A	4750	175	349	PSVAGRPRRKGGGRQPAQTRA VGI AGTEPPLY YLGLWGPVGVDQ G*QP ASFPGPPQPVPKAPSNTKEA\SPSNA HSSSLGRLPSSPLPRPASNTGSLSPR QGTMTTL*GATHLPQHSD*EESTRE SPPTLEQLPPSVQLIRMP CPPLPVT Q
4455	9952	A	4751	2	354	ENCQINN LRFLHRKP KKEYTKPTA SRRK*IVNIRIERNGIEQKNNRTSSSS SSSSSSSSSSSLTFR*MDGRRSSSSS SSSSSSSSSQ*QRK\KTRLIKI*NERG DITADLTEIK*LLILQKLNNY
4456	9953	A	4752	121	363	WRDFKTKTVIRAK*GYLIITG*NHO

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						EDTTVINMYAPKTA PKKYM KQKL TDWKRAV/DSKTTAGDLNILLIMD KTKQKINRV
4457	9954	A	4753	178	439	GPALINALLKWRIPSGEDREP*GRD WEKEKE/R*LEEGRERGGKGEGGK RRNKGRKEGREERGKGERE EGYIM CIHGIGNRSLAVLGA
4458	9955	A	4754	193	355	GLFSIEEH*HDSTHLGINTLALISRLFI EK*LLKR VYQVTQACELYAWNPN DQCLPPPLVRPVQHRGAYPGEDWQ IDYTQMPPCKGFKY*LVFIDTFTVWI EAFPTKIEKAIV
4459	9956	A	4755	3	227	NIKIGKEEVKLSLFAGDVYLEKPKD STKKLLELI/NFSKVAAY*INIQKVA FLYANSE*SEKEIRNIIPFTIAT
4460	9957	A	4756	115	487	CSLCFVAEWSPWCGWTQLIYPW*/E/ ITHSPVHTQRLGLETHRTAEMRLFS FSLFFFLRQSFALVTQPGVQRCDLG LLQPPSPGFK*FSCFSLPSSWDYRHA PPRLANFVFLVQTGF\ SMLATL VSN
4461	9958	A	4757	2	436	GTEAEQPSYQPGLELPQGDQEEP*G LAGKTGLGPRFRPTTGGSGQTLLLEV EGLSHSPFQSPGIPGEFEKARKIL*A GS*HNSC*ATE/GLGERPGGICGVSS SVSTQGPMP*CGQQGN*ALESCRG ATAALSEQSPASPSSRAARA
4462	9959	A	4758	76	194	
4463	9960	A	4759	310	551	SSKQSSAKPPFCLPNPGKVCRSGRS RT*GCNLQKGS GPEKGRRFGHPPE WTIFPSVQRQQA*FSDSPPTNGIP GEWKG
4464	9961	A	4760	1	1165	LRWQREEGQKAGVHVGTMTQHLR PQPGAAVLPAALAPPPKHQFSLQAS SPSRLGRAGLAGGPSRAGLLC*WRR LSFLPSSFPSPRSWGARSRRRARGQ VGPREPAGRSAGDRGVGGRFGGPL ALSFFATGLLRASCAPAFQEVTVLG KAVQWRLEPGEPFTEG*ALAGTLG LGKH*QGRQK*GWG*PSLANARQ LGKPLQVLGWLGHVEGRPGRAVK VTGVRSWSCLPGSTGVGDRSRATQ LPAGP*VSLRVDQGEAVTGWGGRA GARGSPGRQGEPRHSARG*GPESLP LPVTRNSLVGGLSESN*ACPCR*QK ERLSIRGVPERRPFGPEPGRGPASC SGLPTTGGTEERRKEGKRAA A ISKA ALPGWARLPDQPGPAATGSK
4465	9962	A	4761	1	389	EETLPLFADDMILYIIKKKQKTKKTT KESTKRY*N**MNVFGKVAGYKV NTQKSIN*QYTI*KVKLAS\FSSSPQK NKIGINLTKEIQNVYSENYKTLKEIK DLNK*ESIPCSQIRRFNIVKMTVLLK LI
4466	9963	A	4762	1	346	RACL*FQLLGRLRQGDGLSLGIRGC SGPGWHHHSPA WATEKDPVSKTNK QNIKH/LRKSPLSRDEKILREKREEE KILAYHYLEKSAIYSISFFFLTKHILN

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						TPVCWFSSEHIIYF
4467	9964	A	4763	2	468	FPSLPSSFFSRFLFCITVMF*VLDPLS LSYLTLLILPHLKFNFKEK/CVNH/CF LLMLLLFLLL\CTY*MCLGPFYFLP CLSFSSVFHFLSLCCIIGNLFRYIFKFI NFELC\CYVLYT*DLFYF*KFSLVIF* IY*FFLSIMLSL*VFFHLKHFIF
4468	9965	A	4764	3	364	RNLKLISEYCKISG*KVNIENQ\VF YISNGQVEFEIKNTIPL*AHT*KMKY LDINVTKYVQDPYEENYKILMKKIK EQME/NIPCL*/I/GRNLTKTSLVLPNLE **ITAIPIKIPASYFVDTN
4469	9966	A	4765	1	755	EESILEEVLEALTSAGEEKKIDRFFC IVEGLRHNSVQLQVACMQLNNGLG TSSGELEFKLHIKNEFMPCGLKEILP NLKCLKNDGLDIQLKGFDEHKKED LVELSHRLEDIRAELDEAYYVYNM VWSTV*ETRAEGYFISILQHLLLRN DYFIRQQYFKLIDECVSHIVLHRDG MDPDFTYRKRLNLDLTQFVD\CV QAKLKEFEKALELYKKEFEFTD PQENSR*NCAKKEAQIYGPFPNSK TF
4470	9967	A	4766	12	321	KSCDWAERLVTLV/WN/PYFKNLSN SYYKQLSPMGGYLNWAHTLTEWI IDNILDQLIFPKLQKEVG*ESWETVV ITNHRDLFSLWLHYLSAVKTPGINGI COHNY
4471	9968	A	4767	2	375	MSSPLPSPWSPCLLPQAPGPTLPVP PAETLSVSPACFLRLPINSPSQ*APA WRQLTADWGGHSALGLPGCPGPSI TWPSHSASHLLPQRNQGPMLGYA HLPGHLPNTNVLPSGHTPALERPK
4472	9969	A	4768	3	338	QSLALSPRLECSGAILAHCHFC/LPG FT*FFCLSLPSSWDYRSPPT/RQLIF VFLVEMGFHHLGQAGLELLTL*SA HLGLPKCWDYRHEPPRPAQRPKLK NLK*LTTVARFTI
4473	9970	A	4769	66	365	LRDEQQHGGPWTSPLSRPPTGKRA RGRSACPQLTH*PGTAARKGASPGR SRALALPTRCPGPACGGREPRLQAR GVP/R*IPPRRGPHGAPSGLP GPVG C
4474	9971	A	4770	3	345	KRGTPLAGEMAEGHCL\CLPLGTEY LTVNPIVHLFNSEIG*KIRPVA\KVR HVYSITASIFFTPLRCLCGEKHISGLR ARSGIVLSLELNHGIDSFAHM*SCDL ILIIITLLSYYI
4475	9972	A	4771	2	352	KRGKPLAGEMEEGHCL\CLPLGTEY LSVKPIVHLFNSEIGKIRPVAGGR HVYSNTASLFFTPLRCLGGEKHKSG LRARPGIVLSLELNHGIDSFAHM*FV DLLIIITLLSYYIPFR
4476	9973	A	4772	1	296	QRSVKISISENGNSHMEIVSFLIFCQ FLLHVFCSTIHIYDCYIFLLI*YPINRQ CLFAY*YSDIKFYSDIN/ISYFLCLLC MSFYPLSTCIYMGLVFIF

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4477	9974	A	4773	2	859	GRWPTQPTSLQGGQTLGDVREAFS RRP*NGERQGAPPACPLPRSLGLWR PWGPLSVTT*NRSWSCYCWLRLV/ GWKGSRAVVKALGSPEAAWHLLG PDAALQPCHFSQPQRRRCRGRPPFLP LSGWAGPWECWPTCQAGRT*IPEG GGSC*GPQVNDLQRHTEENVLRC DLPHPALAAWGTVSPG/SHAPAQ*T EV*RSAQSSFRPQCPLTSPARGTPGS SRLLCGVPP/CGPLLMLCPLPVPEV GLGPFLRELLNTKKLNCFVNKQKV PNKPACHLGDGPSLPHQIC
4478	9975	A	4774	158	517	RCRSGYVDQVAGLFCFVLRQSLTF VTQAGVQWHDLSLQPLPPRFN*FS CHILLSSWDYRCMPPLANFGIFLR/E RGFTMLGMLVLNC*PQ/CDPPTSAS QSAGITGMGPPHLGLSCSIKK
4479	9976	A	4775	1	165	GSLLPLLFIILEVLAKAIRQEKSIGN EKEKV*LSLLTDHMI/YM*NPTVKK LTT*KLTT
4480	9977	A	4776	2	516	QNPCISERQYCCEKLPLERSSRPQDS AGQPVT/HAHCSLSSTVDLCPLLAT HRISCWH*QDEVQGGRD/SVDKGD LVALSLPAGHGDTDGPISLDVPDGA PDPQRTKAAIDHLHQKILKITEQIKI EQEARDNVAEYLKLANNADKQQ VSRIKQVVQKKNPAAQTIGQLD
4481	9978	A	4777	154	406	CTDIQGYPGSRSAQAGVQWHNL/ CLSLPSSWDYRRPLPRPANFLYF*ER RGFTVLARMVISIS*PCDPPASASQG AGITGVSHRT
4482	9979	A	4778	1	429	ARLETNSRSVAHGGVQCHDLSSQQ PPPPGFKGFSGLSLPSSWDYRRPPPC PR*F*YFY*RRGFTVLARMVISIS*PC DPPALASQSAGITGLSHCAR/LERES HSIA/RAGGQWFHLGSLQPPPPRFK* FSCLSLPSSWDHRCPPVD
4483	9980	A	4779	1381	1787	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVISIS*PRDPPTSA SQSAGITGMSH
4484	9981	A	4780	1147	1553	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVISIS*PRDPPTSA SQSAGITGMSH
4485	9982	A	4781	1456	1862	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVISIS*PRDPPTSA SQSAGITGMSH
4486	9983	A	4782	889	1295	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D

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						SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
4487	9984	A	4783	743	1149	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
4488	9985	A	4784	2583	3580	DRVSLLLPRLECNAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHAWLFFCS/RD TVSLCYPGWSRVA*SRITATSA\PL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR\YPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYLYFHRDEGLCCPGWS* TPELK
4489	9986	A	4785	1966	2372	LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH
4490	9987	A	4786	3	305	FFFLRKSL/GSV/TQAGVQWRGLRSL QPPPPRFKRFSCSLSSWDYRCVPP RPA/NFLYF**RWGFTTLARMVVIS* PCDPPASASQSAGITGISHRAQPIKY
4491	9988	A	4787	1172	1688	VFFGVFVFVFVFVFFPKLTSGTIPWA SPEVMIYPPTH*VCEAPSPFYVFSH LFSVLQSPSHLVCLFLCSF*DGVSCLR QAGVQWRSLSLQPLTPWFKRFSC LSLPSGWHH/RRPANFCIF/M*RRGF TMLPRMVSISSPRDPPASASQSAGIT GMSHRARPQSSVFKQSFLSR
4492	9989	A	4788	641	1074	VLNLVEFVTRELAFTSNVFFCFFVF FCFFLRRL/DSVTQAGVHWLDLGS LQAPPPRFTPFSCSLPSSWDYRRPP RRPANFLYF**RRGFTRLARMVVIS* PCDPPASASQSAGITGVSHRAPTN VNKAITNGLFTYFFNEE
4493	9990	A	4789	7273	7925	IVSLFLFILLVFWWWCFFFFFFFETE SCSVAVAQAGVQWHNLGSL\QAPP PGFTH/LFSCSLPSSWDYRRPPRP VNFFFFFFH*RRGFMTL\ARMVLIS *PQVICPASASQSAGITGLSHRVRQ GPHNLLTNQVKNKFFFFFFLETESHV TQAGVQ*HDLGSLQSPPGKRFSC LSLLSS*DYRLPPHPTHF/CVFLVE NGNSPCWPGWS*TPDLR

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4494	9991	A	4790	156	391	IPHSYIRKFYSFKMAILSP/KLIYSINA ISKKIK*AFLKKTDELILTFI*KGKES VLDKPILKKKNIVGLKICDFETYY
4495	9992	A	4791	365	506	GRHHACLIVDRALVFPS/CQVGRAA HFLPLPGPCPAWTPPSRSLRPGP
4496	9993	A	4792	2	503	LTHPAGARPVLLTTPESFEGPCFGTP HGQSLSQSAFSRGSLSGDTVGVGTG QVGS/LLSGGGVRAG/GAGGGGGA GFGSRLALKAAGERGEKPREPVPPP *QR\GPHTKAPWT*AGQGQPPGRAC SPG/PPAEPASQPLTPGPGRRLPGGK RSRRDRARGAARKMGLLFPLD
4497	9994	A	4793	3	389	FQDLIKR*KATIKTLWY*HKNRY/D IDQQNRIEN/SKHRLSHLIFDKGTRTI Q/YGREQLSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSP IPDIGFHNDFLNMTPKAQATTCK
4498	9995	A	4794	27	285	VFFFFFFFFLRRSLALLPRLECSGTIVF LVETGF/TMLARMVIS*PRDLPALA SQSAGITGVSHRARPASFNFLTINILP PLLLWTF
4499	9996	A	4795	12	336	SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSRLTFSSHSLNMELVQD LTASAPMYSSTRDPP/CLGLPKCW DYKREPPRAH
4500	9997	A	4796	74	463	HISQHDSYQLQVLLASYKTASFLFFF LRQSL/DSVTQAGVQWRDLGSLQA PPPGFTPFSCPQSPK*L/SSWDYRRPP PRPANFFCIFIVEKECFTLLARMVIS WPRDLPASASQSAGITGMSHRARP AQVS
4501	9998	A	4797	1	337	KKLISGFNVIPIKTPANPCVKIDKLIL KFIWHCKARRIGKAMWNKIKYGGI IQ*DLKICHKVRIEIVWY*LQGRQ/I DQ/WEQ/IQSPEIDPNIYSHLTYDKSP TAIQRRIYPF
4502	9999	A	4798	3	331	KNYKTLLREI/KEELN*WKDIPRLW LRRLNIVKMSFL/SKFIYRLDSIPIK/ MPSRHLFL*KLILKQILKFIWEGKGP GIAKTILKKNKFGGFTLLNFNTYNK AANSRVLVLG
4503	10000	A	4799	3	340	INRLNIFTMAIFSTLIYRFNTIPIKIPA GFVEMDKLILKLWVKFAHGIGKT TLKKNRVP/IKFSSSSSSSSSYWNE DRNINQWN*IDNLKINPCVCGQLIF NKDAKTNEER
4504	10001	A	4800	46	195	SPATLGRPEVGPDS*GPGDRDHAGL TMVKPPVFYLNKYWIMRSGDRDHP G
4505	10002	C	4801	353	442	MPLLYVQRLFARTGLCATLFGMM SPLYV*
4506	10003	A	4802	1	273	FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPE*LGLQA PATAPG*FFVFLVETGLCKHNEKSP LSVQGRIYVLRNQKG
4507	10004	A	4803	57	231	

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4508	10005	A	4804	2	169	
4509	10006	A	4805	698	1231	
4510	10007	A	4806	58	2674	
4511	10008	A	4807	7	235	
4512	10009	A	4808	1	245	FFFFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPPE*LGLQA PATAPG*FFVFLVETGFHLVSQDGL DLLTS
4513	10010	A	4809	175	394	NFLRYSHFKKCNRRPGAVVTPVIPA LWEAEAGGS/CRSGDRDHPG*QGE GKRGSLFKFQEVSGAPNKFWSWLPL
4514	10011	A	4810	65	2712	SGSGHCLAEAAASMGPGWGWKLRT VALLAAAGTAVGDRCERNEFQCQ DGKCISYKWWCDGSAECQDGSDES QETCLSVTCKSGDFSCGGRVNRCP QFWRCDDGQVDCDNGSDEQGCPPKT CSQDEFRCDDGKCISRQFVCDSDRD CLDGSNEASCPVLTGCPASFQCNSS TCIPQLWACDNDPDCEDGSDWPQ RCRGLYVFQGDSSPCSAFEFHCLSG ECIHSSWRCDGGPDCKDKSDEENC AVATCRPDEFQCSGNCIHGSRQCD REYDCKDMSDEVGCVNETLCEGPN KFKCHSGECITLDKVCNMARDCRD WSDEPIKECGTNECLDNNGGCSHV CNDLKIGYECLCPDGFQLVAQRRC DIDECQDPDTCSQLCVNLEGGYKC QCEEGFQLDPHTKACKAVGSIAYLF FTNRHEVARRMTRTRSGYTSFIPNLR NVVALNTEGPSNRIYWSDLQSRMIC STQLDRAHGVSSYDTVISRDIQAPD GLAVDWIHSNIYWTDVSLGTVSVA DTKGVKRKTLFRENGSKPRAIVVDP VHGKHRPCT/WPGVLCTCQVTSAT* DVRATIRR*ML/WFPQRTLEKAHLV SGREKQEEIIRCLRVKVLTYEMQ DLGGG*TRL*ITQAKMNAENWL*L EEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVL FHNLTQPRG VNW CERTTLSNGGCQYLCLPAPQI NPHSPKFTACPDGMLLARDMRSC LTEAEAAVATQETSTVRLKVSSTAV RTQHTTTTRPVPDTSRLPGATPGLTT VEIVTMSHQALGDVAGRGNEKKPS SVRALSIVLPIVLLVFLCLGVFLLWK NWRLKNINSINFDPVYQKTTEDEV HICHNQDGYSPSRQMSLEDDVA
4515	10012	A	4811	49	361	STSYPTGSHAFL*PQNVVDAETNS* HINNVLRLKIKLLEENTETKNCHD LGLSTDYY/SVTPKA*ATTTKIDKL ELIKIKNFCTSKDITYKVKRLLIGNNI CK
4516	10013	A	4812	2	346	EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCK

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4517	10014	A	4813	2	356	EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCKSF
4518	10015	A	4814	1	357	VRPHHTNKKRVRLR/VRVNIKVRD KVSTEVKDKIKNQAAVIVKLGVIK AGPWVRVKDWVRLEVKIKNRDQV RGEAEVRRIGQQLRTKTRPKLVNHP KRNGSIN*NHITVECYSTIKKQ
4519	10016	A	4815	1	323	PVRGTEQSNKSWASGLQPGWGAE QLAWGSFNLSKWPSGGGDPQIPILLS RVQNMGRRLAR*EAPCQPQPLPSR RSSPVPHQHL/PPCHPCGASLSPALA WPPPPPSRS
4520	10017	A	4816	1908	2324	ILASSLRANPGFIRNFHLFFFFFYFLR RSL/DSVAQAGVQWHDLSLQAPPP GFTPFSCLSLPNSWDYRRPP/RHHAR LISFFLFLVEMGFTMLARMVSIF*P WDLATSASQNAGITGVSHHTPRP VIKYLPSPPNLAG
4521	10018	A	4817	1	273	RPRRRYPHSWWFL/QEVAIFTLIEKV VFYYSHRLFLHPAFYKKIRKIHKKW TAPIGVISL*AHPIEHA VSNMLPVD VNLRSIRTVLHFHQ
4522	10019	A	4818	3	293	DHVSPGVQDQAGQYKTPASLQKQ KQKTNRHGSAYLWSELLGSLRQED HLNPGVRCSELLLGHCSPAWAAK *DPVC*KNKTKNLIAGGHPRFSWIQ
4523	10020	A	4819	2	170	KLGFIIKIDFSSVKDNVKGMRRAQAT DW/DFIKIKDFSSVKDNVKGMRRAQ TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN
4524	10021	A	4820	52	228	WASGHVVRPYRVLNNFISNQKMD KEDLSGIAEMFKTPVKELLIVL*TCL IVAFKSDNS
4525	10022	A	4821	22	376	TGTVIKIAWY*HKDRHMDQ*NRINS SETNPNI*SKVQRPFWRASSSSSSS SSSSSSSSSSS/PSSSSSSSSSSSSS SSSSSSSFIQNTGINLTDGFLGNVF LDMTPKAQAKE
4526	10023	A	4822	151	379	SIPGIQSWFNIQKSINVFYHIVILNTQ HRSSSSSSSSSSSSSSSY*LMIKF/LNK LGIEGNFLILIKAIHGKPTVNH
4527	10024	A	4823	3	479	RDEVSPHCPGWSQTPGLKQSSCLGL PKC*AYRHEPLGL/ILFFH*ATQETQ ARAGWSYASHFVDERTEAQR/V*G TCPRSHANYVLEDLICVLF*DRVCS VAQAGVQWHDLSLQPPPGFK*FS CLSLPSSWDYRRFATTAS*ILAF*VE MGVRHFARLV
4528	10025	A	4824	1	57	GKRYTRSDELQRLRRAHTGVEKKLV CPECSQRSMRSDRLTGHIRSHQNK GIH*SDELQRLRRAHTG
4529	10026	A	4825	3	602	VDKNHTLSLLCQPSHGDCSRFSAST CLIRSRFHFNFNTFKIF*KLGDSMLT AVSVARDCGMILPQDKVIIAEALPP

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						KDGKVAKINWHYADSLTQCSHPSA IDPEAIPVRL/CP**LRGSSNDSLFC NEWIILSDTGGIFK/HLVPKGSNLG VCVCSHECIATVF*KNLYYCFQLML HGTVFARMAPDQKTQLIEALQNVE
4530	10027	A	4826	3	241	TSFSCLSLSSWDYRCPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR
4531	10028	A	4827	3	241	TSFSCLSLSSWDYRCPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR
4532	10029	A	4828	2	321	KAVLRRKFIATNT*KK*TSQIKNLL KKLQEKNKFKPKVSRRTIQRSEQK *IQTRKPGEKINKTKGSSSSSSSSSS SSSSSSQREDLNQIGNEREDITTGTT EIQ
4533	10030	A	4829	132	290	LVTSE***IYQIFFFSPEMESHVSQA GVRWSNL\SSLHPLPPGFKRFSCFSL
4534	10031	A	4830	645	1201	GGRDLLRTHSVGPSTPQTIPVLTPPG *CACTQDVSPHS/PPMKELWPGA PQGSPGRLSPQPPH*RSPHSPTLW PAL/PGLASTEGWGAIALYILEKNW GREGLNLPPA*PFCPPQSPHGS LVF PSK CASREAPTSNPCLQPQIPRLPSR PKAQ PAPHLGGA AHTRISAGVAR VCAGAFGGQA
4535	10032	A	4832	115	454	TMMTSWINCFRKG*DDVEHHALHI NLRGKKFILFLPIQEGLTRGRKQ*AN TVGHFQLGFRLYKISGLEKLKLSKL STQWLLKPLHPDQL*TRAELLG*ES LDKYDQDPEALIR
4536	10033	A	4833	1	638	ERQSVPGFKASQDRLTLLVRAYTN Q*LKLRLPLIFHFENPRALKNCAYS TLVLCQWNNKA WMSAHLFTGW LTKYFKLTIETYCSEKTPFKILLFI DNLAGHPRALMEM*KEMNVFMPA KTTSIMLPLIASSFN SYLRNRIHRTF VVVAQSWLQCPTTAISDIQIGPVAM GLLLIPSAFVLCWLSIQVSKLKH HSHHSYFLRFWRLTA
4537	10034	A	4834	2	6053	KEILQEYLEISSLVQDEVVAIHREM AAAAARIQPEAEYQGFLRQYGSAP DVPPCVTFDESLLEEGEPELGELQL NELTVESVQHTVQLLGKRQVLQEA LQGLQVALCSQAKLQAQCELLQTK LEHLGPGEPPVLLLQDDRHSSTSSSE QEREGGRTPTEILKSHISGIFRPKFS LPPPLQLIPEVQKPLHEQLWYHGAIP RAEVAELLVHSGDFLVRESQ GKQE YVLSVLWDGLPRHFIIQSLDGSRL RMEAADPGSPALQNL YRLEGE GFPS IPLIDHLLSTQQPLTKKSGVVLHRA VPKDKWVLNHEDLVLGEQIGRPVQ RGSNSQRA WVRGPNTGAPHPGVGS RMGRKRREL RDWEGRGRSPRFQ GNFGEVFSGRRLRADNTLVAVKSCR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ETLPPDLKAKFLQEARKLKQYSHPN VRLIGVCTQKQPIYIVMELVQGGDF LTFLRTEGARLRVKTLLQMVGDAA AGMEYLESKCCIHRLAARNCLVT EKNVLKISDFGMSREEADGVYAAS GGLRQVPVKWTAPEALNYGRYSSE SDVWSFGILLWETFSLGASPYPNLS NQQTREFVEKGGRLPCPELCPDAVF RLMEQCWAYEPGQRPSFSTIYQELQ SIRKRHRPRCSSSAAPAHMLTALHS PGLLPASTLPAGCSAVSSLCPCCCQ GFLFRAETIKPLVPTHEHSWHVHSSG RQVSEGTSAGNIEQARKGKGLEEC AVPTGGSTPLPEGRNDRDLRLPGPE PASEAGGPARGRRTERSGCPGAQL GPRQRPPEQGATGERAPAFACVAA CTRAAVPGRVCVEASMKLKKQVT VCGAAIFCVAVFSLYMLDRVQHD PTRHQNGGNFPRSQISVLQNRIEQL QLLEENHEIISHIKDSVLELTANAEG PPAMLPHYTVNGSWVVPPEPRPSFF SISQDCQFALGGRGQKPELQMLTV SEELPFDNVDGGVWRQGFDISYDP HDWDAEDLQVFVVPVPHSHNDPGWI KTFDKYYTEQTQHILNSMVSKLQE DPRRRFLWAEVSFFAKWLVGNGQL EIATGGWVMPDEANSHYFALIDQLI EGHQWLERNLGATPRSGWAVDPFG YSSTMPYLLRRANLTSMLIQRVHY AIKKHFAATHSLEFMWRQTWSDSDS STDIFCHMMPFYSYDVPHTCGPDPK ICCQDFKRLPGGRINCPWKVPPRAI TEANVAERAALLLDQYRKKSQFR SNVLLVPLGDDFRYDKPQEWDAQF FNYQRLFDFFNSRPNLHVQAQFGTL SDYFDALYKRTGVEPGARPPGFPVL SGDFFSYADREDHYWTGYYSRPF YKSLDRVLEAHLRGAEVLYSLAAA HARRSLAGRYPLSDFTLLTEARRT LGLFQHDAITGTAKEAVVDYGV RLLRSLVNLKQVIIHAAHYLVLDK ETYHFDPEAPFLQVVGWEEAEPMM VLPFRLTEFQDDTRLSDALPERTVI QLDSSPRFVVLNPLEQERFSMVFL LVNSPRVRVLSEEGQPLAVQISAHW SSATEAVPDVYQVSPVRLPALGLG VLQLQLGLDGHRTLPSVRIYLHGR QLSVSRHEAFPLRVIDSGTSDFALS RYMQVWFSGLTGLLKSIRRVDEEH EQQVDMQVLVYGTRTSKDKSGAY LFLPDGEA\SPSPRSPCCVSLKALS SQRWFRTMSTFTRRSFGTICQGWR GCLWYHPWWTSGTTSTRSWPCTS IQTSTAR/VIFFTDLNGFQVQPRRYL KKLPLQANFYMPVMAYIQDAQKR LTLHTAQALGVSSLKDGQLEVILDR RLMQDDNRGLGQGLKDNKRTCNR FRLLLERRTVGSEPDFFSKLAAMFR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GLIFHSSRSNGNREVQDSHSTSYPSLL SHLTSMYLNAPALALPVARMLPG PGLRSFHLPLASSLPDFHLLNRLTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFD GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG
4538	10035	A	4835	1	6606	MGFSSSELCSPPQGHGVLLQMQEAE RLLEGMRKWMAQRVKSDEYAGL LHHMSLQDSGGQSRAISPDSPISQS WAEITIQTEGLSRLLRQHAEDLNSG PLSKLSLLIRERQQLRKYSEQWQQ LQQELTKTHSQDIEKLKSQYRALAR DSAQAKRKYQEASKDKDRDKAKD KYVRSLWKLFAHNRVYVLGVRAA QLHHQHHLHQLLLPGLLRSLQDLHE EMACILKEILQEYLEISSLVQDEVVA IHREMAAAAARIQPEAEYQGFLRQ YGSAPDVPPCVTFDESLEEGERPLEP GELQLNELTVESVQHTLTSVTDELA VATEMVFRREQEMVTQLQQELRNEE ENTHPRERVQLLGKRQVLQEQALQG LQVALCSQAKLQAQQELLQTKLEH LGPGEPPPVLQLQDDRHSSTSSSEQR EGGRTPTLEILKSHISGIFRPKFSLPP PLQLIPEVQKPLHEQLWYHGAIPRA EVAELLVHSGDFLVRESQKQEYV LSVLWDGLPRHFIIQSLDGSRLRM EAADPGSPALQNLRLGEGGFPSIPL LIDHLLSTQQPLTKKSGVVLHRAVP KDKWVLNHEDLVLGEQIGRPVQRG SNSQRAWVRGPNTGAPHPGVGSRM GRKRRREL RDWEGRGRSPRPFGN FGEVFSGLRADNTLVAVKSCRETL PPDLKAKFLQEARILKQYSHPNIVR LIGVCTQKQPIYIVMELVQGGDFLT FLRTEGARLRVKTLQLQMGVDAAG MEYLESKCCIHRDLAARNCLVTEK NVLKISDFGMSREEADGVYAASGG LRQVPVKWTAPEALNYGRYSSES VWSFGILLWETFSLGASYPNLSNQ QTREFVEKGGRLPCPELCPDAVFRL MEQCWAYEPGQRPSFTIYQELQSI RKRHRKHRAFTERKGTGRMCTD RRQHFPFARGAQRQRPKATWAGAG FRGWRTRAEPQRSAPAARGPAGE LQQRAEQGATGGRAPAFACVA AACTRAAVPGRVCVEASMKLKKQVTVC GAAIFCVAVFSLYLMLDRVQHDPT RHQNGGNFPRSQISVLQNRIEQLEQ LLEENHEIISHIKDSVLELTANAEGP PAMLPYYTVNGSWVVPPEPRPSFFS ISPQDCQFALGGRGQKPELQMLTVS EELPFDNVDGGVWRQGFDISYDPH DWDAEDLQVFVPHSHNDPGWIKT FDKYYTEQTQHILNSMVSKLQEDPR RRFLWAEVSFFAKWLVGNGQLEIA

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						TGGWVMPDEANSHYFALIDQLIEG HQLERNLGGATPRSGWAVDPFGYS STMPYLLRRANLTSMLIQRVHYAIK KHFAATHSLEFMWRQTWSDSDSTD IFCHMMPFYSDVPHTCGPDPKICC QDFKRLPGGRINCPWKVPPRAITE ANVAERAALLDQYRKKSRLFRSN VLLVPLGDDFRYDKPQEWDAQFFN YQRLDFFNSRPNLHVQAQFGTSLD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYTSTRPFYK SLDRVLEAHLRGAEVLYSLAAHA RRSLAGRYPLSDFTLTEARRTLG LFQHDAITGTAKEAVVVDYGVRL LRSLVNLKQVIIHAAHYLVLDKET YHFDPEAPFLQVVGWEEAEPMMVL PFRLTEFQDDTRLSDALPERTVIQL DSSPRFVVLNPLEQERFSMVFLV NSPRVRVLSEEGQPLAVQISAHWSS ATEAVPDVYQVSVVRLPALGLGV LQLQLGLDGHRTLPSVRIYLGHRQ LSVSRHEAFPLRVIDSGTSDFALSNR YMQVWFSGLTGLLKSIRRVDEEHE QQVDMQVLVYGTRTSKDKSGAYL FLPDGEA/SPTSPRSPCCVSLKALSS QRWLRTMSTFTRRSFGTICQGWGR CLWYHPWWTSGTTSTRSWPCTSI QTSTAR/VIFFDLNGFQVQPRRYLK KLPLQANFYPMVMAYIQDAQKRL TLHTAQALGVSSLKDGQLEVILDRR LMQDDNRGLGQGLKDNKRTCNR RLLERRTVGSEPDFFSKLAAMFRG LIFHSSRSGNREVQDSHSTSYPSLLS HLTSMYLNAPALALPVARMQLPGP GLRSFHLPLASSLPDFHLLNLRTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFD GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG
4539	10036	B	4836	114	255	VQPRRYLKKLPLQANFYPMVMAY IQDAQKRLTLHTAQALGVSSLKDX*
4540	10037	A	4837	1	452	LDGRQLSV/SRHEG/FP/LRCIDS/GTS ELALS/N/RMQVWFSGL/TGLLKS RRVDERHEQQVHMQLVYGTRTS KDKSGAYLFMPDGEAKP/TSRSP CCVSLKALSSQRWLRTMSTFTRRS FTICQGWGRCLWYHPWWTSGTTS TRSLHFSFN
4541	10038	A	4838	3	3543	QLGRLGPERRGGRALTVCEASMK LKKQVTVCGAIFCVAVFSLYLML DRVQHDPTRHQNGGNFPRSQISVLQ NRIEQLEQLLEENHEIISHIKDSVLEL TANAEGPPAMLPYYTVNGSWVPP EPRPSFFSISPQDCQFALGGRGQKPE LQMLTVSEELPFDNVDGGVWRQGF DISYDPHDWDAEDLQVFVPHSHN DPGWIKTFDKYYTEQTQHILNSMVS

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						KLQEDPRRRFLWAEVSFFAKWW NINVQKRAAVRRLVGNQGLEIATG GWVMPDEANSHYFALIDQLIEGHQ WLERNLGATPRSGWAVDPFGYSST MPYLLRRANLTSMLIQRVHYAIKK HFAATHSLEFMWRQTWSDSSTDI FCHMMPFYSYDVPHTCGPDPKICC QDFDKRLPGGRINCPWKVPPRAITE ANVAERAALLDQYRKKSQLFERN VLLVPLGDDFRYDKPQEWDAQFFN YQRLDFFNSRPNLHVQAQFGTSLD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYTTSRPFYK SLDRVLEAHLRGAEVLYSLAAHA RRSGLAGRYPLSDFTLLTEARRTL LFQHDAITGTAKEAVVDYGVRL LRSLVNLKQVIIHAAHYLVLDKET YHFDPEAPFLQVDDTRLSDALPER TVIQLDSSPRFVLFNPLEQERFSMV SLLVNSPRVRVLSEEGQPLAVQISA HWSSATEAVPDVYQVSPVRLPAL GLGVLQLQLGLDGHRTLPSVRIYL HGRQLSVSRHEAFPLRVIDSGTSDF ALSNRYMQVWFSGLTGLLKSGSLC FLA\SIRRVDEEHEQQVDMQVLVYG TRTSKDKSGAYLFLPDGEASPTSPR SPPSCVSLKALSSQRWLRTMSTFTR RSGFTICQGWGCLWYHPWWTS GTTSTRSWPCTSIQTSTAR/VIFFTDL NGFQVQPRRYLKKLPLQANFYMP VMAYIQDAQKRLTLHTAALGVSS LKDGQLEVILDRRLMQDDNRGLGQ GLKDNKRTCNRFRLLERRTVGSE VQDSHSTSYPSLLSHLTSMYLNAPA LALPVARMQLPGLRSFHPPLASSL PCDFHLLNRLTLQAEEDTLPSAETA LILHRKGFDCGLEAKNLGFNCTTSQ GKVALGSLFHGLDVVFLQPTSLTLL YPLASPSNSTDVYLEPMEIATFRLRL G
4542	10039	A	4839	2	438	FVPAKVAGAAEPDEDGGRSLRDC GDYTPSERLGPKGAMLWFQGAIPA AIATAKRSGAVFVVFVASDDEQSTQ MAASWEDDKVTEASSNSFVAIKIDT K/QMHLLKSETSVANGSQSESSVST PSASFEPNNTCENSQSRNAELCEI
4543	10040	A	4840	1	1608	
4544	10041	A	4841	1	3117	MAPEWRPGTTASLPSGPGARSVC SLRSPEAGSASFVRLCGPRNLGWFGP HLRLRTSAHARQRHPKTRASAREN TSRHSRNPVSVPQDLSLASRCAG SIPITLESCLPVGLSKDVWPLTIEPKV KVFIFFNLKLPDCPSTMKNPASLLFSL FEGEWAI AEVLSDIWCTGVLAINK DQVLTIGFDINEFLSCSSSSKSMSC SLTGSLALQPDQQQDHETDSSPAS AYQRIWEAFANQSRAERDAFLQDT FPEGFLWGASTGAFNVEGGWAVG

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						GRGVQPKHVKEAFRLLNKSIIRVET PDVNLQDEEEIQMEVDEGAGGING HADSPAPVNGINGYNEDINQESAPK ASRLGFSEYCRISNLIVLHLRKVEE EEDSALKRSELVNWYLKEIESEIDS EELINKKRIEKVIHRLTHYVEYFSS LHASQITHYKVFLSWAQLLPAGSTQ NPDEKTVQCYRRLKALKTARLQP MVILHHQTLPASTLRRTEAFADLFA DYATFAFHSFGDLVGIWFTFSDLEE VIKELPHQESRASQLQTLSDAHRKA YEIYHESYAFQGWLAFTHMSQTLA NKIRVRGMAQESCSHGSSVGYLQH PGSEQVQFPRTTSPCSSQQLQGHQC TAGPPPPPGGGMVMMQLSVPNNPQ SCAHSPQWKQNKYYCDHQRGQK CVEFSSVDNIVQTSLNCTDPVVCVP SSFFIGDSGIPLEVIAGSVSADELVT RIHKVRQMHLKSETSVANGSQSES SVSTPSASFEPNNTCENSQSRNAEL CEIPPTSDTKSDTATGGESAGHATFL FREPSGCSQDQPAEDLNIRVERLTK KLEERREEKRKEEEQREIKKEIERR KTGKEMLDYKRKQEEELTKRMLEE RNREKAEDRAARERIKQQIALDRAE RAARFAKTKEEVEAAKAAALLAKQ AEMEVKRESYARERSTVARIQFRLP DGSSFTNQFSPDAPLEEARQFAAQT SVRVTSSEPPNPASSSKSEKREPVRK RVLEKRGDDFKKEGKIYRLRTQDD GEDENNTWNGNSTQQM
4545	10042	A	4842	3	790	GARGTFLSPASVESSVLLCLLVPHP VLSRGPPASPPSSYHPSLPGGG/GGQ *PLPEYGLESSEQN*GLSPGEDPGNP GGPFWGSGAPAGSLMEA*GNKRDA PPPPGDPSCSAPC/GDPPGMQGIQDS LPCHTASQKGGAFPGPMAPGRVL HQQGPL*GPSRLSQESPSAGPPMPQ LPSWVLCQVRPRAWGCWEPKGPPG TQFPPRFPDPSGTPCPPGYLEIFLLDP IPPRNWLAPLAAAQ**/PWGRWE MPMALPRGGLPLYT
4546	10043	A	4843	1	1026	
4547	10044	A	4844	1	722	MALEQRLKGGSGAALRSKAFPAEG TAGAKALQESDWSIGGAVSKPVF VQSVRELVADPCASNPCHHGNCSSS SSSSSDGYLCICNEGYPNCEQAL PSLPATGWTE/CHGTPTASACSCYS GA*/QSCLALRQR*HCLPGSRKQG\ KSCRNEMGSSGGDPYCLWECQF* QLCGWPPGIL*SATEHLSQDSARCH CLTDFALEGHGHRIPTVLPHRWTKC DPPSGFRGTGPPGGDARLGE
4548	10045	A	4845	2	2028	CSPAAPRRPVRSCCPRWPCCCCSSE RGPEAAPWPTRCPPRPCL/LPGPCAA QPCRNGGVCTSRPEPDQHPAPAGE PGYSCTCPAGISGANCLVADPCAS NPCHHGNCSSSSSSSDGYLCICNEG

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						YEGPNCEQALPSLPATGWT/AIHGT PTASACSCYSGA*QNPASLSGNGDT AYLAAENRAESCRNEMGSSGGDPR YCLWECQF*QLCGWPPGIL*SATEH LSQDSARCHCLTDFALEGHGHIPT VLPHRWTKCDPPSGFRGTGPPGGD ARLGE*SLY\CFVND SVTKS/NCGFA LNSGGEVSTCVPGESHANDLECSG KGKCTTKPSEATFSCTCEEQYVGTF CEEYDACQRKPCQNNASCIDANEK QDGSNFTCVCLPGY\NGELCQSKID YCILDPCRNGATCISSLSGFTCQCPE GYFGSACEEKVDPCASS\QNNGT CYVDGVHFTCNCSPGFTGPTCAQLI DFCALSPCAHGTCRSVGT SYKCLCD PGYHGLYCEEEYNECL SAPCLNAA TCRDLVNGYECVCLA EYKGTHCEL YKDPCA\KSACLNGATCDS DGLNG TCICAPGFTG*ECDIDINEC/ATVTP CHHGG\SLG DQPNGY\TCHCPHGW VGANCEIHLHWEVPGTWAESLTNM PRHFPLTFIHWEFPFLRGPFHPYADHP DRGDLPHQPH
4549	10046	A	4846	1	703	TISCPAVRSRRPRRISCLSCPGGGGA ASGLQRAAGGTGLSWVPAGLRVCC SQRSWRPAKEEQPVQTPRRTGKGG EISDMKPYKNKNEGNLENEGKPEDE V*PDDEGKSY*EEKPYA*GNTECEG KLKADGEPGDEGQLEDNGSQEKQG KSECEGKPQGEKGPASQAKPESQPR AAEKRPA*RLCGPGKAKK/NKPDQ GDRITFPQGLSGGLTGKASEQ*GDD ERMWRCVKGSRGA
4550	10047	A	4847	180	866	GAYVHGGRLCVQSLFQGVSSSDF CPPIPTLVPTLRPRAPCLWCTQDPAR PPCQSQRRLGPFQGVAGLKPSPGLL PNILLPESPSKRFNHGQLPVPQTVFG GGGSRGPPLLVPPSLPLFVFPFCGCF LSQPRGHRSPSSP*EEG*STPLLSVC HSHTDLWGLSWAVPAGWTGPSALF SPQAVNRLPITRPAPTHPHSFPREAP GRW*TPLPTS YQSLLFY GKDLPVK
4551	10048	A	4848	112	679	KI*NMWCYSDTGQFN VVKLSVLL*I IYIFNKILSSFLVKTGKLSLKS VN/NK QQSRITKTSKEN\KRGGFMR*DIKTF YVFAVIKSVLYMQI*ID*WKIIESSET DLHISSHLIFDKDNKMEKSLKK\WDI VYSSHRKIINLDL*HIPYVNINMIWN IDLKIKRFF* IAT/ENIFVTFSNVGND FLKYQLKSKIKKLKMRMVVYQMV P
4552	10049	A	4849	33	394	GSVWHHPFEGALRGPIPGAAGKPG LGTPSHPGLSPHPAACAACPRLPGL CSCAPGSAPLRLRP*/PAPCGSSDS VPRTP/GRRGLGSPGPPAPAAPKAE* LLQGGEFFSDPQPLAPEPRQLR
4553	10050	A	4850	2	269	LSGVCTVHIRGVCVWAGGNPSGTE LPGPLPPRPSASPPHPPQ*GVALP\

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						PVLFCFLVLPHPPTPNLIYPPCTVPFS PLPAPFAFFCW
4554	10051	A	4851	1	543	LLSKWIIITPSGAGSGDPPPAASPRR KQRMKIMKTTRSQTTPGRAPAASA SSPTL*TPGRDLESRLRP*PTNLPVR TPPGTAAVCPLLHRP/PQKAPVLGP ARV*ERGE/DANATPKREGLKRA/PP NDTLDFLWLGTPSSTKIKWTRPPAV EPLLVLHPTPTLPPLPVVPIVTQRVE YQGRFF
4555	10052	A	4852	831	1301	FFVFTFKYKNTILLCVINQGPSSKNL FFFQGRDIHQFILSFVFRAGHLVPSQ ASPTSKRPKPFSLIPNPYLLS*FPLLIE KLVINFLKKKFPTTRASP*PNQSTSR SSPFSYPGRRVPPLQTSSVPELRTPY WTGAPPLNGSSGYVSPTLPPPLMH
4556	10053	A	4853	1	1222	
4557	10054	A	4854	2	563	AHVIIYRFSMH*VITDVIPMLEVRSV YEINDVGTPEGEQ/TPPLTPVGGSN PQPIPAQSHPTSSSSSDGLRDNVPW LKVKNSPLKQSPGYQTELVIQLVW VGGEPPQIASLAVNSSYGLVDFGN CNGIAMVDYLQKAVLLNLGTIELY GSNDPYRREPRSPRKSQRPSGAGLC DISEGLVPSKA
4558	10055	A	4855	648	1377	EYLHGGWEHLQKRSLSPATGGGQG QLGAEGGP/GPGGGAAPAHPLAPN QACGVGLIDWRPRWTRGGTAAAG ARTPNLNPGAALTP/GRHSCVSVKK GSESELSRRR/TLPVVSPPGGGGCE MLRPDPASSP/SSQTP*PVPGAQAQT LALSCPPNSCPAKEVGAAGF*APLH LLSPSVGEGGGASGSTPKVSSFPLPF GGPLHSP*Y*PGPENWEGGDEGPL SHPARVPAAQSETECVPTESPQ
4559	10056	A	4856	3	394	SQAPS/GVAAHTPLS*AWTQPWNS IHMALASTRPNMPLRSGPA/CMPQL QLQELFTRSLVESELRIAPSEYPDES PIEQLEERRQLLEQPISLDVMLEPYI LRRSKLDLLYTSDSDLQLYKEQGE GQGDR
4560	10057	A	4857	3	666	SLLPKIFIGCLRRASSGPGAGNMLGS PSPQPLVSILGIAESWSTLPQGQPPA NPEAWAGPAGAKTDKSKT*GHFTP ETLPNVPKKDPLQLGA*KPGGSKPS EE/VWSQ/SPGPWLRNSGFFPPLNP RWGPFPTLWERF*NCSQPFRLRN PPVPL*GVLRASNPWPPHPHHPA NMPPAPPRVLRSSSTSAPPPWGCT QGPRGARAGA*AGAASS*SRGR
4561	10058	A	4858	3	361	FFFFRKWVNIFANYM*KKLILKIYQ QL*KLNHKVQ*LDL*MNKQNFHQK TTQM/AKKHLTGCTKLLICREMKK KTQ*QRNHLTPIRMATYFLKNAN/C W**CNKNETHVGCWWKTKM*SLF
4562	10059	A	4859	3	397	DQPTDIILDEQ*LelfHLRTGIRRG PVSSLPFN/IRAIRQEK*IKGIQLGKEI

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						KLALFADMILYLENPEDS/AQKL/LR LINNFSQVSGYKINAQKLGAFLYTN NVQAE/SQIKNPIPFTVAIKKLKYLKI HLAKE
4563	10060	A	4860	2	328	AHIDAVNEAMRLLLEHGFHAPTMSW PVSGTLMVEPIETEDHA*LDRFWDA LINLLQGIADIEDGRICPRVNPLKMS PHSLTCVTSSHWDRA\YSEKGAAFP LPFVKPENK
4564	10061	A	4861	13	410	NKMRRQATDRDKMLAKDTFDK\GT LEIYNQFLKFNNKKMSIPIK*WAKN L/NSHLTREDIQVANKPMKRCSTSY FIKEMQIKAMTRSRCADIKMAKIQT TDDIKC*RTCTRSTNFPFPALHLFYQ LTFRKSISH
4565	10062	A	4862	3	293	DKGLKGFRGFPTFTSFGQPTWLGLG LDLPEPGN*GPGFGCGP/NSRVGPTL SNLGPGERGPPGPPGLGV*ALKGK RADKKGGASFFPGF*KFPVGLP
4566	10063	A	4863	125	366	GIPGERRLEPPG/PKGPPLSPQIKGN NGPGPQN*VFFGGFKTKVPFGAQQ GS/GNPGPKPIFPPGPPKGRKYRVGP MAPPLQ
4567	10064	A	4864	79	336	HIATFNALSYVQASKRDKKFFACAP NYSYAVLCECLSSSIHLSSACSHVH C*RHDDALLWQPHGSIIRDDMR*HI ATFNALSYVQASKRDKKFFACAPN YSYAVLCEC\HRRVFIYRQPAPMST VFYNRKDCLQ/TVDRMLIHKVASLK TNDPILSIQAPK
4568	10065	A	4865	2	512	KIQIASIRNEIGH/LLTDATYIQRRLR E*CGQLQANKFDNLNGRDKFPGRH KLPKLIQKEMEAGRSGPLSPRVLG LQA*ATVSGLTGKFYKTCKEEIPIL TILFQKTEKGTQ\SS*EETSTILIPNQ EGKKNFQNGCLSMDPGTGKVPLTK ILVNQIQQSVIHKDNISI
4569	10066	A	4866	466	1451	EVCGLKKARISLFFF*DGVSLLCCPG WSAVAQSRLTATSASRV\K*FSCLSL LSSWDYKRPPRPANFLHF**RQGF TMLARLVIS/WIS*SVPPWPPKVLE L*AKAGDSLEPGSSRLQ
4570	10067	A	4867	3	379	NKSCQGPRTSFASAGWALKNPRWQ EQKEGLGKAGRPSGMNSSASSPTPG RKRELGMGSPSLRSPP*CE\GRSDR LG*PP*GGQGGGGH GAPSTPGPGG\ GPGDFHSKPPDPSLVPRPTEARGSP GP
4571	10068	A	4868	2	1718	SEGAPRRGAWGGPPARSHTLAPT PLPP/GPLSLCFACLKWLGVDRD AG*LGSQKAGGRGHPGMGQGKGT PPAHAW*PTGWCTGKP*KLGFLCPF HIPVSLACFLLSCAASDFSVLTWQ LWGP*EPPTEGGHSPFPSCRC/HRQE EGFLPVWQSPRQRPRMRPDSAPPST SARASKVGPGRGLPLNFG/QRPNL TPYGPAPALALS*PPQRWEELAEGA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PGPQPPVASKGPFSS*PKVLREPAVE TSSCASAPLAVFVRGVHTCIGG*AP GLSGGHPLTVSF*IGGIEGLDCLSPQ *AWGPGLGLEVCCGSHQASPPGPG VLGAPCPPPPCPPQGG/PAQPVGPS/P SHHGGERE*RGRPHSKLPLPPGVWG GC*RIHSRGPPGLSQPLFCF*PRRLS\ PAQPA*SKGGSRLVLSFCFLLPGS* GTRASGRGHSPSLKPGPGRAGRQ\G ETRGS\GSPGE*GCWSQNWDRGPA GQPWATSRVSIVRGWRVPGVAGAG FLAVLPWAPPSEARWQEQADQNPSA FGPKWEAAFLPNLPCQGGQQRGSPSP PPPPGCRNGDPSQGLGAGAEYSLGP LPYT
4572	10069	A	4869	253	451	RWKA WFGREIKGNNPRCKRGGGK HGTG/EEIKGNNPRWKRGGGKHGT GGK/YKGNNPRWKRGGGKHGTGG K/YKGNNPRWKRGGGKHGTGGKL K/SNNPRW*REGGKHGSGGK/YKGN NPRCKRGGGKHGTGGKLK/SNNPR WKRA GKGHGSGGKFKEIIPDGSVK VESMER
4573	10070	A	4870	2	269	EGGLGLNRFPPPPGPPRRPAAACMS AP*PQR/HWPP/SPREEKASLNEPGG PGRGRGRGSGQLHGEGGPRGGE/R GNWPGGMEGEGGIDAPAS
4574	10071	A	4871	20	312	SVMNGTSICKCRANDETGLSPSPAG PKSRSRRLS*LWRPSAATDSGSPPT* PVPTSPPPAPTAPRPGSRAPSSPLA PTLTGPGG\PLRPPPPAEEP
4575	10072	A	4872	299	472	KSISVATANPGKCLSCTNSTFTFTTC RILHPSDITQVTPR*/GVPGKSGASLL SSAVFS
4576	10073	A	4873	1	3454	MKHTLIPRIKNACLQMSSLAVPVNS LVCLGKILEYLDKWLVDGILPFLQ QIPSKESAVLMGILGIYKCTFTHKL ITKEQLTGKVLPHLIPLSIENNLNQF NSFISIIKEMLNRLSEHKTLEQLHI MQEQQKSLDIGNQMNVSEETKVTN IGNQQIDKVFSHIGADLLTGSDSEN KEDGALNVPPAGAKPTQQRPTDMS ALNNLFGPQKPKVSMNQLSQQKPN QWLNQFVPPQVSPA TGSSVMGTQM NMIGQSAFDVCSNEDLPEVELVSL EEQLPQYRLKVDTLFLYENQDWTQ SPHQRQHASDALSPVLAETFRYMI LGTDRVEQMTKTYNDIDMVTHLLA ERDRDLELAARIGQALLKRNVHLS QNESLEEQLGQAFDQVNQLQHEL KKDELLRIVSIASEESETDSSCSTPLR FNESFSLSQGLLQLEMLQEKLKELE EENMALRSKACHIKTETVTYEEKEQ QLVSDCVKELRETNAQMSRMTEEL SGKSDELIRYQEELSSLLSQIVDLQH KLKEHVIEKEELKLHLQASKDAQR QLTMELHELQDRNMECLGMLHESQ EEIKELRSRSGPTAHL YFSQSYGAFT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GESLAAEIEGTMRKLSLDEESSLF KQKAQQRVFDTVRIANDTRGRSIS FPALLPIPGSNRSSVIMTAKPFESGL QQTEDKSLNQGSSSEEVAGSSQK MGQPGPSGSDSLATALHRLSLRRQ NYLSEKQFFAEWQRKIQVLADQK EGVSGCVTPTESLASLCTTQSEITDL SSASCLRGFMPEKLQIVKPLEGSQT LYHWQQLAQPNLGTILDPRPGVITK GFTQLPGDAIYHISDLEEDDEEGITF QVQQPLEVEEKLSTSKPVTGIFLPP TSAGGPVTVATANPGK\CLSCTNST F/TLFTTCR/IYLHPSDITQVTPSSGV PFHLSCG\SSGSSFHSNTAVNSPALS YRLSIGESITNRRDSNYNLSVGTME VGPKFLQER\GIS\AKVYHSP\SENPL QPLPK\SLAIPSTPPNSPSHSPCPSPL PFEPVHLSENFLASRPAETFLQEM YGLRPSRNPPDVGQLKMNLVDRLK RLGIARVVKNPGAQENGRCQEAIEG PQKPDSAVYLNSSGSLGGLRRNQS LPVIMGSFAAPVCTSSPKMGVLKED
4577	10074	A	4875	1	638	LA WGGKKGKASSDSGGLVDSISTL TPTPGDTNT/HSDLIVRGGAYGGQW AHGVLAQVQPSVGAETV*PQMGE *TDVCGSQSPHICSLTLRVGATML GKAR\WKPLG*TLPR\KIV\NSKATC SPGGTAKVSAAIRGLGRCRVVTPTA ASFHSS*\WLWVKTGGSRRKKDSES WVNLTRTPIATAVPDMTTDSLGGIQ SIPGHPVLQPIDPGESL
4578	10075	A	4876	31	448	PKSLLSLLVKINYGYVPK*QATKAK LDNWDYIKLQSFCTTKIMNRVRRQ PAE*ENIFANQTSKGLISKIYKELK QLNSKKANNLIKWNSSDDLNR/HFSN EDIQMASRYMKK\STSQIIREMQIK TTMRYHFMPIRMTT
4579	10076	A	4877	3	286	KFTFKRHHHLQLLKRK*DS*V*T*Q MFMEQIKEDLSKQRDNCS*IGKLSI AKNIYVSNIPG*FDAIPIKIPARFFYA FGLYCRNSVSLSPRLN
4580	10077	A	4878	3	236	ATHSTLPSFQGPVSLASMTVVGIDG KASRPLQTPVCQLDQHSFLHS/FLV IPTCPVPLL*GILTKLSASLTIPRLQ P
4581	10078	C	4879	206	262	MVAIGTGYRRPGLRFTLN*
4582	10079	A	4880	2	756	LTSSRGARPAPLRAPAR/LDPAFRAN PLRSYSGSLPTFPYLHCSNMPKAC SPWRPAADMGT\PGARFTSPPDFQ GPARAPPDAAGTATLSKARAPLSGR NPFQGRPCPSQRKENSRRRTSPG SRRVTDTGRLAGAPCSATPDSGI*T RLPFRIGRGAPEAIAPSLRNGARPSL RTD*PMFQLLGYNWNPSVVRPSKV LRLNICYYTP\SHAPAAAPPGPADFQ GPARAHRTPEPRRFRHGPLSRGE P
4583	10080	A	4881	3	322	MGSVTGPLYSGYKEEVVCCTLVEV

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FPSLLQVSRNPRMPFDLGLIFCLG GQGFPRATTVSGHWPE*LSQSSSSP KLRPPTL*SKPAHPGAAEALKAVPR TSAGAR
4584	10081	C	4882	240	500	MQNGLSGAYFPSVWAAKDSQERR RSPATGRNDSPRAPLPRSSARRPSK ANLHTLGQLKLSSRCRAPLRRAA RTRXSXDQXWRRXTT*
4585	10082	A	4883	22	696	CTFGSFPFGLSAWSFRASLPAPAP GPNERFRSPGAGGFWGVDAAGQPA PAEVLGTALRASAAPGCAD*NPKKI KWHPG/SFCSPGEGMEILQQVCSKQ LPPCNLSKEDLLQNPYFSKLLNL QHVDSEGLSLTLAKEQAQAWKEVR LHKTTWLRSEILHRVIELLDVYYV KIQDTNVTSEDKKFHETLEQRLVT ELMRLLSPSQEREIPPLGLEKADLL E
4586	10083	A	4884	1	594	AVVHFRLPLPGPFILCLSGPRFPQP AAPGPNERFRSPGAGGFWGVDAAG QPSPAEVLGTALRAPAPGLQVCF KGSAGGASGKRSSGRVIPA/MWPET VVALGNPWTVQTEGKVGAGEPVL HFDSSRAL*GSVSCENNL*NQFNRS SCSV*RQALRI*KTPSEHLKCLGPC SSVFNTSECRVENRSLNCPFTPCNL
4587	10084	A	4885	2	326	VKTAEFVNKWQKNSTKLWNSQAQI DSSSLVNQINDLRQTEIWMGDRIMN LESRIQMCDWNTSDFCVTPQYNE TEH*WKKVKRHLEGREENLT*IVK LKEQDFEASQ
4588	10085	A	4886	2	373	VLLTPEERTVVIALWRKVNVAALC R*GAWA**L*AYPWTHRFESFGDI DSSDAVMGKPIVNAHGKNVLGAFS DGQSHLDNLLGTYSQSELHCDKL HVDPENFKLLGNVLCVLARNFGK EF
4589	10086	A	4887	3	332	HLSIINLVNQLNSPLKAYTLPVWIP SS\RGPTICCLQEIHFASKNTYKLKV KELSSSFQANEKEKHADKTGFKVPK L*REKNGHYIMIKRSVQKENIYIYM FLIADPDIC
4590	10087	A	4889	1	304	HSCSSMRMPPLPTPPP/IVLCPPHPSP LIKALVSSKPP*VPSAETWPVAAL GA*VPAVLGWPLHTENVLPVPPLPL EMPRIQWHFMLCSFPQRSRADEST
4591	10088	A	4890	1	254	RPRRQFGIEGSFLNQIKNIYKKSTAN VILYVDRLNAFSLISGSSSSSSSSSS SSSS*LPVNIIRQ/EKVI*GMQIVKEE LNLSL
4592	10089	A	4891	310	415	SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRRL/DSVAQAGVQWRDLGS LQRPFGFTPFSCSLSPSSWDYRRPP PRLANFFVFSVETGF/TVSARMVIS *PRDPPASASQSAGDTGVSQAPV
4593	10090	A	4892	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS

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						GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHAWLFFFC/SD TVSLCYPGWSRVA*SRITATSAIPGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR\YPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYLFYFHRDEGSLCCPGWS* TPELK
4594	10091	C	4893	40	180	MSFEAEIVLSPDRTTALHPGLQIETL SHIIIIILISTISFHQLLH*
4595	10092	C	4894	4827	5060	MWIYFWTLNSVPVIYMSLMSIPHY FDYCCFIVSDIMLPEITFTFILLMLV ALAIRGPLHFRRHFRJNL SIATKNA*
4596	10093	A	4895	2	311	FILHVCDKLILFVSGDTFQTVSPRFL APRTFLAPLQNP*PLSPCAVHISFSRP LPARSPLPP/PRPPPPPTCSTAIPATH NPILTTHTSTPPPTLPTINLTSSP
4597	10094	A	4896	2	374	DLTPKV*SRKGKIGKLD FIRT KTFW SAKDHVKRLKRQTTDWEKIFLNHIS NK/GLLSRIYK*LQTQY*KTPSNPI/K KTAKDVKEHFTEEDIQMACNPMKR CSTSLAVRELQIKTTVRYLKIEFNF
4598	10095	A	4897	1	684	
4599	10096	A	4898	1	1349	
4600	10097	A	4899	1	821	MLQTWSGYDNPRVTQKVPPFQLNC LPMTVLLILYAEVATDWNRVGLT QGQLLHSLRLDPWSGLTQRTFPTGA MEISPDYLPPEFIVENTERIDEREKG REQPPKKT PENKAWPKMLKGKKA KGKKVAPAPAVVKKQEAKKVNP LFEERPKNFGIGQDIQPKRDLTRFVK WPRYIRLQQQRAILYKRLKVPPAIN QFTQALDRQTATQLLKLAKHYRPE TSKRRRLLAQAEKKAAGKG/VRPT KR/PPVL*AGVNTVTTLVENKEAQL DLYCAI
4601	10098	A	4900	1	868	GTRPKMPKGKKAAGKKVAPAPAV VKKQEG\AKKVVNPLFEKRPKNFG IGQDIQPKRDLTRFVK\WPRYIRLQR \QRAILYKRLKVPPAINQFTQALGP RKQATQLA*AWPTKYRPRDKAREG SRDLFGPGPRKKAAPKGTFTKRP PVPSKQ\G*TTVTTLGGGPRKASAG WWIAHDVDF\LELGLSFLA\ALCRK NGGSPYCIKKGKQDWGRL\VNKK TCTTGRLSHR*TSED/NKALLKLVE AIRTNYNDRYDEIRRHWWGNNVLP KSVARIAKLEKAKAKELATKLG
4602	10099	A	4901	145	745	RRRGTSQCNLITIVNHISEITVIMFIE CSLCIKVIRLFHILILLDFSSKPAPPPP

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						PCGAPGL*TATLLSRLRTARDLGR L*ASPASPLCAVPSPAAAAFL/SLPLP LCPSSSSARELRSPTPGLSGQPAPAA SPGPG/PAG/PPPPPLAVRPRFAPHL QLCPGPPFSRPSVLPASSRCQPGLSA PSLPSSPRPPPLRGLGRS
4603	10100	A	4902	94	432	TFLFFLIFSSEYWKFKQKQYSLEKSL FVAYNHKDG*THFLKGNNQFISIA/ LFTLGDIIYCKDIFGRLGLQP/TDISS DSPFLSFSSSIYILTGWQARWLTPVI PAFWEAKAG
4604	10101	A	4903	109	422	FFEDGVLSRSVAQAGVQWR\NLSS LQPLPPRFK*FSCFSLRSRWDYRHA PPCPA\FVFLVETGVTLARMVLIS *PRDPPASASQSAGITGVSHCAPSRH SLS
4605	10102	A	4904	3	364	HEETAYDINILS**TQTFNMARLE*N CCNTIKSISEK/PTANSIR*AKKQEGF FQISGIRQGCLLSSFLFILEVLARGN R*DKN/GIQIGKKKVELSLFSETMRF NIWKRLWKPHITRANK
4606	10103	A	4905	50	394	LSYSWHSIHLMLKIISWHFDGQFSA LVIL*LSVAVDTADYSHFLETASLL DFEFTVLSWFSSYL/TDMFLFTLVFS LAPFSIQLLNIGISQGSVLSPLLYAS ASGYMSLNIMYRH
4607	10104	A	4906	49	366	SGSSLA AVFWGPKGPAQAP/GPWAP WASPSGPDLPRLHPADPQRQLST VPLPLSRPPALSLIAPMALSHSCSNIP P*TPPPASLRPELTPARS/PPTR*SHS PPP
4608	10105	A	4907	119	246	FCFHHLNLPFLIF/NVCLCV*QSHS VTQAGEQWRNLGSLQPPPPRFKPF CLSLPSS*DYRHAPPQLADFCISSRD GVSPCWPGWSQTPDLR
4609	10106	A	4908	1	280	ESRSVAQAGVLWRDLCSLQPPPPVF K*FSCLSLPSSWNYRCAPCPASFFV FLVEAQGFTMLARLVLS*PQ/CDPP TSASQSAGITGMSHCTWP
4610	10107	A	4909	406	661	SQTPDLR*SAHLSLPKCWDYRR/AA TAPGQNISFKLPNPWEKAKHLMKS T*RLKHFTNFALFV*NCIDD/WMEF ALVAQAGMQWHDLGSLQPLPPQFK WFSCAPASPKCWDYRREPPCPANFF FFLYF**RLGFTMLARVVSNS*PQ/C DPPTSASQSAGITGMSHCAWPPFFF LFFSFFFETGSHCVAQAGLK/PLKLL RSSCLGLRKCDYRREPLRLAPSW TFRM
4611	10108	A	4910	3	459	ELRDGEKVLDLCAAPGGKLIALLQC ACPGYLHCNEYDSLRLRWLRQTLE SFIPQPLINVIKVSELDGRKMGDAQP EMFDKVLVDAPCSNDRSWLFSSDS QKAS/W*DKSKEEFAFFYRLGC*GL QLRPLRPGGILVYSTCTLSKAENPR CDQ
4612	10109	A	4911	1	95	TPKVHASWQK/MAD*SGQCPVLQIP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LSSLMMQ
4613	10110	A	4912	253	1531	SWKLAEKVWEAQLPGFPSPQC RCGRGQSRQVRCVGNNGDEVSEQ ECASSPPQPPSREACDMGPCTTAWF HSDWSSKCSAECGTGIQRRSVVCLG SGAALGPGQGEAGAGTGQSCPTGS RPPDMRACSLGPCERTWRWYTG WGECSSECCSGTQRRDIICVSKLGT EFNVTSPSNCSHLPRPPALQPCQGG ACQDRWFSTPWSPCSRSCQGGTQT REVQ/CA*APTRPSAPDALLNCGPPG SAPVNSQPC/MPAP**SMARDSSSTF APWVGTPGPGFCVLPLLTQPPVCRSL RTCPGSGLPRIPPERGPGHLHGFLCH HRSPIGLGPLWNPLGSSSLFPGQQ GMSSR*TEGVGKVNGTQSDFSGT GQAHVGGCDGVCCTYCLRCCFWG LHGICVWSNVYHFSKRRLHRTLEG TRPVFLEDFS
4614	10111	A	4913	131	355	STADTLP**TPKLSPQLMDTILPSQS VAMFHT*DHSAPTGTGAPPHHTPS RPLNTRGPTTEEFSPRPPPQHRPSSC
4615	10112	A	4914	3	420	QQPPTRLD*GPKQLMPHSPHNPHIT* NPAVLSLPPQTKLLGPPVVRGPLLIR *SPQLLPACLP*RSTRPGTLKPKAT PA\PPPTTVHKPVASLRSHLRADGPG APPHTTSPRPLNTRGPTTEEFSPRPPP QHRPSPPTK
4616	10113	A	4915	11	375	
4617	10114	A	4916	3	260	
4618	10115	A	4917	3	208	
4619	10116	A	4918	1	422	
4620	10117	A	4919	127	4348	GASISDIQTETTEEDSVLLMHTLLAA TKDSLAMDPPVVNRPKSKTKKAPI KTITKAAPAAPPVPAANEIATNPKPI TWQALNLPVITQISQALPTTEVTNT QASSVTAQPKKANKMKRVTA QGSQSPTGHEGGTIQLKSPLQVLKL PVISQNIHAPIANESASSQALITSIKP KKASKAKKAANKAIASATEVSLAA TATHTATTQGGITNETASIHHTAASI RTKKASKARKTIKVINTEHIEA LNVTDAAATRQIEASVVAIRPKKSKG KKAASRGPNVSEISEAPLATQIVTN QALAATLRVKRGSARKAATKARA TESQTPNADQGAQAKIASAQTNVS ALETQVAAAVQALADDYLAQLSLE PTTRTRGKRNRKSKHLNGDERSGS NYRRIPWGRRPAPPRDVAILQERAN KLVKYLKVKDQTKPIKRSMDLRDV IQEYDEYFPEIERASYTLEKMFRVN LKEIDKQSSLEMLISTQESSAGILGTT KDTPKLGLLMVILSVIFMNGNKASE AVIWEVLRKLGRLPGVRHSLFGEV RKLITDEFVKQKYLEYKRVPNRPP EYEFFWGLRSYHETSKMKVLKFAC RVQKKDPKDWAVQYREAVEMEVO AAAVAVAEAEARAEARAQMIGEE

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						AVAGPWNWDDMDIDCLTREELGD DAQAWSRFSFEIARAQENADAST NVNFSRGASTRAGFSDGASISFNGA PSSSGGFSGGPGITFGVAPSTSASF NTASISFGGTLSTSSSFSSAASISFGC AHSTSTSFSEASISFGGMPCTSAF GGVSSFSGPLSTSATFSGGASSGFG GTLSTTAGFSGVLSTSTSFSGAPTT TVFSSALSTSTGFGGILSTVCFGG PSSSGSFGGTLSTICFGGSPCTSTGF GGTLSTSVFSGSSSTANFGGTLST SICFDGSPSTGAGFGGALNTSASF VLNTSTGFGGAMSTADFGGTLST VCFGGSPGTSVSFGSALNTNAGYG GAVSTNTDFGGTLSTVCFGGSPST SAGFGGALNTNASFGCAVSTSASF GAVSTSACFSGAPITNPGFGGAFST AGFGGALSTAADFGGTPSNSIGFGA APSTSVSFGGAHGTSLCFGGAPST LCFGSASNTNLCFGGPPSTSACFSG ATSPSFCDGPSTSTGFSFGNGLSTNA GFGGGLNTSAGFGGGLGTSAGFSG GLSTSSGFDGGLGTSAGFGGGPGTS TGFGGGLGTSAGFSGGLGTSAGFG GGLVTSDGFGGGLGTNASFGSTLGT SAGFSGGLSTSDGFGSRPNASFDRG LSTHFGSGSNTSTGFTGEPSTSTGF SSGPSSIVGFSGGPSTGVGFCSPST SGFSGGPSTGAGFGGGPNTGAGFG GGPSTSAGFGSGAA\SLGACGFSYG
4621	10118	A	4920	3	1380	NMLGKYL*VKDQTKIPKRSHMLR DVIQEYDEYFPKIIERASYTLEKKFR VNLKEIDKHSSSYILISTQESSAGILG TTKDTPKLGLLMVILSVIFMNGNKA SEAVIWEVLRKLGL/RPGV*LGSLSA CCPCCPLAREDPRIASVWWSGGT GWGAGLGRGPRVLTCDVDDGQMV KLSAVSLLNVLCF*A*MLDRPSRIP DKEGIWVLNCLLLVAMCSLLSSLH* DCPMC*ERSPSMLGKWPLALNLGQ FLICGSWGLIFPNCQG*GIHSFGGSE GKLITDEFVKQKYL\EYKRVPNRSP P\EY\EFFWGLALPTTETSKM\KVLK FACRVQKKDPKDWAVQYREAVEM EVQAAAVAVAEAEARAEWFQHQH WLYLANPAPSNGASSSGPKFYCW PAVDPSTGVGFCSGPKHQVASSGGP STGAGFGGGP\NTGAGFGGGPEHQ WLWQVEPPVLPVAF
4622	10119	A	4921	1	412	TRMGLPDASRRRTCRMDPEGWQE AMSSA*GRITLQRLSTGPEGQGGRE KVGPEGGSNPQQPKAAGVLSKHL PGAPAQPPQRPPSSPPLAGPLTERV EKVCDFLDAAGDYLN/GTPG*PSPG ESPAAQDPPVPPWPP
4623	10120	A	4922	117	295	
4624	10121	A	4923	1	3564	
4625	10122	A	4924	1	355	LPGIEVLWQGPVVSKVIPVESIEEV

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						CKSIKRAPVIWDTIHVN/DF*SALTP YQIVTTKFYFRIKKIVHWGPFPHSSQ KILSICEKYQWLSVPLTHNLTKFLSII VNYSRYHCKIPQLV
4626	10123	A	4925	3	3145	AAAEGELGAWRGNSGRPKIIGRAA EAENEDRTLGRLLPGNERSQPRSP MLLAPQLKAEAAADKGLAPVPPPF SSGHSGPCEREGEGQRGRGRSRRG AHLELKPSPLRAGAPTDRGRGGP AEVAAAGGRRMVQKESQATLEERE SELSSNPAASAGASLEPPAAPAPGE DNPAGAGGA AVAGAAGGARRFLC GVVEGFYGRPWVMEQRKELFRRLQ KWELNTYL YAPKDDYKHRMFWRE MYSVEEAQMLTLISAAREYEIEFIY AISPGLDITFSNPKEVSTLKRKLDQV SQFGCRSFALLFDDIDHNMCAADK EVFSSFAHAQVSITNEIYQYLGE PET FLFCPTEYCGTFCYPNVSQSPYLRT VGEKLLPGIEVLWTGPKVVSKEIPV ESIEEVSKIIRAPVIWDNIHANDYD QKRLFLGPYKGRSTELIPRLKGVL NPNCEFEANYVAIHTLATWYKSNM NGVRKDVVMTDSEDSTVSIQIKLE NEGSDIEDTDVLYSPQMALKLALT EWLQEFVPHQYSSRQVAHSGAKA SVVDGTPLVAAPSLNATTVVTTVY QEPIMSQGAALSGETTLTKEEEKK QPDEEPMMDMVVEKQEETHKNDN QILSEIVEAKMAEELKPMDDKESI AESKSPMSMQEDCISDIAPMQTDE QTNKEQFVPGPNEKPLYTAEPVTLE DLQLLADLFYLPYEHGPKGAQMLR EFQWLRANSSVSVNCKGKDSEKI EEWRSRAAKFEEMCGLVMGMFTR LSNCANRTILYDMYSYVWDIKSIMS MVKS FVQWLGRSHSSAQFLIGDQ EPWAFRGGLAGEFQRLPIDGANDL FFQPPPLTPTSKVYTIRPYFPKDEAS VYKICREMYDDGVGLPFQSQPDIG DKLVGGLLSLSDYCFVLEDEDGIC GYALGTVDVTPFIKKCKISWIPFMQ EKYTKPNGDKELSEA EKIMLSFHEE QEVLPETFLANFP SLIKMDIHKKVT DPSVAKSMMACLLSSLKANGSRGA FCEVRPDDKRILEFY SKLGC FEIAK MEGF PKDVVILGRSL
4627	10124	A	4926	3	251	HERHELQMLVDAPCSDLAQELROS CATVQRLQHTLQQVLD/Q/REEVRQ SKQLLQYLLALYNEVSLLS*QDIF NVALDVCMCRS
4628	10125	A	4927	1	408	GTSLNSLSKTKAKDLFIGDVIHNAG PHRDKKLKYYIPEVVYSGLYPPYAG GG\GLYSGHLALRLNHIADSVQF*P R*DPYTVR*LLKPSSAGYDPTFVLLI GTDGIYTYTPSSCENGLGSCEEPHL MSFRSYFHG
4629	10126	A	4928	187	378	LCQKTMSLFTHSFCFSVGRNMEGV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LMDVDCESVYPIV*ASN*GLASAEV GGSFEPRSLRPAWAT
4630	10127	A	4929	26	121	PDRTMGG\REQRQSPGAQRTFFQLL LSFFVES
4631	10128	A	4930	3	867	
4632	10129	A	4931	1	558	EVRVKCVKALKG\LYGIPDLTACL KLFTGRFKDWMVSMIMDREYSVA VEAVRLLILILKINMEGVLMDDVDCE SVYPIV*ASI*GLASAVGEFLYWKL FYPECEIRTMGGREQRQSPGAQRTF FQLLL\SFFVESKSHFVTQGGSGQF SAHRNLC\PGSGNFHVSASRVAGIA GAPPHTWLIYVFFS
4633	10130	B	4932	1	1617	MKNGVQWAE\LAGHDYVLDLVSDL ELLRDFPRQKSYFIVGTEGPAASRG GPKVVFGNSWDSDEDMSTRPQPQE HMPKVLDSDGYSSHNDGTNGETE AQRGTATHQGQPTMAAVSESDSLG EPAVPHKGLDCY\LDLFDPVLSYGD ADLEKPTAIA\YRMKGGGQPGGGSS SGTEDTPRRPPEPKPIPLDASTLAL QQAFIHKQAVLLAREMTLQATALQ QQPLSAA\RLSLPAEKPPAPEAQPTS VGTGPPAKPVLLRATPKPLRPAPLA KAPRIPIKPVAAPVLAQDQASPETSL HRDAATVTQM\HFLTQGGRLLSLLD DSSLHLWEIVHHNGCAHLEEALSFQ LPSRPGFDGASAPLSL\TRVTVLLV AAGDIAALGTEGSSVFFLDVTTLTL LEGQTLAPGEVLR\SVPPDYRCGKA LGPVESLQGH\LRDPTKILIGYSRGLL VIWNQASQCVDHIF\LGNNQLESCL WGRDSSTVSSHSDGSYA\VWSVDA GSFPTLQPTVATTPYGR\ACTPVAHD HIDELVRGAVFSEKHFCIEDL*
4634	10131	A	4933	1	811	HASAGAGCWHLPGIIEGAAQKGKR GRQVIAVARTADVIMMLDATKGE VQRLLEKELESVGIRLNKHKPNIFY KPKKGGGISFNSTVTLTQCSEKLVO LILHEYKIFNAEVL\FRED CSPDEFID VIVG\NRVYMPCLYVYNKIDQISM E EVDRL\ARKPNSVGSSSCGMKLNLA DYLL\EMLW\EYLA\ALTCILHQGRR RDRRARFSQDAI\LRKGASVEHVCH RIHR\SLASQFQVTPWVWGAPAPSY S\PQAGGALTH\TMEHEDVIQIVKK
4635	10132	A	4934	1	431	QRFPAAFPG\PGARRDAPPHSPPAEC RAHAATWRLKPRPHRPHSLTAPLP VHWAGTTEPLSPRPATGTESARRC ISGDTQSFLRLARPCRQPGPS*DRC RPGVVSCLDREKNAGHWLSMAFS LLWVLATQHCHLPEESLTM
4636	10133	A	4935	56	252	GAQERGCPREKHGNAELAEGLVLIL RGRGKPPSASLAGRE*I*SRGPEWK VTVNQTAKAKERTGP
4637	10134	A	4936	81	896	CGLVTPACLDPWVGIAPLPDTLIVL RGGGSALLPAPIPPVTLEEKQTLTRL LAARGATIQELNTIRKALSQ\NGGG

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						LAQAAYPAQVVSLILSDVAGDPVE VIASGPTVASSHNVDCLHILNRYG LRAALPRSVKTVLSRADSDPHGPHT CGHVLNVIIGSNVLALAEAPAAGRG TG\YQAVVLSAAMQGWGTPAAHR DDRYQCHGHPPLVPAASVMA*VTF WEFRGGLOGGQMAEQARLADGG FPLPLRMRTSPSASSAFPCFSLGQPL S
4638	10135	A	4937	100	332	NKPQPQLLYRIKLTSTPFHPIQKVGL RQMIDLNIPPRIKLLLENIK*YLSDL GV\TK*KLTKFNFLKIKHFCSPSSC
4639	10136	A	4938	692	900	NKLLWLGAVTPACNPSTLGG*GGQI MRSGVRDQPVQHGE\TWSLLKIQKL AGHGWPAPGSPSCLAGLRQE
4640	10137	A	4939	87	322	ARLVQNTGAQLKEVQYKLFQGLF FE*/QSHSVAQAGYSAVIIAHCNLSL LGSSDPFFSAS*VAGTTGMCQHAW LIFDR
4641	10138	A	4940	91	356	GHAFLFGGYSSSHWPSTYPPHAPV PPPPPSPPYPSLPPFHSPLPIKPFPLPP /SPSPSPSL*SPPTPPPTLLIPSPSPPP ASPPLQ
4642	10139	A	4941	2	332	CGGPPGSPDTRGGSLIPQGV*AA/GP MEQVPLVAPSSAIPA VPGSLSGTPSH QPVLGTHTPSCPGLTYIPPESELP DCPAPGRQRPCPGQTPLPTPCPPSFI FSKQPR
4643	10140	A	4942	637	1560	VWQLDKSMRAAQPWAPAGGAAGS EWAGLKR\RPLGWSSFSPAAAQSP ELLGHPQSPWPSEAPWKACQVSF QGT/RVAASYHNAQHGTERRHSSC *GLGS*/CNSPTWARLSTHCPQ/HSR NTPRTQHCPHYPPRGLAKRWLCGE GPNPYSHPLREGPLRRRVGRGMGK EVHLFYRAWHSGIHFPS/TPSRTSHQ DSPHLEN*TSPLIDLTPTWAPPMCK RIL*KCTCNSLPQKPSMALQCI*NEI NKTSTTSPT\CLAPH*APATLACSPF LQPAELLPIGTLHVIFHPRTLFPKS RTGSFLSSPQVSV
4644	10141	A	4943	2	335	ALHPTLTLDLYFTIYTKIHST*IVDL DVKPKTLKLEESIR/VKLCDLRLSK ISWILKAQSIEEQTD\TWDLKT*NNY SSNGTVKRIKRQVED\WHKV FARRI SDTGLVSRISC
4645	10142	A	4944	2	345	FFFFFFETESRSVAQAGVQWRDLSS LQAPPPG\SRHSLASAS*VAGTTGVC HHARLIFVFLVETGFHHVSQDGLN LLTS*SAGLGLPKCWDSEKLFFFFG DKSFRFCCPGWSTMV
4646	10143	A	4945	178	388	RREPLHPANLLLFFFFFFEMESPSVA QAGVQWRDLSSLQAPPPGSCHSPT SLS*VAGRLRNKNCLNPDAW
4647	10144	A	4946	546	850	FSVLFFYFESESCSVLQAGVQWRDL GSLQPPPPGSSHSPTSAS*VAGTTGT CHHTQLIFIFLVETGFHHIGQASLKL

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						LTS*FAHLGLPKFWDYRCEPPHPA
4648	10145	A	4947	169	358	GNGFLFCTQVEVQGAFL*YLNLLAP GVK\LFSCLTLLKPWDSGTFPTFSFN FFIYLAKEKGFNG
4649	10146	A	4948	1	145	ANSAAMPSLGCSASSGLVFWPQGL YLLGVVSVSPLPPTPTTVTFPEQI*LL SPQVSSSPVSEGSSQHPA*SLRPFHV PRS/SPVSSLQPFAPAKSPGPSATCAF SAPSLSLLTLLASGDSSFWGPGPIQM SAGGSIVMCS*GLVFWPQGLYLLG VVSVSPLPPTPTTVTFPEQI
4650	10147	A	4949	1	295	GTSSRLRLHRTDELTA PSIYRSTKST LDGSLAANEREPFTLGKKPPFSDKP SIPAGRSLGEHLPKIQKPPLPPTTER HDWSRRLAGKKPPVPKHGWVP*/R EDDNE*DELTA PSIYRSTKSTLDGSL AANEREPFTLGKKPPFSDKPSIPAGR SLGEHLPKIQKPPLPPTTERHDWSR RLAGKKPPVPKHGWVP
4651	10148	A	4950	119	1036	HASCLKTQALQEC SVGVGGGLPV PAGPPRCFCPALPAAALALQGTFFA TGG*A WGLSSPDWTFSTKKLVME ARSHGEGGAQGPATLTGPPGEGAL RASQ/PGTAGSELRHRARGPAQICST RTR\PAPWWT*SLPPPGHSRAVGF RCGPASP\GVPVNAVALPPSTCGE ESRLPQEEGGIHMA/PGTPLCSGDCI CCED*PQSRSGQFGADSL*RAKGGT LPSGPSARRRSPL*ASESASCCRRAS SIGPPAAQGERADSRALGTAPPGE LALRPTPGGIGTPPAGGSEDISREVD PAKRHGLGA
4652	10149	A	4951	2	1262	GSAAGSTYEPSSMRLEALQVLTLLA RGYFSMTQAYLMELGEVICKCMGE ADPSIQLHGAKLLEELGTGLIQQYK PDSTAAPDQRAPVFLVVMFWTMM LNGPFSRFSADSEHPTLQASACDAL SSILPEAFSNLPNDRQMLCITVLLGL NDSKNRLVKAATSRALGVYVLFPC LRQDVIFVADAANAILMSLEDKSLN VRAKAAWSLGNLTDTLIVNMETPD PSFQEEFSGLLLLKMLRSAIEASKDK DKLSTISIYYFNGQENRKEKNWNER EYKLEIPYELCTEVDANKWTAPWT SQAYNALTSVVTSCKNFKVRIRSAA ALSVPKGREYGSVDQYARIWNAL VTA\LKSEDTIDFLEFNTVSSLRTQ ICQ\ALIHLLKLG/RSASDLP\MKET LELSGNMVQSYILQSLKRSRIGR
4653	10150	A	4952	52	730	KSACDALSSILPEAFRNLNDRQML CITVLLGLNDSKNRLVKAATSRAL GVYVLFPCLRQDVIFVADAANAMV MSLEDKSLNVRKAAWSLGNLTD LIVNMETPDPSFQGRVLWSPAENG YDQALEASKDKDKVKRHAV\RAL GNLLHFLQPSHI/GKTPHLQKFI*GSL SRALNLLF*QKLAMKVRWNACYA MGNVFKNPALPLGTAPWTSQAYNA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LTSVVT
4654	10151	A	4953	3	363	HELEFEIKNTIPFILAP/N/NIKYLGIT/ LTKYVLYLN/DLYAENYKTLMK*IR DLNGDPLSCKVKNLIKINKYMK\EIL CSRIGKDSNIV*VSLLPQL\ACRLNAI PIKIPANHFVEVN*LILKFI
4655	10152	A	4954	179	438	ENIMSKTSTENCTKQCHFVHVN*Y SIFFFFLRQSL/DSVTQAGVQWRHLG SLQAPPPGFTFSPRFSLPSSWDYRCP PTSLANFFCILVETGF\TVLARMVSIS *PRAPPASAS*SARCKLHLPGSHRSP ASASPVAGTTGARQQA\WLIFFVF
4656	10153	A	4955	1	264	QFPKPSPRGP/TPTKSLFHILSPPNQ*I SPPP*QLPPSLYQIPPTIRLSPLPLAES PSPLSVGLGGPLGWVGQLLCLSPFG GPKHVEV
4657	10154	A	4956	3	369	HERHELVKEFNKVSGYKINAHKSV ALLYTN/DDQAENQIKSSTPFTIAAK SVK/YLGIYLTKEVKDLYKENYKTL LKEIVDNTNKRKHIP*P*MGRINIVK MTTLPKAIYKFNSMPIKISPSHFG
4658	10155	A	4957	2	338	GCWDN*ISTCKRMKLDCSMLHMK INSM/WIKDVNIKSSSYEK\NIGVNLP DNVLGNGFINMMPKAQASKEKIIN WDSAKLK/IRK*RQLTEWEKLCANP IYSHLIPVLCYLYLV
4659	10156	A	4958	42	447	IELVTVLQFYRAFYLFERYAGFLFY YYFLFFVEIRFHYIFQAGLS/ELLGSS DPPTSGLPKCWDYRR/DHRTWPDM QDFLMFHIFPKLFSFPDMCFLASE*P SANTWLLL\VVQSSFSLLSHTYHPPG KASTLWFS
4660	10157	A	4959	377	1220	FRKVVP\LAESHPAVPG\GKVRTSR PKSPRALPT*/PGLFNPGCQRETPSP LG/PPGQHP/VPGQLNSKRKQIPHNE LVEQTLRSGLTSAQPAHPTGGYSCS KLRLPGPLPNPNGLCRCSDGRIPGDR EPLALSRT*IHLRACTGPDAAAQVL PGLLPCPHLPHLSGMFDSWLAPP LPDPCQRPTPPQAPSSEANNQRSQA PGCGPHSLRDSSELQGCQCPGAQAF RGSGLFQLTQLTGPLHGTR*RLSPK NSQALKPHM*AVGRILHWPPAARP GNSGRYPDD
4661	10158	A	4960	3	353	HEVPAKGPRPHLTDCPTTQDFLPGF SPRPASGPPPSLSLRLFQQPG*TVW SPGPPCPVVPDCTSASGQVPFLPPAF RFKNVF*PSRPSGTRGGP/PP*VCTS R/PLP*TSEPQPQPG
4662	10159	A	4961	301	343	TRMAHFWS*STKPSPMGPIQWSHM PGAFSE\SSSCHSHSAFLPPYFSGPS NRPPIRALCRNLPLPLPNKPRAPSAA DEDNSLNVEWYVPYITRPQA*AALI KINQDGTFLVRDSSKK
4663	10160	A	4962	2	319	ARGPGPSGKSGARSGLGNTPRRG AGLGRVPWSLCY*EGVESGRPEGA GPGTSPGVGFIGAYHGRGVTKVGG

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPG/GQACGVWSDPKSPGEPVEPIPG GSWPPQREP
4664	10161	C	4963	109	372	MQAWINIRKSVYVIHCVNKIKXXX XXXXXXXXXXXXXXXXXXXXXXXXX XKLRLRLPQPVKGHLQKPMADIPN GKKLKASTTKIMNKTSS*
4665	10162	A	4964	3	990	RTLRECYK/HI*ANELNNLDEMSKL KDA/TLLQLTQEEIETLKYNNEIE*I M/NKLPTKKSPGPHGFTG*FYQMFO EEFTPILSRL**KIKEEGTVPNLLYEV /SIIMIPKPKDKITRPVSLMIIGAKIFK QNI*HTQVYAHIHRIVYHDHNGFM QAWFNI*KSVYVIHCVNRIKDKNH MIVSIGA/EKAFDKIQHPFMVKTCT QERTF/FILLKGIY/NKPMADIPNGKK LKA\PLRSGTRRVPDFRWKWO/CP LPLLFSIVLEVLARAVRQEKEIKGM QIRKVVKLFTDGMILYVEKSKESTI KTSKLINRFNKGSEYKANIKK*VVF L*SSNQQT
4666	10163	A	4965	3	314	HENDSNPETDNRQEGPSQENIGRVS D/MAFVPSAWTASGGVAWGNPGES GSRTGGVRAETLAPRLQV*PAHLIG HPRSNRGQGRPPWKAGKLKCCQEV LFRFAAF
4667	10164	A	4966	2	329	ARGEERKAFRCIYDCVIHE/CEECR KAFRCIYDCVIHERIHNGEKLYEC*E CETSLSSNSVLIQHQRHTAEKPYEC NECGKAFHRTSVFLQHQRFTGEQ LYKCNECWKTRFCSSRFIVHQRIHN G*KPYECNECGKAFHRTSVFLQHQR FTHTGEQLYKCNECWKTRFCSSRFI VHQRIHNG
4668	10165	A	4967	61	533	WTEPVRHPDIHSQKREPSLMPPTVT GPGTTNMLFQPHRGPEKSRVPLHSS SSSSSSSSSSSSSSSPKTF/FGAPK/LP PSAPTSPDLAQAS*GLKSWKPWSGE RRFGCSKQRRALPTAS*FQGQSHAA PETPSYVGQDQSPSPGG*RPSTSPEG DSCFP
4669	10166	A	4968	22	482	GKGP GPPGGVCKSTLPPAKPWRGPP HLPLPLGL*EKALPRALGQWEGRES FWDQPGKLPLQN/PPRSLGVAMGT QAVEIPDGRPLDLSPTPAHSFSFLAL KPLLGEARVHFRASAWPLPTRAWT LDLPQLGWGFWDCLMALESRSSG ESPSLL
4670	10167	A	4969	146	1299	GAPGPWPTGTTWLPGAAGAVPDPG FLLPSSAALSRSTAS*FSQPPVPAL TVPWPRCGC*TSCPAVPQSP/GLPR TLVPACRGLPLSSVPSSPASRPKLPL HSPSSWSIPPEGSWGPLPTTLPLPWG L/PRLQSREHKPALSAATWQGLVVD PSPHPLLAFLPLSSAQVHF*PGLRSW VGPFGLRKQP*HTGLSSLTTGCCP AWLTSWPRISQSERKAHP*CLPL*Q ALSPPISYFNLTVDLRNRDYHSASS SSSSSSSSSSSSSSSRRLSWSPKHHPL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPSFILSWPQGIPRGLKNPGKTRGGL GWWKKGFLANWLSKKPRRKKGPS FPPLVL*FQGPRALPVPRNPHPKLG ASSQSPSPWWGKRPKPKSPGNGTS WLPPK
4671	10168	A	4970	298	954	QVQGHEDFLGARNTTLCSSFSCPGP GILGAEILETVGWCEKVCMLRAEK GSPHCFVIPGPEPCSPRNPFLAGAGP ESKPWWVEAKQKP*SGLLLPLVVFS VPRS*NCEPGVGERSGRGVHLGFLQP GYP*PHQGFWEILQGQLSRLFPNSSL PPH/MPLKPQQKSHSSHKQKGRGKN EEKTLCQVICRQRMGLVP*QHPTPC GAPSPHPHPQTPPKQVPYL
4672	10169	A	4971	4	410	PIERPHELKHRLPHVQKLVEDVGDG VIPAALEEGQAGWSHGFLVFLVEIK SAEGP/PGPADSRVRGVRPQRSQSA GPA*RAGRQDGVCRSLGQGRGGGR ATSLVLHPPGYPGCWFSVGVPSLPQ YTGIRSSSPRTRG
4673	10170	A	4972	148	268	LQPR*PLTCAPPPCPVQTQTHPISVS QTLLGLEFCCSLSL
4674	10171	A	4973	397	1449	RSHPSGTGRRTSRLESWFLGVSCKK SKVREGPLGPA**AG*RGVRPQRSQ SAGPA*RAGKRQDGG/SPEPRAGVG GEVGTQSP/GPSGASGYPGMLVSKP VGGTSASWLPAGCPIPS*LS*QRSQG SPSSCLIGHLLALWAAFGLVTSPLP QYTGIRSSSPTA*ATVQGDGSHKGG TGGTGLGRGRNTQPDACGRGHR SPTR/RPHGNPNNGNTGCAEGGQARS LLPKLAPKLPGWVPSVPVAVGPGD FGWRQAQYQSSLWDLSSPRNTLGR SATSAGPAPPALLGAGSGRSSGTSP AAPGCSSRCHCWASAPAGVSGGPG\ GRGAEAPPSPTLAQRGSPPG\AAIFP PACGIPP
4675	10172	A	4974	2	637	ARAKEV*DLYTERTK/PLLKEIKEDR NKWKHTSCLWIARLNIVKMSILCKL VHRLSAITIKI/PCWLCLAEIDKLILK/ FIWKFK/RSRVAKTVLKKKRVRL TLSNFKTYFRVTVIKIEWLWQKD KYIDQWNRIKSLEINSYICGLLIFYK SAKTIS*ENSVSWYLDNWIPTCERM KLAPYIIYKKIK\WIKDLNIRAITVKL IKENIGPGARL
4676	10173	A	4975	254	590	KARYILPDLMIGLDFFFFLGETKFP FAPQPGGHQGDG* LTPPRSGNYRLGPPPLNFFVF*KKR GGPHVGQTGFELLT*KDPPPLASQR AEITGGTHHA
4677	10174	A	4976	103	378	CFLYSICRGADTQRRFKLSDSLINST ECLHVHCRGLEISLADCAYT*ILTK GNHNPLS*YTFMRN\AKQPVN*YHR CTETFSLTRMELLVSV
4678	10175	A	4977	2	327	RQCLALWPRLECSGVIIAHHSLHLL GSSDPPTSAS*VAGTTGMHHAQLI/ LFWVLIDTG*CYVAQTGLEPLNSGH

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						PPTSASQSAGIIGLRHRAQPCVFQSS QKRGPELF
4679	10176	A	4978	19	1009	KTTQQQNLFFSSAHETFTNTDHL GHETSDFDMF*HIQVI*STFLYHNVIK LEVNSRKISGKCPNMWKLNTVLS NTKIINFLDNKQNETIKI/RAETNELE NR/RTEKIN*TKM*FFEMINTIDKSL AR*SRGKRHKLLISGMTNVVSHCVS LPTLFLFQSCFDYILTTLHFLINF/QN RFNNLYKMIRGY*QLYKN*FDKLH EMKNFL*/RY*LPILTQEEI/S/HLNSPI YILKIEIVVLNLPNTKTYW*TLKF/EE MIPVHRLFQKQETLPNPFYEVSITPI PKI/QD/D*TKENFRPISLVDKIPSK NLSNYICSLNASHPQRSTDPNLQ NF
4680	10177	A	4979	3	358	STSNAYHSNSLHQIQIKEKKNHTILSI DAEKAFYKIQEPLLAITL*NRNSGN/ FLNMLMTTY**PKVNVILIGNITIPY* YFAFLP*KLRTQRSRLSSLFNLVK NPANVTVISINIKRK
4681	10178	A	4980	3	341	FFETESNSVAQAGVQWHDLGSLQP PSPG\SSNSPASASRVAGITGACPNV QLISVGFLFFVFWFFFETESLSVAQA TGVQWVRSWAYCNLRLPGSGRFLC LCLPSSWGLQGV
4682	10179	A	4981	658	1001	LILSARPPKGEKGSFLLAEFSSYFHS GLFSSARSFFFFFFFETESHCVQA GVQWLDLGSLLQPPPG\SSNSPASAS QVAGTTGVCHHAQLIFVLLVETGF HHVGQAGLELLTS
4683	10180	A	4982	53	394	PQQSGFWFIYFSKQGCFFVNILNIC SFVLFFFETESCSVAQAGVQWHDL GSLQPPPG\SSDSPASASRVAGITG ACHQTWLIFVFLVDMGFRHVGQAS LKLLTSGFKKWVT
4684	10181	A	4983	66	516	HFYQFFPHFSGRMDLWSSLLCHFF MTSQFVTFVLLYFIFVYILSV*LD F*MRKQT*LISG*ASI*YRYV*LQNL YVLKLYITPLSL*AHVLIYL/CYLKS ESHSVTQAGVQSHNLSLPPRFK*FP CLSLPNG*DYRNVPPHPANFCIS
4685	10182	A	4984	3	324	HENRMKYEISINMWKLNNIFLNKL WVKEITSRLQKYFECSENKTTTYQK L*DAKKMNQCQGYLWVFMALSA* ISKRKRLINILSFYLSKLEK*EPTK PKASSRKVV
4686	10183	A	4985	108	277	ARVIRANFCIFGKDRVSPCCPG/W/ SPELPGLKRSPSLPKCWDYP*AT APGQHPYS
4687	10184	A	4986	29	454	
4688	10185	A	4987	116	424	
4689	10186	A	4988	1	1217	PPTTCTPACQGLSGAAMKSLVLLC LAQLWGWSAPHGPGLIYRQPNCD DPETEEAALVAIDYINQNLPGYK HTLNQIDEVKVWPQQPSGELFEI IDTLETTCHVLDPTVARCSVRQLKEH

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						AVEGDCDFQLLKLDGKFSVVYAKC D\SSQDSAEDVRKVCQDCPLLAPLN DTRVAHAEKAALAAFNQNGNSN FQLEEISR\AQLVPL\PPSYTV\LEFTV SG\TDCVAK\EATEAAKCNLLAEKA IMAFVKATLK*ESLGGGRRLLQLTCT VF\QTQPCDLHSPNPEGANEAVPTP V\VDP\DAAPPSPPLG\APGLPP\AGSP PELPCFYWAAPP\G\HQLHR\AHY\D LR\HTFHGVWVFIGGHPSGRKCSHP PGKHGTVGSSLVFWCCCCLGPVVP SIVPG\RIRHFKVLG
4690	10187	A	4989	1	443	KKFVIPDFEFTGHVGRIFEDVKELT GGKVAAYIPQLAKSNPDWVSLC TVDGQRHSGHTKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAIIVS SLIKMDCNKA EKFDVFLQHLNKK
4691	10188	A	4990	3	217	ATKRKKKMKDKDKA\KLEAMGTS KTNEEDKRRGLDKRTPDQAAFEKM QEKRD\FSRHLDTL\TEHYDIPKVHH
4692	10189	A	4991	3	475	AATESGMVAYYQVQKGPLKLKG VAKLGVT\K/RVRPEGPRDSVFIPLPK FLGTPGPDPTRRLLMFFSRKKKKK DKDKAK\LEAMGT\SKKNEEEKR RGL\DKRTPAQAAFEKM\QEKRHME RILMKA\SKTHKQ\RVEDFNRLGTL \TEHYDIPKV\TWTK
4693	10190	A	4992	783	5158	PKSGRRRDVEGGVCCFLSLRNSR YLLSTHILERGKASLCHPGWNAL VPSPLTAASASWVQVILLPLSLPSG WDYSLHLEELTGESPTSERAFNYH PTTCLRRKILQDSEHTASTRGPMTL DRPGEGATMLKTFTVLLFCIRMSLG MTSIVMDPQPELWIESNYPQAPWE NITLWCRSPSRISSKFLLKDKTQMT WIRPSHKTFQVSFLIGALTESNAGL YRCCYWKETGWSKPSKVLELEAPG QLPKPIFWIQAETPALPGCNVNILCH GWLQDLVFMFLKEGYAEPVDYQV PTGTMAIFSIDNLTPEDGVYICRTH IQILPTLWSEPSNPLKLVVAGLYPK PTLTAHPGPIMAPGESNLRCQGPY GMTFALMRVEDLEKSFYHKKTIKN EANFFFQSLKIQDTGHYLCFYDAS YRGSLLSDVLKIWVTDTPKTWLL ARPSAVVQMGQNVSLRCRGPVDG VGLALYKKGEDKPLQFLDATSIDD NTSFFLNNVTYSDTGIYSCHYLLTW KTSIRMPSHNTVELMVVDKPPKPSL SAWPSTVF\KLGKAITLQCRVSHPV EFSLEWEERETFQRFVNGDFIISNV DGKGTGTYSYSYRVETHPNMWSHR SEPLKLMGPAGYLTWNYVLNEAIR LSLIMQLVALLLVWLWIRWKCRRL RIREAWLLGTAQGV\TMLFIVTALLC CGLCNGVLIETEIVMPTPKPELWA ETNFPLAPWKNLTLWCRSPSGSTKE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FVLLKDGTGWIATRPASEQVRAAFP LGALTQSHTGSYHCHSWEEMAVSE PSEALELVGTDILPKPVISASPTIRGQ ELQLRCKGWLAGMGFALYKEGEQ EPVQQLGAVGREAFFTIQRMEDKD EGNYSCRTHTEKLPFKWSEPSEPLE LVIKEMYPKPFFKTWASPVVTPGAR VTFNCSTPHQHMSFILYKDGSEIASS DRSWASPGASAAHFLIISVGIGDGG NYSCRYYDFSIWSESPDPVELVVTE FYPKPTLLAQPGPVVFP GKSVILRC QGTFQGMRFALLQEGAHVPLQFRS VSGNSADFLHTVGAEDSGNYSCIY YETTMSNRGSYLSMPLMIWVTDTF PKPWLFAPSSVVP MGQNVTLWCR GPVHGVGYILHKEGEATSMQLWGS TSNDGAFPITNISGTSMGRYSCCYH PDWTSSIKIQPSNTLELLVTGLLPKP SLLAQPGPMVAPGENMTLQCQGEL PDSTFVLLKEGAQEPLEQQRPSGYR ADFWMPAVRGEDSGIYSCVYYLDS TPFAASNHSLSLEIWVTDKPPKPSLS AWPSTMFKLKGDITLQCRGPLPGVE FVLEHDGEEAPQQFSEDGDFVINNV EGKGIGNYSCSYRLQAYPDIWSEPS DPLELVGAAGPVAQECTVGNIVRSS LIVVVVVALGVVLAIEWKKWPRLR TRGSETDGRDQTIALEECNQEPEPG TPANSPSSTSQRISVELPVPI
4694	10191	A	4993	1	369	GTFQLPKPIFWIEAETPALPGCNVNI LCHGWLQDLVFM LFKEGYAKPVD YQVPTGVTMAIFSIDNLTPEDEGVYI CRTHIQMLPTLWSEPSNPLAKLVVA GGCGLWLLASGNCCPRYHGWS
4695	10192	A	4994	183	429	ISIKSMKLISDYKYCIYIYRYHRDVI RLGIIDIYSVLHPTSAQYTFSSLHGT LTTDRNILGHKT LNKFKRIEIRQYL FSDQ
4696	10193	A	4995	2	270	TSGCLQGSCCVTGPPGAVGRASRSR PSTRPPSRARPLGSPGCSARAQDAA DLPLPPPPPPCCSPSAGCRCSLGCF RRCPLRSSRRSRF
4697	10194	A	4996	1	428	NPCLSERQGCCEKLPLERSSTPQDS AGHPVT/HAHCSLSPVDLCPLLLAT HRISCWHCQDEVQGGTD\SADTGD LEALSLLAGHGD TDGHIILDVPDGA PYPQRTKAGIDHLHQKILKHEQITIE HEARDDNAPDYPKLANN
4698	10195	A	4997	131	412	RKWLKLLPCSFFSSKNIYAETFSPCV CIRVCIHVCVYTCVYTCVCIHVCSC PC/VGQASALKSVSLCQLHCILVLTP MLTLRFDKKFFTQDSHFI
4699	10196	A	4998	2	175	KFTWKHKGPRIARNILKRKIKVEGF TLPNFKTYKAAVTETVWYWHKD SGLDHFVLL
4700	10197	A	4999	2	175	KFTWNHKGPRRIARNNLEKENKVEG FTLPNFKSYYKAAVTETVWYWHK DSGLDHFVLL

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4701	10198	A	5000	1	909	MVLEVSVSDDRAVWRLWRAPIGES QQRSLGFWWSKVLPYSADNYFPFER QLLACYWALLETDRLTVGHQVTLQ PELPIMNWVLSDPSSHKVGHVHQH SIIKWKWYIRDQTRAGPEGTTTPVIT Q/WDAHEQSGLSGRDGGKQRFVLT GVDTYSGYWFAYPAHNASAKTSIY GFTECLIHCHGIPHSIASDQGTLF KEVWQWAHAHGIHWSYHIPHHPIA AGLIEWWNGLLKSQQLQCGDNTL QGWGKDLQKAMYSLNQRLIYSTVS PISRIHGSRNQRVEVEVAPLTITLSD PLAKFFFLP
4702	10199	A	5001	1	1014	
4703	10200	A	5002	349	718	AGPEGTTTAACP//CQQQRPILSLRY GTISWG/DQSATWWQVDYIRTL WKWQSASAKTTIHGLTKLIHHDIP HSIASD*GTCFMAKEVWQWYCF SQDSRVQESRGGIGSCTTHHPCSF PN
4704	10201	A	5003	1	558	
4705	10202	A	5004	1	2205	MGAVFEALWQYSPPELPAKASVMVQ EASKAIGQCQSSAAKLRRSGKESVT EPWARVLGALEMAARLYKVTS CHGIHTPSWRCLCFSTGGKERHAH DLPHVTAQSQGHQGGQKISRTALK EPTVHKVTASLSPVATSPQPMPLP SDFPPLSEEINPMLPEATVIASPK EIA RQDNVDSPQEPPTPQFSSRPIT RLK SQWAPRGPECVIGIDILSSWQNP HIG SLTGRVRAIMVGKAKWKPLELPL RKIVNQKQYHILGGTVEISATIKDLK DTEAVTPTTSPFNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAVPD V/VSLLEQINTSPGTWFEWSPKKAL QQVQAAVQAALPFGPYDPADPMVL EVSVADRDALWLSLWNAAGESQRR PLGFWKALLSSADNYSFPERQLLA SYWALVETERLTVGHQVTLRPELPI MNWVLSDPSSHKVSGAQQRSIIKLK WYIHDWVRAGPEGTTTSVITQWAH EQSGHGGRDGGHAWAQHGLPLT KADLATATARIHRSRNQGVKVEVA PLTITPSDPLAKFLLISATSTSLEVT VPEGEMLPPRDTTKIATFGTQTGFL ALQLADGLLWDLVIIPGKGKPSRDL VESPSPYSTYEGIDGWDEPAPTAT KPPVMPAPALPPDTRSGSKAPT VPT PYPQMEHHQVQLASNNSTEALGH LSPQSSWVQTPGQNSGAIPNHLGK DMISPPQMAPAGVKWESQKY
4706	10203	A	5005	155	531	GNLWSVDLRPGTPLRQNFRTIRQQ HSRFTKNHCSQTPLIPRQTGSGVD LSKLQQTCS*GSCLVCTIDLANAFFS IPVHKA/HQKQFAFSWQYFTVLP R LTWLQPC*VPNLPAETNTEPSNGT
4707	10204	A	5006	1	518	MTVDYCKLNQVVIPIAAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP

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						VHKAQQKQFAFSWQQQYTFVLP QWYINSPALCHNLIRRDLCFSLPL DITLVHYIDDIMLIGSTIKWVVHSS/ DSIIKWKWYVHDWARAGPEGTTN GLAG*SGTCKKHEWKTGDKGIRGR G
4708	10205	A	5007	1	2592	MVRKAKWKPLQLPLPRKIVNQKQH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCRMTVDYC KLTQVMTPIAAVVPDVVSLKQINT YPGTCK\FLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAQLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEALQQAQVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYSPFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLS DPSR HKVGHAQQHSIIKLKWIYICDQARA VPEGTC*LNKEVAQMP/MGTTRKW TAAALQSLSGISLKDSGEGKSSQWT ELQAVHLVVHFAWKEKWPGTWKK HDWKTGDNEIWGRGIWMDCSEWS KTVKIFVSHAHEPSGHGGRDGGYA WAQEHLSFTKADLATGIVECPICQ QQRPTLSPRYGTIPQGQTFILTGINT YSIYGFAYPAHNASAKITIRGLTECL IHGHHGIPHS/IVSD*GTHFTAKDV\ET RIHRPRNQGEVEVAPLTITRSDTL AKFLLPVPTTFRSANLEVLLLEGGT LPPGDPTTIPLNWKRLRPRGHFGLPL PLSQQAKKGVSVLAGVTDLDYQDE FSLLLHNRVTAAPFSLHSSFAILD NMIEKANKCHVEGVHDVSDPAQRR ECDRHTGSSCHLLRGPPQLQSQLVS GPRSPKSDSGESCLAWDPTFKAQVS PLAQGSPRNSVQEPSRGTGSPKSLG ALIALWPSWYLSSDPDPQGSNSRNL EISACQKYLSPAFGNSDYSTAEDFN SDYTLKSPENSIGYARLEKHRRLYG GDGGDGGGDDVRGGKRGDDASR KGVTERV
4709	10206	A	5008	1	942	MVGKAKWKPLELPLPRKIVNQKQH HIPEGIAEIAATIKDLKDAGVVIPTTS PFNSPIWPVQKTDGSRMTVDYCK LNQVVTPIAAAVPDVVSFLEEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFVLPQDYINSLA L*HNLIWRDLDFLLQDITLVHYI DDIMLIGSNDHKVGGAAQHSIIKWK LYIHDQAQTGPEGTTTSVIAQWAHE QSGPGSRDGGYAWAQHGLPLTK ADLATTTAECPCVQQQRPTLSPRYG TIPSLPLTKALTLQLKKCSSGPMLM EFTGLAMFPIILKQLD
4710	10207	A	5009	1	1795	MRKCGKPQFKLGQTNKANSRIQEE LIHKSLSIEQEGEKPQVQSAFHRMW QPADSQCDIIDSADIWADPLVRHREI

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						ITGSGGINRRRTRGGRGRGGEEAAGG AENCGSREERERAGVGTAVTQLQN LNTIGIIGSRGGRGQVAANHQRQG GHSYCKGQKQNSNQNSVTHVEL WHWLNHSVPRSEIDRKPTTFLNL YKQKTSRDLWPFTRVTLHRGKRND QTFQGLLDTGSEMLIPEDTKHHCG PPVKVEAYGGQVINGVLAQIQLTV GPVSGSHTPVVIYPVPECIIGILSS WQNPHIGSLTSRKTDGSRMTVHY HKLNQMVTPIAAAIPDVVSLEQVN TSPGSWYAAIDLANAFFPIPVHKAH QKQFAFSWQGGQYTFTVLPQGETL VNFSLPQDITLFHYIDDIMQIGSSDQ EVANTLDLLPRKSTTPSG/LYGFWR QHIS/HLGLLLTPIY*VTQKAA/SFEW GLEQEALQQVQATVQASLPLGVY DPADPMVIEM/SLSDPSSHKVGAQ QHSIIKWCRYVCDQA*ASPEGTS*L YCTSFIMEKEEVC/LSLEQTLTDMG LPILHAMLLWIHLWIHGLPYPSSWY STQQCL
4711	10208	A	5010	3	169	DFQPFTRVTVHWGKGNDQTFRGLL DTGSELTLPIDPKHHYGPVKVG/ AYGAQLL
4712	10209	A	5011	1	562	
4713	10210	A	5012	3	591	DPADPMVLEVSEADRDA\VPISSEQ QRPLGFWSKALPSSANNYSFFKRQL LACYWVLVEIEHLMGHQVTMRPE LPIINCVLSDPCSHKVGHAAQHSIIK WRWYIHDWAEGTSKLHEEVAQIPM VSTPSLPQAPMASWEVPYDQLTEE EKTRAWFTDGSARHAGATQKQWTA VALQPLSGTSLQDSSEEKSSQWTEI
4714	10211	A	5013	2	586	
4715	10212	A	5014	3	514	
4716	10213	A	5015	1	994	MVRKAKWKPLQLPLPRKIVNQKQH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCWRMTVDYC KLTQVMTPIAAVVPDVVSLKQINT YPGTCK\FLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAQLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEALQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYSPFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLSDP SRHKVGHAAQHSIIKLKWIYICDQARA VPEGTC*LNKEVAQMPPM
4717	10214	A	5016	1	643	MVGKAKWKPLELPLPRKIVNQKQH HIPEGIAEIAATIKDLKDAGVVIPTTS PFNSPIWPVQKTDGSRMTVDYCK LNQVVTPIAAVVPDVVSFLEEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFTVLPQDYINSLA L*HNLIWRDLDDYFALLQDITLVHYI DDIMLIGSNDHKVGGAAQHSIIKWK

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						LYIHDQAQTGPEGT
4718	10215	A	5017	3	1074	VTASLSPVVATSPQPMLPSDFPPLS EENPMLPEATVIASPKFIARQDNVD SPQEPPTPQFSSRPITRLKSQWAPR GPECVIGIDILSSWQNP HIGSLTGRV RAIMVGKAKWKPLELPLPRKIVNQ KQYHILGGTVEISATIKDLKDTEAV TPTTSPFNSPIWPVQKTDGSRMTV DYCKLNQVVTPIAAAVPDV/VSLLE QINTSPGTWFEWSPKKALQQVQAA VQAALPFGPYDPADPMVLEVSAD RDAIWSLWNAAGESQRRPLGFWS KALLSSADNYSFPERQLASYWAL VETERLTVGHQVTLRPELPIMNWV LSDPSSHKVSGAQQRSIIKLKWIH DWVRAGPEGT
4719	10216	A	5018	1	1482	MAPNSRVQELVLGQVAVICQGLLS LQPRTEGYTVGFLTFEVLDLTGSSA CRWPIVGLHSVILLDKVTKKDEL RDSNSWLQKQILSLKFSKTALSES SCRQRAEIVENQTQGLIMRPLAFHR GNCIGERGMTILFRGYWTEPTLIPED PKHHCSPPVKVRAVEDGSWKMTV DYHKLQVMIPVTAAPDVVSLLE KINTSPALFHNLVQRNLDCFSLPQDI TLVHYVDDIMLIGSSEEVANTLDL LVRRLCAKGWEINLTKIQGPSSLVK FLGVQWCGASQDIPSKVKNKLLHL ALPTTKKEAQCLVGLFGFWKQLIPH LATPIIPQRAHEQSGHGGRNGGYTW AQHGLPLTKADLATATAECPICQQ QRENGA/PRYGTIPRGDQPATWWQ VDYVGPLPSWKGQQFVLTRIDTYS AYGFAYPTCNASAKTTIHSLTACLI HRHGIPHSIASDQGSHTAKEVQQW AHAHGIHWSYHVPYYPEATGLIEW
4720	10217	A	5019	1	1494	
4721	10218	A	5020	101	304	
4722	10219	A	5021	1	1912	MTVDYCKLNQVVIPIAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP VHKAQQKQFAFSWQQQYTFVLP QWYINSPALCHNLIRRLDCFSPL DITLVHYIDDIMLIGPRQLACY/W ALVETEHLTISHQVTMRPELPIMNW VLFDPSHKVGCAQQHSIIKWVY VHDWARAGPEGTTTPVISQWPHEQ CGHGGRDGGYAWAQQCRLPLTKA DLNTATAKRPICQQQRPTLSPQYGT IPQGDQPATWWWVDYMGSLPSWK GQRFVLTGIDTYSYGFAYPACNAS AKTAICGLTECLIHHDIPHISASDQ GTHFMAKEVRQWAHDHGIHWSYH VSHHPEAAGLIEWWNGLLKSQQLC QLGDNTWQGWGKVLQKVYALN QHPIYGTVSPIAKIHRSRNQGLEVAP LTITPRDPLAKFLFPATLQSAGLE VLVPEEGLPPGDTMIPLNWKLRLP PRHFGLLLPLNQAKKGVTVLAGV

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						TDLDYKDEITLLLHNGGKEEYAWN TGDPLGLLLILPCPMIKVNGKLQQL KPEALVPKGVVFPDGTMLSLSW KLRLPSGHVGLLMPLSQQVQKGV VLAVIDPGHTSAASLVLRSCVWS GSDTIVSPGSQDFRLGINDTTGFPV PD
4723	10220	A	5022	3	835	DLWPFTRVTVH/WGKANDQTFQGL LDTGSELTLPGYPKRHCCPPVKVR VYGGQTDGSRMTVGYHKLNQVV TPIAAAVPDVVSLEQINTPSTWY GQVAAFAPPTTKKEAQRLVGLDF GGNTLLIWVYYSGLSSDLKGCQFE WDPEQERLCKAFSAHSQWFGCQGL GRSVDWKIDDKKLGKMRMDLSE LGKNREEYWYPVQQAQKGVKVL VVIDQTIKMKSVYYFTMEKTCQRQ ATTAELEPEKNVIGVDETVEGQSYH SSKQKDIPFQGEK
4724	10221	A	5023	2	1300	DLWPFTRVTLHRGKRNDQTFQGLL DTGSELMIPEDTKHHCGPPVKVEA YGGQVINGVLAQIQLTVGPVSGT HPVVIYPVPECIIGILSSWQNPFIG SLTSRKTDGSRMTVHYHKLNQVM VTPIAAAIIPDVVSLEQVNTSPGSW YAAIDLANAFFIPVHKAHQKQFAF SWQQQQYTFTVLHQGYNSPALYH NLIWRDLDRFSLPDITLIHYIDDMT LIGSSEQDVANTLDLL/SDLSRGGF* *SSG*DDPFCGHHSASFSPHPCNRP MGP*TK*PWGQGWRLRMGSATCTP THQG*PGYGHC*VPNLPAETNTKP SIWHHSSG*SASYQAAG*LYWTSFI MERA EVRP/TWSTCLLWIWVCLSCT QCFCQDYHLWTHGMPYPLSRYSAQ HCL*PRHSLYS*RSVAVGSCSWNSL VLPCSPSS*SSWI
4725	10222	A	5024	2	790	PRGRNRRRKTFQERRMTL NESPEKI GK WIECYGHPPASKLVEIYIHTVFV EDKLSICIRSFNKKADGSRMTVD YCKLNQVVTAIAAAIPDVVSLEQI NTSPDTWYAAIDLANALFSIPVHKG YINSLALCHNVIWRELD CFS LPRDT TLVHYIDIMLIGSSVQEVENKLDL LVKDKLLHLAPPTTKEEVQHMVGL FGFWRQH IPHLGVLHQPIYRVIRKA A/SFEWGPEQE KALQQVQAAVGGK QSENNLGHQ RSPGLWFS
4726	10223	A	5025	281	1461	VRVLS PVEKELKLWKNTHKLLSYP TVGAAVTQLQNLTAMGVIGSHGAR GOVVALNRQRQGDLPFTRVTVH WGKG/NMQIFGGLD TGSELTLP DPKHHCGPPVKVGAYGGQVINGVL AQVQITVGPQTHPVVISPVPECIIGID ILSSWQNP HIGSLTGIMVGKAKWK QLELPLPRKIVNQKPYCIPGGTVEIS ATIKDLKDAGVVIFTTSLFNSPIWPV QKTDGSRMTVGYRRLNQVVTPIA

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						AAVPDVVSLEQINTSPGTWYAAID MANAFFSIPVHKAHQKQFAFTWQG QQYAFTVLPQGYINSPALCHNLIWR DPDCFLLLQNITLLVHYVDDIMLIGS SEQEVANALDLLVFSDLAIKWVM HSSIASSSGSGICVIRLKKVLAQ
4727	10224	A	5026	1	3179	MAEDKEEQVPSYTDGSRQRENEED TRVKTPDKTIRSHETYSLPREQYGG NYAHDSIISHQVPPTTCGNYGSTIQD EIWVGDSHSGYVRPVPVPRSLNSDIS YFGVGGKQAVFFVGQSARMISKPA DSQDVHELVLKEDFEKKEKNKEAI YSGYIRNRKDDYDNHTGIDLVTGII ATIKGSNEEDTDTPFIGKVRTLEFP FVNGSAEIMLMPSNQQHKTDEKGR ANLGVFSVFAPRGEHTLQVKAIYN KSIIEGPIIKLMILPDPEKPVRLNVKY DKDASFLAGGLFTAPPLPAQLMSSL SCAWIIESVLNSWRKGCNKLNRQR ALHKKQDRGKLPEDRELQHTKKQT NWAGLLIPAMNNNVDMTARKLQR DLQPFTSVTVHCRKGNDQTFGGPL DAGSELTLPKDPKHHCPPVKVGA YGGQVINGVLAHPLIWLTVQKTDGS /WRMTVDYCKLNQVVIPIAAVSD VVSLEQINTSPGTWYAAIDLANAF FSIPVHKAQQKQFAFSWQQGQYTF TVLPQWYINSPALCHNLIIRDLDLDC SLPLDITLVHYIDDIMLIGSSEQEVA NTLDLFVRHLRARGWEINPTKIQGP STSVKFLGFQWCGACQAIPSKMRD KLLHLVPPTTKKEAQCLQLLACY/ WALVETEHLTISHQVTMRPELPMN WVLFDPSSHKVGCAQQHSIWKW YVHDWARAGPEGTT/HPCHFPMAP *TMWPWWQGWRLCMGSAM*TST H*G*PEYSHR*APNLPTAETNTEPSI WHHSSG*STSYLVVG*LYGISSIMER AEVCPHWNRYLLWIWVCLSCMQC FCQDCHLWTHGMPYPPS*YPTQHC L*PRHSLYG*RSAAVGS*SWNSLV PCFPSS*SSWIDRMVEWPFEVTITVS TR*QYLAGLGQSSPEGRVCSESASNI WYCFSHSQDSQVQESRARS GTTHH HP*GSTSKIFASFSCNITVCWPRGLS SRGRNAATTRHNDIKLEVKIATQT LWAPPTFKSTG*EGSYSVGWGD*PG L*R*NHSPTP*WR*GRVCMEYRRSI RASLNITMPYD*GQWETTAAQARSS
4728	10225	A	5027	2	1284	CHCGPP/VKVEAYGSQVLKGVLAQ VQLTVGPVGPRTHPVVFIPVPECIIGI DMLSSRQNPHTGSLTGRVWTIMVR KAKWKPLELPLRKIVNQKQYHIPE GIVEISATIKDLKDAGVVIPTTSPFNS PIWPVQKTDGSRMTVGYCKLNQ VVTPIAAAVPDVVSLEQINTPPGT WYAAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEINMT

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						KIQGPSTSVKFLGVQWCGACQDIPS KVVDKLLHLVPPTIKKEAQCLVGLF GFWRQHPLHGMPLQPIYRVQTMA ASFEWGS\EQEKALQQAG\QAAVQA ALPLGP/HKDPADPLVLEVS\SDRD AVWRLWQASI/GHKVGHAAQQHSIIK WKWYIRDWARADPEGTTKGQGGQR RWWQLAERQDSRDREAAIGERQET AVGKTARDGEAVCD
4729	10226	A	5028	422	1252	TTLFSVQIFQWRQLENLYFREKKFS VEVHDPRRASVTRRTFGHSGIAVHT WYACPALIKSIWAMAIHQHYLD RKQSKSKIHAARSLSEIANDLTRTRT LENSKLANMGSKGKIHS\SSGSLSS GSGARRHCILLPGSQESDSSQSACK DMLAALKSRQE\ALETLRQRLEEL KKLCLREAELTGKLPVEYPLDPGEE PPIVRRRIGP\AFKLDEQKILPKGEEA ELERLEREFAIQSQITEADRRLASDP NVSKKLKKQRKTKYINAVKKLQVY
4730	10227	A	5029	1	400	RHEERTTGILTSEGLASDTSLICVIED FFDTALIISRSSEGGKIQMLDSFLLSL GFLVTEKTVNHLLQQEERPCMDTL DCG/LQVAISEALCRLTIKKS\RDDEL HKWFDDEVIAEAFKEIKDREFETDS RRFLN
4731	10228	A	5030	1	612	
4732	10229	A	5031	64	323	LFPTLWLLDLLGTVEEILPSLSENIS VWGMKDSVPQGVISLKEK\ASTSPD EPVPRSHHVVSLLKSTCLYIFTSGT TGMIOFFWKA
4733	10230	A	5032	287	508	YYSIFLIYYYYYFLRWSFALVAQAV VQWCDLGS\QPLSPGFKRFS\PSALS SWDYRHEQPRPANFIFLVETGFL
4734	10231	A	5033	1	3627	
4735	10232	A	5034	3	3613	
4736	10233	A	5035	353	406	MLHLQGIILMIVLYSCCRELIHSFLK DSKSMPCNWGESDGPVTGARHPSW EEEEDGGVWNTTGSQGSASSHNSA SWGQGGKKQMK/CSLKKE
4737	10234	A	5036	1	514	ECKDCGKSFTVSSSLTEHARIHTGE KPYECKQCGKAFTGRSGLTKHMRT HTGEKPYECKDCGKAYNRVYLLNE HVKTHTEEKPFTCTVCRKSFRNSSC LNKHI\HIHTGIKPYECKDCGKTFTV SSSLTEHIRTHTGEKPYECKVCGKA FTTSSHLIVHIRTHTGEKPYICK
4738	10235	A	5037	1	3222	
4739	10236	A	5038	1	4267	MGPWAWKLRWTVALLAAAGTA VGDR CERNEFQCQDGK CISYKWVC DGS AECQDGSDESQETCLSVTCKSG DFSCGGRVNR CIPQFWRC DGQVDC DNGSDEQGC PPKTCSQDEF RCHDG KCISRQFVCDS DRDCLDGSDEASCP VLTCPAS FQCNSSTCIPQLWACDN DPDCEDGSDEWPQRCRGLYVFQGD SSPCSAFEHCLSGECIHSSWRCDG

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						GPDCKDKSDEENCAVATCRPDEFQ CSDGNCIHGSRQCDREYDCKDMSD EVGCVNVTLCCEGPNKFKCHSGECIT LDKVCNMARDCRDWSDEPIKECGT NECLDNNGGCSHVCNDLKIGYECL CPDGFQLVAQRRCEDIDECQDPDTC SQLCVNLEGGYKCQCCEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKM TLDREYTSILIPNLNRNVVALDTEVA SNRIYWSDLSQRMICSTQLDRAHGV SSYDTVISRDIQAPDGLAVDWIHSNI YWTDVSLGTVSVADTKGVKRTLF RENGSKPRAIVVDPVHGFMYWTD WGTPAKIKKGGNGVDIYSLVTENI QWPNGITLDLLSGRLYWVDSKLHSI SSIDVNGGNRKTILEDKRLAHPFSL AVFEDKVFWTDIINEAIFSANRLTGS DVNLLAENLLSPEDMVL FHNLTQP RGVNWCERTTLSNGGCQYLCLPAP QINPHSPKFTACPDGMILLARDMRS CLTEAEAAVATQETSTVRLKVVPD KTVRWCAVSEHEATKCQSFRDHM KSVIPSDGPSVACVKKASYLDCIRAI AANEADAVTLDAGLVYDAYLAPN NLKPVVAEFYGSKEDPQTFYYAVA VVKKDSGFQMNQLRGKKSCHTGL GRSAGWNIPIGLLYCDLPEPRKPLE KAVANFFSGSCAPCADGTDFFPQLC QLCPGCGCSTLNQYFGYSGAFKCL KDGAGDVAFVKHSTIFENLANKAD RDQYELLCLDNTRKPVDEYKDCHL AQVPSHTVVARSMSGKEDLIWELL NQAQEHFGKDKSKEFQLFSSPHGK DLLFKDSAHGFLKVPQRMDAKMY LGYEYVTAIRNLREGTCPEAPTDEC KPVKWCALSHHERLKCDEWSVNS VGKIECVSAETTEDCIAKIMNGEAD AMSLDGGFVYIAGKCGLVPVLAEN YNKSDNCEDTPEAGYFAVAVVKK SASDLTWDNLKGKKSCHTAVGRTA GWNIPMGLLYNKINHCRFDEFFSEG CAPGSKKDSSLCKLCMGSGNLNCE PNNKRGDTTGYTGAFRCLVEKGD VAFCKHQTVP TGT LGGEKNPD PW AKDLNEKDYELLCLGWVP GKPV EEYAN\CHLARAPNHRCGSHGKDK EACVHK\ILRSTASHLFGASNVTDCS GNFWLVRS\ETKDLLFRDDTVCLW AKLHDRNTYEKYLGE EYVKA VGN LRCSTSSLLEACTFRP
4740	10237	A	5039	2	342	LSRVVL SAAATAAPSLRNAA/FLGP GVLQATRTFHTGQPHLVPVPLPEY GGVRYGLIPEEFFQFLYPKTGVTG PYVLGTGLILYALSKEIYVISAETFT ALSCSAFELFRDHF
4741	10238	A	5040	53	940	DCYLDVSLTMLS RVVLSAAATAPT IIMKNAAFLGPGVLQATRTFHTGQP HLCPMYPIPEY GGVRYGLIPEE

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						FFQFLY/PLKTGVNTDPNVPETWG LNLVTVLFQRKYMVEFRRRGPSLA LIKY*GGKWVYGNLKKYGSPLVAG LWLD*TPMEQKLGPT*EE/ARQGGF PSQHIQNAIDYGRSLYQALVQKRH YLFADVQRNNIAMALEVTYRERLYR VYK\EVKNRLDYHISVQNHDAVRN GTTNSLLNWVEKHVRAKLFPPQA RKEDILPKWHCRPIKLLAKEGSKAQ AQLW
4742	10239	A	5041	2	205	APVTSW/IQPKDGSCPFSESTKTISLY ISSEQQFHLRPSSEDDFIEDTADML\ VSFSGYSSAPKNQEQ
4743	10240	A	5042	1	360	SPCLSERQFCCEKLPLQRSSRPQDSA GQPVT/HAHCSLASTVDLCPPLLAT HRISCWHCQDEVHGGRD\SVDKGD LEALSLPAGHGD TDGPISLDVPDGA PDPQRTKAAIDHLHHKILKSTE
4744	10241	A	5043	106	396	
4745	10242	A	5044	77	4026	
4746	10243	A	5045	1	344	LDFIQTMLQVVGVSVAVPV/IPWI AIPLVPLGIIFILRRYFLETSRDVKR LESTTRSPVFSHLSSSLQGLWTIRAY KAEERCQELFDAHQDLHSGLSISGN GFKGQDLLFLA
4747	10244	A	5047	3	378	ERDGALTLPLTPGLSPPPPLPP/HTSS QAHYRLSAFGQQFLFNLTANAGFIA PLFTVTLLGTPGVNQTKFYSEEEAE LKHCFYKGYVNTNSEHTAVISLCSG MLGTFRSHDGDYFIEPLQSMDEQE
4748	10245	A	5049	2	278	FVNHGCSQTLHFVFKVGNRFQTAR FYRDVLGMKVQAGADRGWRARLE PAPEPALAEGGENGCVVNLSRRVS DLRPCAVFSFRSVASCRWGS
4749	10246	A	5050	1	1539	MRLTPFSLSTGNSFRYSRRLKKNIFG TAPALRVSEMSLRPSSRIFFCFSRNG LDFTIVITLAQPPVPGISFIVAKPRLF PGAGSAGCGLLERLFLSLLGTGLR WCLRGCFPGARFCSTTSPEGHTTFT GLRRSARTQRLAQGPKPGPPAATV ARQTSRVSPAPPCSLRPGLRHESAPS GIGDVTARGALRGLGCTVRVTAAC GGNHGCSQ/LCLHFVFKVGNRLQT AAFHIGTSMGMKVQQHEEFEEG\CK AA\CNGPIYDG\KWSKTMVG/YLGP EDDHFVAELTYNYG\VG DYKLGND FMG\ITLA\SSQAVSNARK\LEWPLT EVAEGVF\ET\EAPGGYKFYLQNRSL PQSDPVLKVTLA\VDLQK\SLNYWC NLLGMKIYEKDEEKQRALLGYAGL TSVSLELQGVKGGVDHAAAF\GRI AFSCPQKE\LPDL\EDLMKRENQKIL TPLVSLDTPGKATVQVVILADPDGH EICFVGDEAFRELSKMDPEGSKLLD DAMAADKSDEWFAKHNP KASG
4750	10247	A	5051	21	223	HPGSRGCSEPRSGHCTPAWGTKVK T/SRLNKNKTKQKKEVKDCMSSTPL

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						AHPPGVWCEWRGLIPSSSP
4751	10248	B	5052	64	543	RGWKRDRDKRDDQDDVSSVRSEG GNIRGSFRGRGRGRGRGRGRGN PRLNFDYSYGYQEHGERTDQPFQTE LNTSMYYYYDDGTGVQVYPVEEA LLKEYIKRQIEYYFSVENLERDFFLR GKMDEQGFPLISLIAGFQRVQALTT NLNLILPPLKDSTE*
4752	10249	A	5053	1	567	AAATSAGA/PGRAVAGAGAGTQRA PGGCPREAPGAAPGVHKARGPGGPF GGEPPPPPP/LVAVAAVAAGSAGR GRPGR\VAAGPAEKRQPPLLPPKGN PWTKKPPQHLSPDTTGPPPPPLETLE AEFGSLKIIKAGKLKTKKSNKASDF SDMENWPTPSELVNTGFQSVLSQG NKKPPNRKEKEEKGEREEQ
4753	10250	A	5054	3	763	SGRPHPVIRESSPSSSLALGGQLGRG RPSGRAAPGRANPSAPAGGPAREGP EFGSLKIIKAGKLKTKKSNKASDFS DMENWPTPSELVNTWISERPQPRK\ KKPQNRKEKEEKVEKRSNSDSKEN RETKLNGPGENRQ/STDEAQSSNQR KRANKHKWVPLHLDVVRSESQERP GSRNSSRCQPEANKPTHNNRRNDT RSW/ESEIEKKE/HDQDDVSSVRSEG GN\SRGSFRGRGRGRGRGRGRGRG NPRLNFDYSSC
4754	10251	A	5055	1	372	RHEQGISFLETESTFMTDQLVDALT TWQNKTGVGLLSA\AHIRFKPTLS QQKSPEQHETVLDGNLIIRYDVDR AISGGSIQTREALIKILDDLIPRDQFN LIVFSTEATQWRPSLPASAEN
4755	10252	A	5056	1	1021	AQAQYSAAVAKGKSAGLVKATGR NMEQFQVSVSVAPNAKITFELVYEE LLKRRLLGVYELLKVRPQQLVKHL QMDIHIFEPQGISFLETESTFMTNQL VDALTTWQNKTKAHIRFKPTLSQQ QKSPEQQETVLDGNLIIRYDVDRS GGSIQIENG YFVHYFAPEGLTTPMK NVVFVIDKSGMSGRIQQTREALI KILDDLSPRDQFNLIVFSTEATQWR PSLPASAENVNKARSFAAGIQALG GTNINDAMLMAVQLLDSSNQEERL PEGSV\SLIILLTDGDPTVGETNPRSI QNNVREAVSGRYSFLGFGFDVS YAFLEKLALDNGGLGRG
4756	10253	A	5057	570	831	HGNYRNVICLLGLFYPHFVGEKKIH IGFFLFFPAIDLKSGSGKVYQGPAGK AADTTIILSDEYFMEVVLGKLDPQK AFFSGRLKAEG
4757	10254	A	5058	1	2229	MGSPLRFDGRVVLVTGAGAGLGRA YALAF AER GALVVVNDLGGDFKG VGKGS LAADKVVEEIRRRGGKAVA NYDSVEEGEKVVK TALDAFGRIDV VVNAGILRDRSFARISDEDWDIIH RVHLRGSFQVTRAAWEHMKKQKY GRIIMTSSASGIYGNFGQANYSAK LGLLGLANSLAIEGRKSNIHCNTIAP

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						NAGSRMTQTVMPEDLVEALKPEYV APLVLWLCHESCEENGGLFEVGAG WIGKLRWERTLGAIVRQKNHPMT EAVKANWKKICDFENASKPQSIQES TGSIIEVLSKIDSEGGV SANHTSRAT STATSGFAGAIGQKLPPFSYAYTELE AIMYALGVGASIKDPKDLKFIYEGS SDFSCLPFTFGVIIGQKSMGGGLAEI PGLSINFAKVLHGEQYLELYKPLPR AGKLGCEAVVADVLDKSGSVVIIM DVYSYSEKELICHNQFSLFLVGSGG FGGKRTSDKVKVAVAI PNRPDAV LTDTTSLNQAALYRLSGDWNPLHID PNFASLAGFDKPIHLGLCTFGFSARR VLQQFADNDVSRFKAIKARFAKPV YPGQTLQTEMWKEGNRIHFQTK\W QETGDIVISNAYVDLAPTSGTQAKT PSEGGK\QITFVFEE\GPRLKDIGP VVVK\KVNAVFEWHITKGGNIGAK WTIDLKSGSGKVYQGPAAKGAADT TIH\ILSDEDF/LWEVVLGQA*PSRKA FFSGRLEGQEGNIMLS\QKLQMLAK DYAKL
4758	10255	A	5059	1	7449	
4759	10256	A	5060	1	7458	MTDSKPITKSKSEANLIPSQEPFPAS DNSGETPQRNGEGHTL/HQDTQPGR ASLPQRPQR\SGRRRNSLPPSHQKPP RNPLSSSDAAPSPELQANGTGTQGL EATDTNGLSSSARPQGGQAGSPSKE DKKQANIKRQLMTNFILGSFDDYSS DEDSVAGSSRESTRKGSRASLGALS LEAYLTTELLALDFGIFIRGSLVFA GYPLTLLHTYRQGSNTSSLVFTGLG SGFIELLGCPRLPQQKAAVQRPSMS GLHLVKRGREHKKLDLHRDFTVAS PAEFVTRFGGDRVIEKVLIANNIA AVKCMRSIRRAYEMFRNERAIRF VVMVTPEDLKANA EYIKMADHYV PVPGGPNNNNYANVELIVDIKRIP VQAVWAGWGHASENPKLPPELLCK NGVAF LGPPSEAMWALGDKIASTV VAQTLQVPTLPWSGSGLTVEWTE DLQQGKRISVPEDVYDKGCVKDVD EGLEAAERIGFPLMIKASEGGGGKG IRKAESAEDFPILFRQVQSEIPGSPIF LMKLAQHARHLEVQILADQYGNA VSLFGRDCSIQRRHQKIVEEAPATIA PLAIFEFMEQCAIRLAKTVGYVSAG TVEYLYSQDGSFHFLELNPRLQVEH PCTEMIADVNLPAALQGFKPSSGT VQELNFRSSKNVWGYFSVAATGGL HEFADSQFGHCFSWG ENREEAISN MVVALKELSIRGDFRTTVEYLINLL ETESFQNNIDITGWLDYLIAEKVQA EKPDI MLGVVCGALNVADAMFR TC MTDFLHSLERGQVLPADSLNLVD VELIYGGVKYILKVARQSLTMFVLI MNGCHIEIDAHRLNDGGLLSYNG

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						NSYTTYMKEEVDSYRITIGNKTCVF EKENDPTVLRSPSAGKLQYTVEDG GHVEAGSSYAEMEVMKMIMTLNV QERGRVKYIKRPGAVLEAGCVVAR LELDDPSKVHPAEPFTGELPAQOTL PILGEKLHQVFHSHVLENLTNVMSGF CLPEPVFSIKLKEWVQKLMMLLRH PSLPLELQEIMTSVAGRIPAPVEKS VRRVMAQYASNITSVLCQFPSQQA TILDCHAATLQRKADREVFINTQSI VQLVQSLGTEQDLVFYEKEKRNQSI LGFEPVNSRHVSHVPETHRYKESHY DKCVINLREQFKPDMSQVLDClFSH AQVAKKNQLVIMLIDELCGPDPSLS DELISILNELTQLSKSEHCKVALRAR QILIASHLPSYELRHNQVESIFLSAID MYGHQFCPENLKKLILSETTIFDVLP TFFYHANKVVCMALEVVRRGYI AYELNSLQHRQLPDGTCVVEFQFM LPSSHPNRMTVPISITNPDLLRHSTE LFMDSGFSPLCQRMGAMVAFRRFE DFTRNFDEVISCFANVPKDTPLFSEA RTSLYSEDDCKSLREEPIHILNVSIG CADHLEDEALVPILRTFVQSKKNIL VDYGLRRITFLIAQFAEDRIYRHLE PALAFQLELNRMNRNFDLTAVPCAN HKMHLYLGAACKVKEGVEVTDHRF FIRAIIRHSDLITKEASFEYLQNEGER LLEAMDELEVAFNNTSVRTDCNHI FLNFVPTVIMDPFKIEESVRYMVMR YGSRLWKLRLVLAQEVKINIRQTTTG SAVPIRLFITNESGYLDISLYKEVT DSRSGNIMFHSFGNKQGPQHGMILN TPYVTKDLLQAKRFQAQTLGTTYIY DFPEMFRQASPAQTRVHVHNVQA LFLKWGSPDKYPKDILTYTELVLDS QGQLVEMNRLPGGNEVGMVAFKM RFKTQEYPEGRDVIVIGNDITFRIGS FGPGEDLLYLASEMARAEIGPKIY VAANS GARIGMAEEIKHMFHVAW VDPEDPHKKKKTVAFSAGNWIRSL TKVFFKGFKYLYLTPQDYTRISLN SVHCKHIEEGGESRYMITDIIGKDD GLGVENLRGSGMIAGESSLAYEEIV TISLVTCAIGIGAYLVRLGQRVIQV ENSHIILT GASALNKVVEPCTVQDIA NHVVSQVVLGREVYTSNNQLGGV QIMHYNGVSHITVPDDFEGVYTILE WLSYMPKDNHSPVPIITPTDPIDREI EFLPSRAPYDPRWMLAGRPHPTLK GTWQSGFFDHGSFKEIMAPWAQTV VTGRARLGGIPGVIAVETRTVEVA VPADPANLDSEAKIIQQAGQVWFPD SAYKTAQAVKDFNREKLPLMIFAN WRGFSGGMKDMYDQVLKFGAYIV DGLRQYKQPILYIPPYAELRGGSW VVIDATINPLCIEMYADKESRGGVL EPEGTVEIKFRKKDLIKSMRRIDPAY

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						KKLMEQLGEPDLSKDRKDLEGR KAREDLLLPIYHQVAVQFADFHDTP GRMLEKGVISDILEWKTARTFLYW RLRRLLEDQVKQEILQASGELSHV HIQSMRLRRWFVETEGAVKAYLWD NNQVVVQWLEQHWQAGDGPRSTI RENITYLKHDSVLKTIRGLVEENPE VAVDCVIYLSQHISPAERAQVVHLL STMDSPAST
4760	10257	A	5061	6	906	EQPALLPRYRSGIRGYMKTIVLDDL RRYL RVEITIFSKARDADANTSGMV GGVRSLSFTSVWVLSPPAHYDKCV INLREQFKPDMSQVLD CIFSQAQVA KKNQLVIMLIDELCGPDPSLDELISI LNELTQLSKSEHCKVALRARQILIAS HLPSYELRHNQVESIFLSAIDMYGH QFCPENLKKLILSETTIFDVLPTFFY HANKVVCMA SLEVYVRRGYIAYEL NSLQHRQLPDGTCVVEFQFMLPSSH PNRMTVPISITNPDLLRHSTELFMD GFSPLCQRMGAMVAFRRFEDFT
4761	10258	A	5062	2	560	APRLDVFSFSQIHRDIKPENILVSQSG ITKLCDFGFARTLAAPGDIYTDYVA TR*PVDIWALGCMIIEMATGNPYLP SSSDLDLLHKIVLKVGNLSPHLQNI SKSPIFAGVVL PQVQHPKNARKKYP KLNGLLADIVHAWLQIDPADRISS DLLHHEYFTRDGF I*KFMP ELKA*L LQEAKSQF
4762	10259	A	5063	1	573	
4763	10260	A	5064	2	791	NLVN LIEVFRQKKKIHLVF EFIDHTV LDELQHYCHGLESKR LRKYLFQILR AIDYLHSNNTVDI WALGCMIIEMA TGNPYLPSSSDLDLLHKIVLKVGNL SPHLQNI FSKSPIFAGVVL PQVQHPK NARKKYPKLNGLLADIVHEIEKEKK PKEIKVRVIKVKGGRGDISEPKKKE YEGGLGQDANENVHPTSPDTKL TIEPPNPINPSTNCNGLKENPHCGGS VTMP PINLTNSNLMAANLSSNLFSP QCEVSCNREEP
4764	10261	A	5065	3	524	TYGPASRGICRVSLGRPRWENAAT WKLAAMASIRLQGLHKPVYHALSD CGDHVVIMNTRHIAFSGNKWEQKV YSSHTGYPGGFRQVTAAQLHLRDP VAIVKLAIYGMLQ/NNLHRRMTME RLHLFPDEYIPEDILKNLVEELPQR KIPKRLDEYTQEEIDAFRLWTPPED YRL
4765	10262	A	5066	1	250	YSSHTGYPGGFRQVTAAQLHLRDP VAIVKLAIYGMLPKNLHRRMTMER LHLFPDET*RLSAIRE*ELQKITVK*L KLSSDEFL
4766	10263	A	5067	129	796	MGKCSHLANFAAIASIRLQGLHKPV YHAFE*L/CGDHVVIMNTRHICIF/H GNKWGTSILFRILAYPGWSLDKVT SLAPAFTLRRSQW/CNL*NLA IYGIP AKKTFTRRTIDWKGLHLFPDELYS

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						RKIFLKKFS*EELPSTTEKYLNVLDE YTTRNRRLFKIVDSTLKIIGYKRIRI AENNSEVIETFLMSFSNLQDGVKQ LLQFEHLFLCAESLWGKVRKV
4767	10264	A	5068	15	350	GPGSAITVGPQPL/RAQRNHRLPVPS PGLSIVMGLRPVPSPGPTGLPGHRQ SSEMRPREAGSLRSSGEKGLPAPVP RPQQSDMTKRTLPRDTPDTPRCPPQ HCPWSRVRGQPQ
4768	10265	A	5069	1	2175	
4769	10266	A	5070	3	86	KNYRG TMS/KTKNGITCQKWSSTSP RRPR
4770	10267	A	5071	2	583	LLLLFLKSGHGEPLDYYVYAQGA SLFSVTNHLGAGSTEECASQCVED KEFTCGAFQYHSKEQQCAIMAENK KSSIIIRMRDVVLF EK*MYLSECQTG NGKNYRG TMSKTKNGITCSKMGPV LFPHRPRFSPATHPSEGLARNPDNDA QGPWCYT TD\PEQRYDYCDIPECEG QEWALGKCFHFCSSPVKINLL
4771	10268	A	5072	844	4515	TVKAPGYSHSHPGALLDLEVGDPN GTNAQLIKCFLPLCPSFPLCPEECM HCSGENYDGKISKTMSGLECQAWD SQSPHAHGYIPSKFPNKNLKKNYCR NPDRELRPWCFTTDPNKRWELCDIP RCTTPPPSSGPTYQCLKGTGENYRG NVA VTVSGHTCQHWSAQTPH THN RTPENFPCKNL DENYCRNPDGKRA PWCHTTNSQVRWEYCKIPSCDSSPV STEQLAPTAPPELTPVVQDCYHGDG QSYRGTSSTTTTGKKCQSWSSMTP HRHQKTPENYPNAGLTMNYCRNPD ADKGPWCFTTDP SVRWEYCNLKKC SGTEASV VAPPV VLLPDVETPSEE DCMFGNGKGYRGKRATTVTGTPC QDWAAQEPHRHSIFTPETNPRAGLE KNATECGGASTELCSTSLCAFTML MDYEGQGEPLDDYVNTQGASLFSV TKKQLGAGSIEECAAKCEEGEEFTC RAFQYHSKEQQCVIMAENRKSSVII RMRDVVLF EKKVYLSECKTGNGK NYRG TMSKTKNGITCQKWSSTSPH RPRFSPATHPSEGLEENYCRNPDND PQGPWCYT TDPEKRYDYCDIL\EC *RRECMFAVGGKLLTGKIFRTMS WDWECQAWGLFRSPHGHGYIPSK FPNKNLKKNYCRNPDRELRPWCFT TDPNKRWELCDIPRCTTPPPSSGPTY QCLKGTGENYRG NVA VTVSGHTCQ HWSAQTPH THNRTPENFPCKNLDE NYCRNPDGKRAPWCHTTNSQVRW EYCKIPSCDSSPVSTEQLAPTAPPEL TPVVQDCYHGDGQSYRGTSSTTTT GKKCQSWSSMTPHRHQKTPENYPN AGLTMNYCRNPDADKGPWCFTTDP SVRWEYCNLKKCSGTEASV VAPP VLLPDVETPSEEDCMFGNGKGYR GKRATTVTGTPCQDWAAQEPHRHS

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						IFTPETNPRAGLEKNYCRNPDGDVG GPWCYTTPRKLVDYCDVPQCAAP SFDCGKPQVEPKKCPGRVVGCV HPHSWPWQVSLRTRFGMHFCGTL ISPEWVLTAHCLSKSPRPSYKVL GAHQEVNLEPHVQEIEVSRLFLEPT RKDIALLLSSPAVITDKVIPACLP PNYVVADRTECFVTGWGETQGTFG AGLLKEAQLPVIENTKVCNRYEFLNG RVQSTELCAGHLAGGTDSCQGDG GPLVCFEKDKYILQGVTSWGLGCA RPNKPGVYVRVSRFVTWIEGVMRN N
4772	10269	A	5073	9	141	FYRLSLGFKCDWFTMEKRVKLEER YRDMAEENLKKDISISLKL
4773	10270	A	5074	3	360	QTKPKESRKRIIMFRTEFNETENRI ESSSSSSSSSFSSSSSYKCLARLT/ RKK/EKIQIIVRSEKIEITNYRIKRIT KGYEELLYANQLYHLMKCPKFLER HKLLKLTQEETKSGV
4774	10271	A	5076	1	245	AAAYYYTAAARRRQKGERRKKRK EEER\KEEKKRKKKEKKRRRRG GRTTKKEEKEKEKKRRTKKEKKK KKKKKKKVSM
4775	10272	A	5077	68	246	SMAFLTIEDTALKFIQNHKRPQIA/ KPILSKNRAESITLFNSKIHYPMTVI KPLRVTST
4776	10273	A	5078	3	364	TSIVAAQMFMVITVMQVRISPQHMT SMWPIMVCELSQFTQLEEDVKDK VESLRSTNKVNRTKVSVDANGPS VGYIPQSELIMYLSACKFLDAALSIP HYKIPLFKIYRWAFIPEVDTE
4777	10274	A	5079	2	1315	GKDAKILCSNPNTGEVLVELPTNTQ RCFDIQWCPNPAVLAAASFAGRIS VYSIMGGSTDGLRQKQVDKLSSFG NLDPFGTGQPLPPLQIPQQTQHSIV LPLKKPPKWIRRPVGASFSGGKLV TFENVRMPHQGAQQQQHHVFI SQVVTEKEFLSRDQLQAVQSQGF INRQKKIDASQTELEKNVWPFLPV TFEDDSRGKYLELLGYRKEDLGK/K DCFGL/GTKWMEPMWLLKTLTKYH ITNHEPAG*PPVTNAAATASSSSTA KPVFIPTDTSSRWALPWRTATSW NRHAPIFFTAQY*RCPRGSYWKYLP ACAVFGNKKNYQETYSR*APHSKD HI*GSYSALPFFSNRPSNQEEAR*CQ QTFGVSV**T*GTDTFTNNHQWFTQ HCKEH*NSKLLRRIDHAYPHS*HQQ LQ*DLCFHASSQSCL
4778	10275	A	5080	18	3600	
4779	10276	A	5081	238	480	SIQFYFFSFQDSKGKHSLSVIGPQN GWNDPPALNRVPKKKKMPENFMPP VPITSPIMNPLGDPQSQMLQQQPSA/ PVPLS
4780	10277	A	5082	352	4060	DYSRRYILRMKLKEVDRTAMQAW SPAQNHPYIYLATGTSAQQLDATFST

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						NASLEIFELDLSDPSLDMKSCATFSS SHRYHKLIWGPYKMDSKGDVSGVL IAGGENGNILYDPSKIIAGDKEVVI AQNDKHTGPVRALDVNIFQTNLVA SGANESEIYIWDLNNFATPMTPGAK TQPPEDISCIAWNRQVQHILASASPS GRATVWDLRKNEPIIKVSDHSNRM HCSGLAWHPDVAQTQMVLA SEDDR LPVIQMWDLRFASSPLRVLENHAR GILAIAWSMADPELLLSGCKDAKIL CSNPNTGEVLYELPTNTQWCFDIQ WCPRNPAVLSAASFDRISVYSIMG GSTDGLRQKQVDKLS SSGNLDPF TGQPLPPLQIPQQT AQHSIVLPLKKP PKWIRRPVGASFSGGKLVTFENVR MPSHQGAEEQQQQHHVFISQVTE KEFLSRSDQLQQA VQSQGFNYCQK KIDASQTEFEKNVWSFLKVN FEDDS RGKYLELLGYRKEDLGKKIALALN KVDGANVALKDSQVAQSDGEESP AAEEQLLGEHIKEEKEESEFLPSSGG TFNISVSGDIDGLITQALLTGNFESA VDLCLHDNRMADAILAIAGGQELL ARTQKKYFAKSQSKITRLITAVVMK NWKEIVESCDLKNWREALAAVLTY AKPDEFSALCDLLGTRLENEGDSSL QTQACLCYICAGNVEKLVACWTKA QDGSHPLSLQDLIEKVILRKAVQL TQAMDTSTVGVLLAAKMSQYANL LAAQGSIAAALFLPDNTNQPNIMQ LRDRLCRAQGE PVAGHESPKIPYEK QQLPKGRPGPVAGHHQMPRVQTQ QYYPHGENPPPPGFIMHGNVNPNA AGQLPTSPGHMHTQVPPYPQPQPY QPAQPYPFGTGGSAMYRPQQPVAP PTSNAYPNTPYISSASSYTGQSQLYA AQHQASSPTSSPATSFPPPPSSGASF QHGGPGAPPSSSAYALPPGTTGTL AASELPASQRTGPQNG\WNDPPALD KVPPKKKKMPENFMPPVPITSPIMN RLGDPQSQMLQQQPSAPVPLSSQSS FPQPHLPGG\QFPWGYSKPFGFKQ GMATIFFQSPNIEGAPGAPIG\NTFQ HVQSLPTKKITKKIPD\EHLILKTT FEDLIQRCLSSATDPQTKRKLDDAS KRLEFLYDKLR\DRTFSTITSGLHNI ARSIETRYSEGLTMHTHIVSTSNFS ETSAFMPVLKVVLTTQANKLGV
4781	10278	A	5084	121	419	DLCFTTPKAGRRQEITKIRAE LNKV EVQETIQKISEKRSWLFNIINKIARLL TRLIQKKD\QINTVRNDKGDITTYPT EIQKTLRDYIEHLYACRVENLQ
4782	10279	A	5085	1	279	TMDSNNTV\DQLDLTDIYRTLHLTS AA YTFSSAHLCSRLRLSHKTS LNKFKKIVIPGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL
4783	10280	A	5086	1	279	TMDSNNTV\DQLDLTDIYRTLHLTS AA YTFSSAHLCSRLRLSHKTS

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						LNKFKKIVIPGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL
4784	10281	A	5087	1	1915	MAILPLLLCLLPLAPASSPPQSATPS PCPRRCRCQTQSLPLSVLCPGAGLL FVPPSLADRRAAELRLADNFIA SVRR RDLANMTGLLHLSLSRNTIRHVAA GAFADLRALRALHLDGNRLTSLGE GQLRGLVNLRLHLSNNQLAALAA GALDDCAETLEDLDLSYNNLEQLP WEALGRLG\NVNTLGLDHNLLASV PAGAFSP\LHKLARLDMTSNRLTTIP PDPLFSRLPLLARPRGSPASALVLA GGNPLHCNCELVWLRLAREDDLE ACASPPALGGRYFWAVGEEEFVCE PPVVTHRSPPLAVPAGRPAALRCRA VGDPPEPRVRWVSPQGRLLGNSSRA RAFPNGTLELLVTEPGDGGIFTCIAA NAAGEATAA VELTVGPPPPQLANS TSCDPP/PGRGLPDALTPSAASASA KVADTGPPTDRGVQV\TEHGATAA LVQWPDQRPIPGIRMYQIQYNSSA DDILVYRMIPAESRSFLLTDLASGRT YDLCVLAVYEDSATGLTATRPVGC ARFSTEP\SLRPCGAPHAPFLGGTMII ALGGVIVASVLVFIFVLLMRYKVHG GQPPGKAKIPAPVSSVCSQTN\GAL GPTPTPAPPAPPAALRAHTVVQLD CRALGARPRTCGLARRPPL
4785	10282	A	5088	1387	1567	GKNLLPLFFFFFFFETVSQSVAQAG VQWRHLGSPKPLPP\GSSDSPASVSQ AAETTGTCHH
4786	10283	A	5089	96	408	SPRKRKTRHSTNPPLECHVGWVMD SRDHGPGTSSVSTSNASPSEGAPLA GRYGCTPHSFPKFQNPSELLKEN GFTQQVYHKYRRRCLSERKRLGIG QSQEMNT
4787	10284	A	5090	390	665	PLNIHYCFLGGKYL VFGFSVAANKT SGAP\GNSPVSAIRAFGDAHPDLVT PGTFIPYCSMAHAQLCFHGHRDAV KFFVA VPGQVISPOSSSS
4788	10285	A	5091	185	386	WEASKKKPRGAQISNAITTYKYL PK VGV\KNYQTEALYKPIQTGKIGHPV FFQKPPLLGDGQNYDTPP
4789	10286	A	5093	3	330	GTGLKARKSASSLPETFPTRTRHGE AALPLSPTWKMTGPGVGNPMIPRQR SMSLLTAVSGQPHFQDSALSQASSS PDLL/LHLSPR\SCPGRVQETLKATD RPPRCPAGCG
4790	10287	A	5094	2	349	PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLKKGENPPNSFYGAIP RIPNPNMDLPSSSPT/RPVSGRNMEA KIFTKFLAGHFKQSFGREIHHDQREF IPGIQGGFNIGN
4791	10288	A	5095	2	353	PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLASSSSSSSSSSSSSS SSPPNMDLPSSSPT/RPVSGRNIEAKI FTKFLPGHFQQSFGRVTHLDQRELI LGNQGGSTICKS

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4792	10289	A	5096	1	262	RGRAGGEPLPATTGAAPPPGRRRLH/ RQLPDRRGLASMPREEKASLNEPG GPGRGRRRGSVQLHGEGGPRGGE GTGREEWNEKAEFTL
4793	10290	A	5097	116	177	LGEHGVYSGVGTGGRLLS*KKGKP WFK*KKLKGGPIPI*RDPRGFSRFSV
4794	10291	C	5098	231	347	MGLGPHLKFFYLKHGLPFFKELNPL KVKIWPRNPWIKKI*
4795	10292	A	5099	518	931	ATRHSMLSCHTYTYIYIKHTHTHVFI YIYTYTYIHTHIYTYTYICHTHIHIYI YIYIHTHFFFFFFFETESRSVTQAGV QWHDLGSLQAASWGHADSPASTS QAAGTTGAHHHAQ/LIFFFVFLVET GPHRASQDS
4796	10293	A	5100	2	1109	DAEMLVMAPRTVLLLLSAALALTE TWAGSHSMRYFDTAMSRPGRGEPR FISVGYVDDTQFVRFDSDAASPREE PRAPWIEQEGPEYWDRNTQIFKTNT QTDRESLRNLRGYYNQSEAGSHTL QSMYGCDVGPDRLLRGHNQYAY DGKDYIALNEDLRSWTAADTAAQI TQRKWEAARVAEQDRAYLEGTCV EWLRRYLENGKDTLERADPPKTHV THHPISDHEATLRCWALGFYPAEIT LTWQRDGEDQTQDTELVEPTRAGD RTFQKWAAVVVPSGEEQRYTCHVQ HEGLPKPLTLRWEPSQSTVPIVGIV AGLAVLVVTAVVAVVAVMCRR KSSGKGGSYSQAASSDSAQGS DV SLTA*KA
4797	10294	A	5101	3	1145	SDSPQTPMRVMAPRTLILLLSGAL ALTETWACSHSMRYFYTAVSRPGR GEPRFIAVGYVDDTQFVRFDSDAAS PRGEPRAPWVEQEGPEYWDRETQ KYKRQAQTDRVSLRNLRGYYNQSE AGSHTLQWMYGCDLGPDRLLRG YDQSAYDGKDYIALNEHLRSCTAA DTAAQITQRKWEAARAAEQRAYL EGTCVEWLRRYLENGKETLQRAEH PKTHVTHHLVSDHEATLRCWALGF YPAEITLTWQRDGEDQTQDTELVE TPAGDGTQFQKWAAVVVPSGEEQRY TCHVQHEGLPEPLTLRWEPSQSTIP IVGIVSGPAVLAVLAVLAVLAVLGA VVAAVIHRKSSGKGGSQAAS SNSAQSDES LIACKA
4798	10295	A	5102	3	242	GFWAPRVCKDIDKWHLSEPEALWF GEGGSPGGCRWGGWLCQGNRA AGGVGAEGACLGLLSATGLLWMT GLQEPREPQV
4799	10296	A	5103	1	138	FPLIPKPGKDPFN/ENFRPIFLMAKN AKILKKILANLIFQPLKKIL
4800	10297	A	5104	59	337	IPYPALPFTSVEAPNSHVKA VMKTS VLLSWEIPENYNSAMPFKILYDDGK MVEEVDGRATQKLIVILNPEKSYSF ELTYRGNCAGGLELMVT
4801	10298	A	5105	54	226	TKAETENLNRPVTEIKSVI/NSLP TK

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						KSPGLDGFIAKFFQTYKREIIPDLLK LLQKLKW
4802	10299	A	5106	2	265	ETVKLLEENI/GQKLFDIGLGSDFLDI TPKAQETKINKWDFIKLSFCTVKE TIKMKRQSVWEKILVSHVSDKWFI SKIQGIYITQYQ
4803	10300	A	5107	1	296	GREKEEGESGEDWGRV\GREKEGG EGREEEGEGGEGGEGGRKEEGE GGREEEGEGGEGGEGGEGGEGE/ GREEEGEGGRQEEGEGGRREGRG GRS
4804	10301	A	5108	1	253	
4805	10302	A	5109	190	472	
4806	10303	A	5110	1	314	HNVPVPHVFMQLQKEITKKNSTFRVHI KAVFYN/HDIYCMPLLNRYKTFDV IVIDPPWQSKSVKRSNRYSLPLQI KQIPIPKLAAPNCLLVTLTNTQKH LRFIK
4807	10304	A	5111	3	362	FFFFFETESLSVPQAGVQ*HDLSSLQ PP/PPGFTPFSCSLSPSSWDYRCPPPR PA/NIFFVFLVETGFHHVSQDGLDLL T/S/GDPPASASQSAGITGVSHRARPP PPQFFIQLPLYNHITLEGR
4808	10305	A	5112	3	385	FFFETESRSVAQAGGQWHDLSLQ APTPGFTPFSCSLSPSSWDYRCPPPC PANFFVFLVETGFHHVSRDGLDFT SDPPTSASQSVGITGVSHCARARPF FKKKKKKKTSILSSSLFSHKQRSFG F
4809	10306	A	5113	1	390	SKAVKV/YRLITRNSYEREMFDKAS LKLGLDKAVLQSMGRDGNITGIQ QFSKKEIEDVLRKGAYAAIMEEDDE GSKFCEEDIDQILLRRTTITIESEGK GSTFAKASFVASGNRTDISLDDPNF WQKWA
4810	10307	A	5114	2	214	GRVDIERAILVQTGQQALEPA\VRL RRAPYPCHTSDLFLNNVGFFFLIM MLTWMVSVASMRPLVSQGE
4811	10308	A	5115	30	379	KRSVNSPGRALSELGVSTELGFLRC VSVVCSLSQEYFLFTLLYFGL/LPF ACLLSSSPVFFVFRCSVPLFFCFLFC VSLCLPFLGFFHVLFFHRLPLIVFSF MEGFYWAWCLVFFCL
4812	10309	A	5116	1	304	GTRETVGLGDTNLAHQCSRLTMVN NDNHSEAYNNLAVLEMRKGVHQQ ARALLQTASALSPHMYETDFNFATI CDMTGYLHRSYVDAQKSEAALSEH VDTQH
4813	10310	A	5117	119	264	
4814	10311	A	5118	720	2798	VYWPHSFLGCPSPNYPLYLGAETRQ GGRARPPFLPLSPFRPRPNPSPFQ VLETQRISYSFLLADTSNTRATSGH AQQPAPILPLREVAGAEDIHVHVPF SLSDLSQIAKRLGSFSSDPDTYIKEF KYLTQSYELTWHDLIILSSTLLPEK KERVWLAAQAHANDLHRQDPTKPI GAAAVPLEPPWKYQPTDPGRASR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NHMITCLIAGLNKAAHKAVNFEKL KEISQRADENPAEFLSRFTEALQKY TRVDPTSREETIVLNNHFISQSAPNI QHKLKKAEDGPQTPQQDLLNLTfK VFNNREEQIKLDKAQRDCAKYQLL AVAIHQPSHSTQGHKKPNGSNPPGP CFKCSKEVTYLGVLSPGAQAMTP AQATLINSPLPSSKNEILSFLRLEGF FRIWIPNFALLAQPLYEAAKGPLNE PLSPIHNILPSFCKLQTALITAPALS PDLSPFVLYTTKNQGIALLGVLGQQ KGNPPSFDPAVYLCKQLDNTVKGQ PTCLKASSAVAVLPLESKKLTFGQS TTIHSPHNLDLLSSWALSSLSPSQI QSLYALFIKNPEFSLAKSAPLNLASL LPISPPPTHSCDILDHLQPQFPNISS KPLTNPDDQLFIDDSSSRAPGSPKIV GYAVVTLNHVIEAKPLPETSSQKA ELVALTRALTLKDKQHWLISEPVQ RPPSSVHST
4815	10312	A	5119	2	697	HGRLLLLLLLLLLPCCEKTTEGEAM KEITAGLPVKVVVDVLRQASKACV VKREFKKAQEQLIKHAVYLARDHFG SKHPKYSDDLGYGYLLNVDNICQ SVAIYQAALDIRQSVFGGKNIHVAT AHEDLAYSSYVHQYSSGKFDNALF HAERAIGIITHILPEDHLLVASSKRV KALILEEIAIDCHNKETEQRLLQEAH VDVHLLSLHLASKSYGDLAVVVLVH MSLLKSY
4816	10313	A	5120	3	277	EEEEAPPPGRERARGKGGDRPRGG NPEHQCGGTPRAEGSSTA/A/PPTCT SSSRTPASTVGPEPCGAGSAATAPG PELSGQNQMGRGPPVEDTE
4817	10314	A	5121	1	337	GTSSCVREVQAMGKKKVLVKVH LKDKFVIDVDKNISISDVTSSLVVL RNDSTYTLHKILPNKVHSLVSLMMV NTVPY/STNETIVSLDGPMVTILFSD KLSFTAPQLYIFTG
4818	10315	A	5122	2	302	ARGLPFFTRNDFSVWTIA/RNKCVG LELSKITMPIAFIQPLIFLHRITEYME HVYLIHRAFCQPQPLERMQVGLKG ARQEFVMKVMPLACLATQSWGPR HL
4819	10316	A	5123	3	346	HENWKLLPCSSKAGLSVLLKADR LFHTSYHSQAVHIRPVCARNARCTIS WELRQTLVVFDLAFITGQGGKDW LF/RMFSRTLTEPCPLASESRVYVDI TTYNQDNETLEVHPPP
4820	10317	A	5124	213	425	QNSQGLFSSGCLPFCGSNTKGILK YIQNH/KKPQIAKATLSKKNKAGSIT LPDFKIYYKALKPKITWYWH
4821	10318	A	5125	1	356	GTSTRIIFYRDGVSEGQRQQLHHE MLAIREACIKLQKDYQPGITFIVVH NIHHTRLLCSDKNHPLGKRGNSPTG SNCGTKITHPTDFYLRRHAGIQG TSRPSYYHVLWD\DNRRFS
4822	10319	A	5126	1	238	HMHSHHMHSHTPHA/HHTHHMHS

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						HHMHSHTHHMHSHHMHSAPHAL TPHACTHTHHMHSHHMHSHHMHA LTPHACTHTPH
4823	10320	A	5127	180	405	IWGEQDTFHSMKWIHLNVNHKT VKLLDDNIG/IKRGDLG/VDNEFLGT TPKAQSMEETIDKLDFIKMKNFCSV KDG
4824	10321	A	5128	61	85	PS*NYPP*KGITFGPLNKK
4825	10322	A	5129	3	2004	RRRRRPASPPAGLALAPRSPASPEP REGETLSPSMQREEGFNTKMADGP DEYDTEAGCVPLLHPPEIKPQSHYN HGYGEPLGRKTHIDDYSTWDIVKA TQYGIYERCRELVEAGYDVRQPK ENVTLHLHWAANNRIDLKYYISKG AIVDQLGGDLNSTPLHWATRQGH SMVVQLMKYGADPSLIDGEGCSCI HLAAQFGHTSIVAYLIAKGQDVDM MDQNGMTPLMWAAAYRTHSVDPTR LLLTFNVS VNLGDKYHKNTALHWA VLGNTTVISLLEAGANVDAQNI KGESAPDLAKQRKIVWINHLQEAR PAKGYDNPSLPRKLKADKEFRQKV MLGTPFLVIWLVGFIADLNIDSWLI KGLMYGGVWATVQFLSKSFFDHS MHSALPLGIYLATKFWMYVTWFF WFWNDLNLFIHLPFLANSVALFYN FGKSWKSDPGIHKATEEQKKKTIVE LAETGSLDLSIFCSTCLIRKPVRKH CGVCNRCIAKFDHHCWPVWGNCVG AGNHRYFMGYLFFLLFMICWMIYG CISYWGLHCETTYTKDGFWTYITQI ATCSPWMFWMFLNSVFHFMWVAV LLMCQMYQISCLGITTNERMNARR YKHFKVTTTSIESPFNHGCVRNIDF FEFRCCGLFRPVIVDWTRQYTIEYD QISGSGYQLV
4826	10323	A	5130	3	144	HEKYHKNTALHWAVLAGNTTVIS LLEAGANVDAQNIKAILRCHMAL
4827	10324	A	5131	148	325	RQGECKIHCKKKLSPGIRSYPVEN/ F/VDTMYDYLQPAYYKLNDLTNAD PCAVRYLLFDQN
4828	10325	A	5132	175	405	NILNSQFSTFLNDYVEFFVVFKIFNFI IIIF*DRVSICCPGWSIMVQSWLTAA LTFGR*SSNLSLPSSWDYRRVP
4829	10326	A	5133	14	26	YSPHEVGWKGRNREKMFCEINVV FPDSVCQEMGFHHVAPAGLELMSS SDSPASASQSAGITSVSHHSCLYTSK GVE*FTGIIFSS
4830	10327	A	5134	177	454	PLLERAKIGPRPEKPMETROGWGPF SPKVPGQKKFWG*LAPISPGMHPN PILGPMV*EGGP*PPGILGPP*PYGKP LF*RKRGSNNGGPYLQ
4831	10328	A	5135	3	92	NAWRTATEEWWTWDWNEDCSEP* HFTYVI
4832	10329	A	5136	1	442	PLIMNSIKSFSDDHAQCGRFEFDRQED DIHLVTLCVTELNDREENENHFPVI YGIAVNIKTAEIYRASQDRGPPEEQL

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						RAARTLAGGPMISIDYDAETEQLRNG PYSWTPFPFHVDFWLHQDDKQIFEN LSTSPLAEPFHFVEHIRSYLD
4833	10330	A	5137	177	566	EPFWSLSYLSLRGGRNVRLCRLSA LVFCQFKAMLLTLTAGNNKTAIEY RASFQDRGPPEQLRAARTLAGGPMI SIYDAKTEQLRIGPYSWTPFPFHVDF WLHQNDKQILKGRVYRLGKS*ISAP WPHL
4834	10331	A	5138	1	981	PLLVEGR*VRLPQSAGDLVRAHPPL EERARLLRGQSVQVGPQGLLYVQ QRELA VTSPKDGSIILGSDDATTCH IVVLRHTGNGATCLTHCDGTDTKA EVPLIMNSIKSFSDDHAQCGRLEVHL VGGFSD\DRQLSQKST\HHFLIEFDR QEDDIHLVTL CVTELNDREENEN\H FPVIYGI\AVILLSLTAVNIKTAIEYR\ ASFQRSGVREEQA/LRAARKL*AGG PMIS\YDAETETTS**DPYFLGHFPF HVGF\WLHQD\DKQILDES FHRPL AE\PPHF\VEHIRSTLMVF*KNTPSA VNTLFPGNKALLYKKNEDGLWEKIS SPGS
4835	10332	A	5139	1	405	AYVTVCNQCGRESKLLSKFYELEL NIQGHKQLTDCISEFLKEEKL*GDN RYFCENCQSKQNA TRKIRLLSLPCT LNLQLMRFVFDROTGH TKKLNTYI GFSEILDMEPYVEHKVW*PTSLNSM LSLKLGGMCMLT
4836	10333	A	5142	2	204	ETGFCHVVQAGLKLGGSSDLPASAP QSAGITGMCHCAQPTKVS VASKVF KGS HKD*ILT*GYANKGA
4837	10334	A	5143	1	360	QQLTVLVAHLGVTLMDQRGYHWL LKSLMTQYQGLLYENP*ITLEIVNTL NPGTLLPNESVPGSALHCRVDVVHE MLSIQRDLTDHTLRDSIEYFIDRS FILGGDPLSGVCSSDFGLST
4838	10335	A	5144	36	380	FVALMGHKMSHNKFKIEIIRSMFSN HNRSQ*SK*IKEIYKCGN*HTSK**M H*GKKSLAKLENNEMNENESTT*Q NLWDAAKTALNEQFML*MPILKKG *MSQINKPTFHLKTIK
4839	10336	A	5145	1	362	ELNLPAPELPRKR TENLFLQLAEYV AHS LNVT S*YVCEGTTMGD*WPWE TQELEPTDPVPDIIPVQKAQTSNFW VLKTSINGQYCIPRKGKDF TIPVGR L N*LGQKLYKSITGTQGQSPG
4840	10337	A	5146	2	428	MFLLVVINLHILFVF*FKLFSWS*AIF L*FLF*FMSESENIYYAEIGIITIVT LKSLIATYCINPSSH CYKVYL VLSY LYCIIVNFDIYFLLLCVPFCYFSLIISL SPLFLLIYMIFLYIHFILLFVIFYTFIP FSFY
4841	10338	A	5147	3	361	TLFQL*DLRKQRLEDLSTLIPRIYPG WKCRT HFLMKKSQIV IAGWYRRY AQHKRNQPTKSTVLVLQSYIRGRK ARKILRELKHQKRCTEAVTTIAAY

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						WHGTHALTETERLKEEARRKH
4842	10339	A	5148	1	424	VHLTADDKVIIAGLWSIVNAQDAV GETLGRLLQGVYPWIQRFSGSFGNLS SASAI VVNPKVTAHGKNVLTSLVD AITHLV DLMGTFAQLRELH*DKLYE DPENLHTLGHVLT VLVVIHFGT*FT AEVQASWLMMDTERANAL
4843	10340	A	5149	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPVKVAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLT VLVLAHFGKEFTP EVQASWQKMVTGVASALSSRYH
4844	10341	A	5150	38	501	APSPDA\MGHFTTEEDKAT\TSLWGK \VNVE\ DAGGETLGRLLVVYPWTQR FFD\SFGNLSSASAIMGNPKVKAH GKKVLT\SLGDAIKHLD\DLKG\TFA QA*SELH\CDK\LVHDPENFKAPGG NVAGDPFLAIPFSAKEFHPLKVARL SWAERWVTW
4845	10342	A	5151	2	198	KVRPPPLKKTFFDSVDYRVLSEVD ERFAELPEFRPEDDLSSFS*PFLSPP CMSTALAHGDFSL
4846	10343	A	5152	1	119	DIMTGPHDEVA AKNIQLTNEIQTLE TE*HEATKEFQVLS
4847	10344	A	5153	3	83	RMVLRMLPLSTDEALCFHAMFQPF LDMIHEAQQAMDIHFHSPDFQHPPT EFIREGDDDRTVLREMHHI*TG*LR VKWRCEEWR*I
4848	10345	A	5154	2	370	GAARLDERTKEGSDDDEDSG*GARA ELEGNKEGESEGOYKAKGERSAWS KLRTEIRQKAEESIDGIKVDDPS*IS MKATYTTMKIS*RQIRKIROREKKN TAKGEGQERQKNL SHKRHDISC
4849	10346	A	5155	106	344	RPCQQMQINVIHPINRMDKKHVIIPI DTSDKI*HPFMIQTLNTLCI**MYLSI IKAIYDPYTADIILTG*TFNAFFSTI
4850	10347	A	5156	198	474	
4851	10348	A	5157	1	131	PQEV PQSFGPPGDKAGC*GAGKMS PRERGGFLKCAEGGHPAPA
4852	10349	A	5158	104	440	FSKIYHFLCCCFVLSKNCPILLHFL KIYLLALGNINISYFYSHSKTLATG LKLTDSDSHISHGTSGSRFKCLLS KAVLMSSLPVYS*LLKLLDVREVS NMVHDTLGIL
4853	10350	A	5159	2	393	EVWPRGLMGYVTVTEPSAVLVVRG VRDRLVITYPHEHHALTSSRLYLLM LFVGDP SGSGSNGSPDS*GLLLFRN DQAHIDLFVCFSVILSCFFLFLSLCEL LWNAKQAMDQRQEQRRLQEMTK MARRPF
4854	10351	A	5160	2	154	FRDGVSLHCSGWS*TPGLK*SSCLS LPKCWDYRHEPPLLFPLWRAIGNIY
4855	10352	A	5161	142	399	HLLTYSEMFLGGVRYFLQSTLPADL SKHAYLYAP*LRLFA*RYTSAFTEW THSANKTVCLMPKLYELTYVGIDTL ATPVIKRYYS

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4856	10353	A	5162	3	410	HEG*PTFSSILHHPGAWAQLQ*PSQ ATTALFTLISVA*QQAGCSPQPGAG NTPPPPPNSGTLTPSPACAHWAQC* ANKDEFVSVPGPQCLWPR*GPSYTAS LPQALRARPSQMTRVPQAPPPTGPG PVVSPCANTN
4857	10354	A	5163	168	435	IIAQ*N*FLKNNFQ*TI*K*NKILFTT RSK**I*QKQQKNLYLEKYKTLLKEI KDLNKWKNISCSWIGTLSIDKLVTL SKLNYRVNVI
4858	10355	A	5164	2	427	QIFRYLIMEKEQEHTYRGFKTVNR WTDAYDYAQHYSEASVASKDVS W*FHDYLGMSRHPDVLQA*QETLQ RHGAGSGGSRNLSGTRNCHVELEH ELADLHLKDSSLIFSFCFIANDCTLF TLAKILPGREIHS DACQHA FM
4859	10356	A	5165	11	1232	MAGAATGSRTPGRSELVEGCGWRC PEHGDRVAELFCRRRCRCVCALCP VLGAHRGHPVGLALEAAVHVQKLS QECLKQLAIKKQQHIDNITQIEDATE KLKANAESSKTWLKGKFTELRLLL DEEEALAKKFIDKNTQTLQVYREQ ADSCREQLDIMNDLSNRVWSISQEP DPVQRLQAYTATEQEMQQQMSLG ELCHPVPLSFEPVKSFFKGLVEAVES TLQTPLDIRLKESINCQLSDPSSTKP GTLLKTSPSPERSLLLKYARTPTLDP DTMHARLR\MSADRLTVRCGLLGS\ LGPVPVLRFDALWQVLARDCFATG RHY\WEVDVQEAGAGWWVGAAY ASLRRRGASAAARLGCNRQSWCLK RYDLEYWAFHDGQRSACGPATTST GSASSWTTRPASSPSTT
4860	10357	A	5166	115	447	MSSWARLCESPVVWYF*HVLVCL HKLRLISQQFLTGINCQLSDPSSTK PGTLLKTSPSPERSLLLCKTPGSGD RVETVEMVGCWVEEDHGNGGPSFF LIRIYLFYLF
4861	10358	A	5167	1	423	ADMKAHLLHSGGMGFSCECSTGF VKHS*LIEHIRTHTGEKPFQCPKCDK SFRLKAQLLSHHGLLTGDRPFHCPE CDKNLRERGHMLRHQRIHRPERPF ACGYCGKGFYKSKLAEHIRVHTKS CPAANELDIKKMLHPLV
4862	10359	A	5168	481	908	EGSQWEAQKALAIQVPCGAVRVP WTTSSPASIPKQSVGKGCDCLR*L GDFAPARGEACECHTEPFRNSRGV GGAWARPGYLVLSLSLQCPDSAC NQDLLAYLQRIALYCHQLNICKVK AEVQNLGGELVVSGVSIS
4863	10360	A	5169	2	2799	EMTAVHAGNINFKWDPKSLEIRTLA VERLLEPLVTQVTTLVNTNSKGPSN KKRGRSKKAHVLAASVEQATENFL EKGDKIAKESQFLKEELVVAVEDV RKQGDLMKAAAGEFADDCSSVKR GNMVRAAPALLSAVTRLLILADMA DVYKLLVQLKVVEDGILKL RNAGN EQDLGNQYKALKPEVDKLNIMAAK

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						RQQELKDVGHRDQMAAARGILQSN VPILYTASQACLPDVAAYKANR DLIYKQLQQA VTGISNAAQATASD DASQHQGGGGGELAYALNNFDKQI IVDPLSFSEERFRPSLEERLESIIISGA ALMADSSCTRDDRRERIVAECNAV RQACRTCSEYMGNAGRKERSDAL NSAIDKMTKKTRDLRRQLRKAVMD HVSDFSLETNVPLLVLEAAKNGNE KEVKEYAQVFREHANKLIEVANLA CSISNNEEGVKLV RMSASQLEAGCP QVINAATWALAPKPQSKLAQENMD LFKEQWEKQVRVLTDAVDDITSIDD FLAVSENHILEDVNKCVIALQEKDV DGLDRTAGAIRGRAARVIHVVTSE MDNYEPGVYTEKVLEATKLLSNTV MPRFTEQVEAAVEALSSDPAQPM ENEFIDASRLVYDGIRDIRKAVLMIR TPEELDDSFETEDFDVRSETSVQT EDDQLIAGQSARAIMAQLPQEQKA KIREQVASFQEEKSKLDAEVSKWD DSGNDIIVLAKQMCMIMMEMTDF RGKGPLKNTSDVISAACKIAEAGSR MDKLGRTIADHCPDSACKQGLVA YLQGIALLYCHQLNICKVKA EVQNL GGELVVSGNCDTCGALQGLKGWPP PLCLATHWVDSAMSLIQA AKNL MN AVVQTVKASYVASTKYQKSQGMA SLNLPVSMKMKAPKPLVKREK QDETQTKIKRASQKKHVNVPVQALS EFKAMDSI
4864	10361	A	5170	25	458	
4865	10362	A	5171	3	764	GPLCIALALQEFGTRRRWACRSLSS SGRRSLFRRMGSVKAVKNKAYFKR YQVKFRRRRKRGKTDYYAR*RLVIQ DKNKYNTPRYRMIVRV TNRDIICQI AYARIEGDMIVCATYAH*LPKYGV KVGLTNYAAAYCTGLLLARLLNR FGMDKIYEGQVEVTGDEYNVESID GQPGAFTCYLDAGLARTTTGNKVF GALKGAVDGGLSIPRSTKRFPGYDS ESKEFNAEVHRKHIMGQNVADYM RYLMQEDEDAS
4866	10363	A	5172	8	400	PLASFDTGDVECALCMRLFYEPDTT PCGHTLCLRCL*RCLYHNAKCP LCK DGLSQ**ASIKYSYNVIVEELIAKFL PEELKEREKLYE*EMEELYNLNNNV PILMCTMAYANVT CPLHMFPCYR LMIRIW
4867	10364	A	5173	2	400	SLPLASFNTCNVECALCMRLFYEPV TTPCGHTFCLKCLERCLDHNAKCP L CKDGLSQCLASRKYIKNVIMEELIA KFLPE*LNERMKLYEYEMEELSNLN NNVPIFVCTMAYPTDPCPLHIFPCY RLMIRIC
4868	10365	A	5174	1	216	AGRTGRPEERAPESKSGSGSESEPS RGGSLRRGGEACGTSDGGPSPF*GS SVVSFTLLSYLGYYSYLLSTV

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4869	10366	A	5175	301	446	SYFSYIILIRGNESEGGFFEN*YFCL LINGGSWSGEPPrRNSHTFNC
4870	10367	A	5176	155	404	AAVPSRILKQYSHPNIVRLIGVCTQK QPIYIVMELVQGERGALSSR*GAQP GQVAALPQEAQQGSSPPAGGDFLTF LRTEGAR
4871	10368	A	5177	172	443	TGMIRGPWTKVGPGAIEKPPVGDGK VPNGCPKSLGNRQPCF*VLEVNEPY VPKKFKAEPFFHANICPLSEKERQF RKQTALVDL*KPKPR
4872	10369	A	5178	3	428	PDQTLCCCAEMGSHCVAQAGLEL LGLSDLPLASQSAITGVGHACAP VLGS*RPSQMLCPFPWWLLSATFY LAVPHLLPCLLFQPHSLRCSRSSSSA NLPVVFPSPGAGCLSLSCMECSFP AKVLVIPFSPSERPPCS
4873	10370	A	5179	2	432	NIVSQNNDLPQTVIWMGDCIISLETR IQMQCDWNTSDFCVTPHS*NETEH HWEIKCHLVGREENLTLDIVKVKE QVFEASQAHLTLLPGTDIFSEAANG LSAINSLKWIKTTGNSTLVNFVLIIC LFLAAAFSPEAASASVD
4874	10371	A	5180	163	585	VEVRAHPKKRQRKKKEKKKSDRYS SSSSSSSDSSSSSDSEDEDKK\KENR RKKKKNRSHKSSSESSMSETESDSKD SLKKKKKSKDGTEKEKDIKGLSKK RKMYSEDKPLSSESLSESEYIEEVQA KKKKSSEEREKATEK
4875	10372	A	5181	18	566	AEQSGEAAARGPVAGPLRPSLWPGFP RRATVCSVQHHGEAGQSGWPYMN PNSNGEIKGSQSQSSGPTIQDYLNRP RPTWEEVKEQLEKKKKGSKALAEF EEKNE*ELEERTGKTQGEIVKWK*E LIQKKDRERKKRRNLVGSSSDSED EDKKQGKRRKKKKNRSHKSSSESSM SETESDSKDSL
4876	10373	A	5182	27	382	SVILSFFFFFFYIAWATVRLCLKQTN ENNDKRDLTSLKVVRK*TLNLHPSI KAMIIRLYFEQLYDNRLANLDEMDI FLATQKLPKLAQEEVKNFSCRVTM DYVNNQNL*TNKGPEPDD
4877	10374	A	5183	2	342	GRSCDPKSVGQTLCVALLSVPLPGD PGQRKLPSQNSEEL*SQKCGPNPM CCSFPVPLAGGPGHSRRSTQSRTR*L KPQLPGWRTEKGAPEEIGKMMLQV IDERPGSALSCRC
4878	10375	A	5184	2	147	AETGFHHASQDGLDLLTS*STRLGL PKCWDYRREPQRPADTWFLKSTT
4879	10376	A	5185	8780	9035	LALQVHTMTPSKFFFIFLVETGFHH VSQDGLDLLTF*STRLGLPKCWDYR SEPPRPAYFYIFLRRSLSLSPRAGVA VSRDHATAL
4880	10377	A	5186	75	355	SNKNPSISCPRTWGECVCQATSRST WFLYPMPYAPIKPTPGDVPGTAPS GRPDSTPS**HRLQGTLPKPAPPLLG VFPKPLLAPLFPEGPGP
4881	10378	A	5187	262	354	VWSPPLTWCLVCQCRY*PGLLM

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						MCFILPT
4882	10379	A	5188	1	104	ESETLPGGVAHACNPITLGG*GGRIT RSGV*DQP
4883	10380	A	5189	1	144	RDKVFALSHRLECSGAIIAHYNLQL LG*NNHRVSDSPVAGMAGVCHHT
4884	10381	A	5190	99	241	CFPGA W V R L Q L T Q A S D G P W Q C S S S Q R L H H A P H V V T L Y L C C A F S P C S P V K L R D F E S A V N N F E K A L E R A K L V H N N E A Q Q A I I S A L D D A N K G I I R E L R K T N Y V E N L K E K S E G E A S L Y E D R I I T R E K D M R R V R D E P E K V V K Q W D H S E D E K E T D E D D E A F G E A L Q S P A S G K Q S V E A G K A R S D L G A V A K G L S G E L G T R S G E T G R K L L E A G R R E S R E I Y R R P S G E L E Q R L S G E F S R Q E P E E L K K L S E V G R R E P E E L G K T Q F G E I G E T K K T G N E M E K E Y E * S H R * R * G S S V L V L D G D I A Q E H G G K D G A E Q L S D A S L G P G S D Y S S H K L L M G P G S A R V A R G S I M H H T L S H S T C V V P S P L A L Q
4885	10382	A	5191	303	427	I V L F E K K I F F F F F E T G S C S V P K A G V Q W C G H S S L Q P * P T G L M
4886	10383	A	5192	82	352	R V P E R V L P R P I P P A S C P V S P P A S R P L * G T P R A A P E T R R R P R T A R D P R G L R W Q T Q P A A P L L A S P G P G V A P V A S G A P I S R N D F Q L C K A R M L L
4887	10384	A	5193	1	248	Q K L K K L A R H G G A C A C G H K L L G W L R W * D H M S L R G Q G C S E S * S C R C T P A W T T E * D P V Y Q H K I L S L * D F L I * K A S S N R S S V I Y E L
4888	10385	A	5194	3	370	A Q W R V D S D G A P K R I A D S A T S P K L L Y V D R V V Q E I L E T E R T Y V Q D L K S I V * D Y L D C I R D Q T K L P L G T E E R S A L F G N I Q D I Y H F N S E L L Q D L E N C E N D P V A I A E C F V S K S E E F H I Y T Q Y C T N Y P R
4889	10386	A	5195	28	183	Y D R K R P V G K E K I G K L D C M K T * N F C A S K N T I K E M K R Q R T V W E K I F A H Y I S E R K
4890	10387	A	5196	1	681	M H P I G I A L S K V P V E S K E G D I M S H T G G S V P Y L D N L N K A S V C R G Q S C R V F Q V K E M V T Q V E S E N N Q E E Q K Q V R L P E S R L T P W E V W F I G K E K E E R D R L Q L K A L E F K E D W K L L K R R V T K K S G S V S V S I S S Q G \ N L T V C D C C E S F L L T K P V S C K H L I K S H S C P A L A V A S / C Q R P E G Y W S D C G T R S H S D Y A D E E D S F V S D S S D Q V S S R R T V T H S Y A P P Q S Q P H R H T Q T G T T A T Y L
4891	10388	A	5197	1	2862	M P G P L G L L C F L A L G L L G S A G P S G A A P P L C A A P C S C D G D R R V D C S G K G L T A V P E G L S A F T Q A L D I S M N N I T Q L P E D A F K N F P F L E E L Q L A G N D L S F I H P K A L S G L K E L K V L T L Q N N Q L K T V P S E A I R G L S A L Q S L R L D A N H I T S V P E D S F E G L V Q L R H L W L D D N S L T E V P V H P L S N L P T L Q A L T L A L N K I S S I P D F A F T N L S S L V V L H L H N N K I R S L S Q H C F D G L D

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						NLETLDLNYNNLGEFPQAIKALPSL KELGFHSNSISVIPDGAFDGNPLLR IHLVDNPLSFVGNSAFHNLSDLHSL VIRGASMVQQFPNLTGTVHLESLTL TGTKISSIPNNLCQEQKMLRTL YNNIRDLPFNGCHALEEISLQRNQI YQIKEGTFQGLISLRILDVSRNLIHEI HSRAFATLGPITNLDVSNELTSFPT EGLNGLNQLKLVGNFKLKEALAAK DFVNLRLSVPYAYQCCAFWGCDS YANLNTENNSLQDHSVAQEKGTAD AANVTSTLENEEHSQIIHCTPSTGA FKPCEYLLGSWMIRLTVWFIFLVAL FFNLLVILTTFASCTSLPSSKFLIGLIS VSNLFMGIYTGILTFLDVSWGRFA EFGIWWETGSGCKVAGFLAVFSSES AIFLLMLATVERSLSAKDIMKNGKS NHLKQFRVAALLAFLGATVAGCFP LFHRGEYSASPLCLPFTGETPSLGF TVTLVLLNSLAFLMAVIYTKLYC NLEKEDLENSQSSMIKHVAWLIFT NCIFFCPVAFFSFAPLITAISISPEIMK SVTLIFFPLPACLPVLYVFFNPKFK EDWKLLKRRVTKKSGSVSVSISSQG GCLEQDFYYDCGMYSHLQGNLTVC DCCES\FLLTKPVSCKHLIKSHSCPA LAVASCQRPEGYWSDCGTQSAHSD YADEEDSFVSDSSDQVQACGRAC FYQ\SRGFPLVRYAYNLPRVKD
4892	10389	A	5198	2	413	VDFFFFLRRSLATVAQAGVQWRDL GSLQAPPPGFTPFSCSLPSSWDYRR PPRPANFFVFFFF**RWGFTVLAR MISIS*PRDPPTSASQSAGITGVSDRT RLDFKKKKKYCGKKDIMYRKVYTS LIQLTKKSLIH
4893	10390	A	5199	1	142	RKMFGNGRARGVIVLPCGKGYQS **GGQAVGSGSASCLPLSLCTFP
4894	10391	A	5200	1	375	GEATMNPSEAEVVCVPTWWPP VSTR*MGGRE*RKERA EKGRGKG MEKEGAGERRGKEKNGDSRERGRE GKSVTDNST*GAAAGLPQSPCPIQA RGVQSPRPQAMSRGEPEYSGIGGW GSGEA
4895	10392	A	5201	109	331	PLYCSPGASYMTLTALGPTQTQVPE QRLFVTCILCQEEQEVKVESRAMVL AAFVQRSSVLSKNRCKFI*DPGKS
4896	10393	A	5203	2	168	FFLDSTLKA*AIKAKINKWNDVKLK SFFKTKETINKM*QPMVWENIFANH LSDKG
4897	10394	A	5204	107	357	DLRWYSSFLWMCCIPGAKWHYPING SSCVMGMGIKYDFTGHWIVKHIGL AADLDSFYEYLLKSYILFGE*DDL* MFNAA YQSIQ
4898	10395	A	5205	3	376	CQSQVPTDHGGQPPGSHPGWKPGP DLPPRFDPPEPSRPGN*GLLGPALCP SDLYAFGPQGISVNQGLPQWRPGW GHPWRLPEPDS*APAIQPLAEPVL WGWGGQRPRVPQQLPTAERCCSDF

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						S
4899	10396	A	5206	1	262	QNIFLHLFFCSFTAQKYPMVHLLQK SDNSFNQELLKSMVKSIMNDVYG PMSQILETLNKCPhFKRQR*VLLLD EYIVLLGRFILFA
4900	10397	A	5207	2	296	NGTHASYGAFYLEYSLLAEFTLVV KHKLPGVYVQPSYRSALMWVGVL SMWEGG*RQGLVRSTVGLGGAVLS SEDRSWGVGSLLSRASAPRLPLAHL RC
4901	10398	A	5208	30	280	FYYAFKEEIPVLYSLFQKIETGGILL NSALLLIPKST*YRRPYKKGKLNRYR PKSFVNINVKILNRI LANQIQKCIKRI TYYS
4902	10399	A	5209	1	277	NFSSLLIHGRMHTGEKPYECKNCGK AFTSAKSLQNHGRTHTG*KPCECKQ CGKAFICSSSCQRHEETHSVNMHSV ILIPKHKRVRVGKGPLR
4903	10400	A	5210	220	585	EILVRSRLRQDPLRSRRGKRHTGRRW DGSGWRATGARE*RRESRGWEME AREAGRRKPASERRKSGSRRAGDF LEPATRSRSEKEVRTLARNGRP*AS PGSHRSSQ*LQPRVACGGRAATKSS
4904	10401	A	5211	1	291	SFLETLLPRLGCSDAIMAHCSLELLG YMRSCHLSLPS*DYRPTPSRLANSFF LIHGGFFTL SWADLQLLGLKQSF RK SWGLTG VSHHAQPPFPYYLY
4905	10402	A	5212	228	379	
4906	10403	A	5213	317	534	ATKEN*INWDLIK*NKQKPFASKDT TKQAKRQHIEWEKKVVNPIYDKAP VSRIKNLLKLNNKNTNNLIVKKK
4907	10404	A	5214	3	366	IGY/NPDTVACV/PILGWNGDNMLE QSANMPWFKGWK VTRKDGNASGT TLLEALDCILPPTRPTDKPLRLPLQD VYKIGGIGTVPVGRVETGVLKPGM VVTFA PVNVTTEVKSVEMHHEAQK AK
4908	10405	A	5215	1	1254	
4909	10406	A	5216	33	1472	KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKFEK EAAEMGKGSFKYAWVLDKLAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD(CAVLIVAA GFVEFEVAG\SKNGQTREHALLAYT LGVKQLIVGVNKMDS TEPPYS\QKR YEEIVKEGSTYIKKIGYYPDTLAFEP ISGWNGDDMLEPSANMPWFKGWK VTRKDGNASG\TTLEALDCILPPTR PTDKALRLPLQDVYKIGGIGTVPVG RVETGVLKPG\MGVTFAPVNVYN GK*KSVEMHHE/AL*SEALSWGNTN GLQLSRNVSVKDVRRGNFAGDSK\ NDPPMEA\AGFTAQVIILNHP\SQKN ARHMPLELDCHTAHIACKFAELKE KIDRRSGKKLEDGPKFLKSGDAAIV DIVSG\KPMCVESFSDYPPLGRFAVR DMRQTVAVGVKAVDKKAAGAGK

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						VTKSAQKAQKAK
4910	10407	A	5217	178	566	KGGATCPESPQDRKRRGNLDMKEL YSENEGMA SNHGKMENE*QPQDQR KPQVTLYSGRQEVKRKGKDRKQGG NRR*GNV*RIKGKPESEGEAKEGKS EREGESEMEGGSEREGKPEIEGKPE SEGEPL
4911	10408	A	5218	27	336	TNPVQQTLPVIWTSTRLPDTHEDKA FSAPQIEDRGTPGLGSRGALGPSPT PDCAG*VVAAGPGAESHPRAPKPT AGMSPGVARLSSPGSGSQGSWQNP ERP
4912	10409	A	5219	2	454	HFNM RDPLTDCPYNKVYKNLKEFS QNGENFCKQVTSVLQQRANLEISY AKGLQKLASKLSKALQNTRKSCVS SAWAWASEGMKSTADLHQKLGA IELEAIKPTYQVLNVQEKKRKSLDN EVEKTANLVISNWNQIKAKKKLM VSTQET*STADLHQKLGAIELEAIK PTYQVLNVQEKKRKSLDNEVEKTA NLVISNWNQIKAKKKLMVSTQET
4913	10410	A	5220	26	130	TTWKYQYKNLERNQKEITELKSTIA EINITRGI*R*FEQTKE*INELEDKI MEIFKDKR*KKGEKSLRGLWPPSRD KEACMPWKLQTEKKKGAERLSEE IMAESFSNLLADMNINS*ELKSTIAEI ENITRGI
4914	10411	A	5221	48	394	SPSMCGSLDPPTLPQTLQVPSMLT HPCPPPPHCPPLAHPSSLLPSTHIY H**HLSPYPNPGTQEGHSGVRLRA TDVASPSVLGQFPSYSISVPREGHA ATVAAKGPLECRA
4915	10412	A	5222	3	726	EQEVDYDPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLRKVGSKCKHPEA KRMPCAEDYLS\VVNLQLCVLH/EK TPVSDRVTKCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLRKVGSKCKHPEA KRMPCAEDYLSRGPEPVMCVA
4916	10413	A	5223	4274	5256	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLQHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT

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						KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIDFVLV SNILPKFNHLCTHTHTHTLTLFST YLKNDRDKTIMCKLSLIG*LLESLEF GGSGENVNYFCNIVCYRK/ADCF SFLKFRYLYEIAARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV
4917	10414	A	5224	1	332	RMPCAEDYLSVVLTQLCVLHDKTP VSDIVAKCCSESLVNSQACLSL*V KDAYVPKEFNTETFTFHADICALSE TERRIMKQTGLDEFVKHKP*ASDER LSAVMDDFAAF
4918	10415	A	5225	7	564	TTRAAGREALSPGQGAGGGEGGA PRHTATGHAAGREGRGGRGADQG* GWPRGARALHDQAEGRGGLPAGLP VQAERPQREPCSGQVGSEPPCHP\A TAGGRKVRPAWPAAAGEAGGHSG TGRAGAAGGAAVGTGGGAAGPGG LPMSGGAGPGGSGAAAPHAAS*VQ PAAGAASAATRNIRMPKTT
4919	10416	A	5226	132	917	PGLFYLGEEQPGPQAGGPAAGQG ATAGAEAAAGCPGGAAAPAVLAG GRAGGRSAGWCAGAPGA*PGLFYL GEEQPGPQAGGPAAGQGATAGAE EAAGCPGGAAAPAVLAGGRAGGRS AGWCAGAPGA*AQP*TTGAAGREA LSPGQGAGGGEGGAEPHTATGHA AGREGRGGRGADQG*SLSQATDLW TSGPSHKWTDLSLWPYPCCSGCSW GQCL*LRAEGRGGLPAGLPVQAERP QREPCSGQVGSEPPCHPVSHTPKGP VPHCLGASPGLLWLATAGGRKVRP AGPAAAGEAGGHSGTGRAGAAGG AAVGTGGCQQRWIR
4920	10417	A	5227	3	1245	AWEFVWHPGGFDRSCPGPQGGEGS EGGEGT*EGSGSLALRPRPLSCPRA GPGPGPRLA*ASVYPWNQKRVGGL WRPQRTPARLCDPHAPEHAWAL*G KPGPAGHPAEAA*RQRE*AAGPRGT AAPAGQDRQHHAGPRGRPARGA AAAERQRAPEKGEEQPGPQAGGP AAGQGAAGAAEAAAGCPGGAAAP AVLAGGRAGGRSAGWCAGAPGA* AQP*TTGAAGREALSPGQGAGGGE GGAEPHTATGHAAGREGRGGRG ADQG*SLSQTTDLWTSGPSHKWTD LSLWPYPCCSGCSWGQCL*LRAEG RGGLPAGLPVQAERPQREPCSGQV GSEPPCHPVSHTPKGPVPHCLGASP GLLWLATAGGRKVRPAGPAAAGE AGGHSGTGRAGAAGGAAGVGTGGG AAGPGGLPM
4921	10418	A	5228	612	795	PGFISAIGGLVGLSSYDFYKEYED KPTSPPIAEMNPGYNI*HDLIKSFKM LAFICISS
4922	10419	A	5229	1	345	SSWSFTLVLTQAGVQWHDLSLQPL

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						PSEFKRFSCLSLPSSWDCRRLPPRPA NFLYF**RWGFTILTSLVLSY*PCVS PTSASQSAGITGVSDHARLIVGDFN TPLLITERSSTQKI
4923	10420	A	5230	1	1212	MPKKRQALVEFEDVLGACNAVNY AADNQIYIAGHPAFVNYSTSQKISRP GSDSDSRSVNSVLLFTILNPIYSITP TRLNVFKNDQDTWDYTNPNLGQGG DPSNPNKRQRQPPLLDGHPAEYG GPHGGYHSHYHDEGYGPPPPHYEG RRMGPPVGEYGPADSPVIMVYGL DQSKMNCDRVFNVFCLYGNVEKV KISLKKQSPGGRPMGEEWLDGYAV DRAITHLNNNFMFGQKLN/CVGA QAREGSRGTGERKGGEWGPAEEHS EAEVLTHTEMGCGSVSKQPAIMPG QSYGLEDGSCSYKDFSESRRNRFST PEQAAKNRIQHPSNVLHFFNAPLEV TEENFFEICDELGVKRPSSVKVFSGK SERSSSGLLEWESKSDALETGLFLN HYQMKNPSINLVT
4924	10421	A	5231	1	421	FDPPGCFFTPIGNPFGPFQGNFHRK NGVQAMVEFDSVQSRQAASLN GADIYSGCCTLKIEYAKPTRLNVFK NDQDTWDYTNPNLGQGGDPSNPN KRQRGTVISQD*PSLLKNYCTCDF FSCSYICAAHVLCGTFQ
4925	10422	A	5232	2	1883	DEQRRRSGAMVKMAAAGGGGGG GRYYGGGSEGGRAPKRLKTDNAG DQHGGGGGGGGGAGAAGGGGGG ENYDDPHKTPASPVVHIRGLIDGVV EADLVEALQEFGPISYVVVMPKKR QALVEFEDVLGACNAVNYAADNQI YIAGHPAFVNYSTSQKISRIE*ND YR\SVNSVLLFTIVNTINWITTDVLY TMCNPGCPVQRIVIFRKNQVQAMV VFDSVQSAQRAKASLNGGDIYSGC CTLKIGYAKPTRLNVFKNDQDTWD YTNP\NLGQGGDPSNPNKRQRQP LLGDHPAEYGGPHGGYHSHYHDEG YGPPPPHYEGRRMGPPVGGHRQCP SRYGPQYGHPPPPPPPEYGPHADSP VLMVYGLDQSKMNGDRVFNVFCL YGNVE\KVFMKSKPGAAMVEMA DGYAVDRAITHLNNNFMFGQKLN CVSKQPAIMPGQSYGLEDGSCSYK DFSESRRNRFSTPEQAAKNRIQHPS NVLHFFNAPLEVTEENFFEICDELG VKRPSSVKVFSGKSERSSSGLLEWE SKSDALETGLFLNHYQMKNP\NGPY PYTLKLCFSPAQHAFLIRCLGRVPFE QENISLSFMPFFGFCFCYLQKILGSP FFFFFFFFLKVVEEGFPP
4926	10423	A	5233	2	337	DMILAERGGVCVMMKTQCCTFIPN TSTTDGSITRALQGLTALSNEANN SGVNDPFTGWLEK*FSKWKGIIASIL TSLAAVMGVLLVRCCVIPCLQRLM QRLIKMALTQTS

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4927	10424	A	5234	62	343	RQLNRNDPNRNKGKKVGIKQCLRF WNNFILTCLIGVSEIEEKKNAGAE*IF EEIMSKNFPKLIKYPNQIEA**TPS KINTEKTTFRH*IIGKR
4928	10425	A	5235	1	359	TDDDLNWLDSRTFREQGVDETET CLLRKFSYSDQNVDSRDPVQLNLL YVQARDDILNGSHPVSEKACEFGG FQAQIQFGPHVEHKKHKGPFLE*MTF CFSFFSFLSSFSFSLFSL
4929	10426	A	5236	2	264	SYYPGEISVPPFNICHFFLSCFYNLS RFFCKKSPASPLCFSIKKSPFVKIHL VFSLVTSFLK*FFFYL*FFPESVISF GSFSNSD
4930	10427	A	5237	3	246	LIPRGQGSTVVLPPYNPATSIFGNDLN EIKMYGHAKTCIWMFMTSSFIIDRT RKRQ*CSSVREWINKQ*CIQTMELV FGRN
4931	10428	A	5238	78	411	VLNSPICNCLYPILCSFLFIHYFVVC FYTFIPVFYLVYHQEIVI*SLTLVFFV CVVKINTRLMVHIFILYICL*LSICNS VYLLHVHIYLEHFL*HILMVVFFKR SDQSS
4932	10429	A	5239	2	175	TKLDFIGIKGFSSVKDNVKGMRQA TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN
4933	10430	A	5240	1	335	VTIRGAGIPDESARNVNYSLASFLKR WLTLMDRGFIFNLINDYISGFSPKDP KVLAEYKFEFLQTICNHEHYIPLNLP MAFAKPKLQRV*DSDLEYSLSDEY CKHHFLGGLL
4934	10431	A	5241	139	354	SPCLPYCCLLCYRYGDGRIMIGFSC GH*VVISTHTGELGQEIFQARNHKD NLTSAVSQTHIKVATCENNL
4935	10432	A	5242	2	332	ILAGAI*DNEIKLM*IEKEVVKLFLF TDDMILCVENSKEHTHSHTQLGLI NEFSRASG*KINVQKLFLYTNVQS KNEIKEPSLCTKASKRIGYLGHLTK EV*DLYSERTKPH*KKNRILRNFTN KRSVRLVQ
4936	10433	A	5243	137	290	GSSDINQTKHVR*VNRQICSRTTQ QSPEDCDFKKDGLVKRCMGTQTRQ SL
4937	10434	A	5244	1	363	LTCSGDKEQIKDKSHVLKKGKGNFE RETS*KKK*SLPPFDDNVEPNLYV EENICKSDSERPRSSSSSSSFT PSQTRQQGPLKSMNDLHSDDYEE ESDEMEDNGPDFEMGKPVNIR
4938	10435	A	5245	2	376	VHLGWCMLPLRTHTEYVKALSYA* DKQLGA*AGLDRQIFLWDANTLSA LTASNNTVTSSLSGNTDSIYRLAM NQLVTIIVSGSNDKALRVWDPLTCA TLVNLKGHTDNGKALVFNRDGTQC LSR
4939	10436	A	5246	60	185	
4940	10437	A	5247	1	146	RWRDLGSPQAGFR*FCCLSLSSW DYRHAPLF*QFYLFILLFCKKYF
4941	10438	A	5248	2	298	TFFTFPFVAKPNPRGPKTPAPYFSPQ

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						GPQKIYPPKFLGPPFNFPPLLGKVF RAPNPRV*LPPGARPSSSSSLLPGF* KIPKPLFY*KKIFTPQKTKK
4942	10439	A	5249	77	370	EYS*SVVFLDLMRRQEELRRMEELH NQE
4943	10440	A	5250	83	467	YSEKSAGLWLNMLEKSLPGHRDTA TQIQHVSPMCQVEPPAKKAATLAE GDKDNDI*PCFVQRQLREGROGRA ARLWEKWLRWYVEKKAKKTALV VKSSIPLDIKPWDNETNIAQLEACM RFIQLDGLV
4944	10441	A	5251	1	359	KYTLSRLATVPPTLNPAEYNISPDTR RAQVEQLAIRAGLK*EYLLQYNNP NRRGLIEDPALIRWTYARSANVYPN FRPTPKNSLLGALCAFGPLFFWYCV FKTDMDRNQKLIREGKLDQ
4945	10442	A	5252	3	349	SSLATVPANLNPAEYSISPDRRAQ VEQLAIRAGLK**YLLQYNNPTRIGI IKDPALIRWTYARSANVYPNFRPIPK NSLLGDLCAYGPLFFWYCVFKPDM DRKETLIPEGKLDQ
4946	10443	A	5254	1	415	NAVIQVAHPLVQKQ*VDYIHNGFL VPVMGPALHKTSVEEMIASTAYLEL FLRSISEPALLRTLRLFLLLHRHDT TILDTLVARIGSNSRLCMVSLSLFKT LLNLSCEDVLLQLGLRYLVPCNHV MLSQKPAVRDVL
4947	10444	A	5255	34	394	YRHYTICCIIGFLNTITMMTVSFHKY GEYFPGT*DLRDIDAGKC*YYAVNF PMRDGIDDES YGHIFKPIISKVMEM YQPIAVVLQCDAYS LYGDSLDCFNL TIIRHSTRLYLI*SYHFTS
4948	10445	A	5256	178	417	ILVPPAGGKGNLI*WNP GPPGARG FPGLTPPRGGKKGRAQPPENLVF* EKTGFPIVQRGGLKPPP GPPKGGE*R GGPP
4949	10446	A	5257	749	1049	DGSSLLGPRPGGKGNQTKGNRPP G*RESPPHPPRRGKKRMAQPPQLI WDFSSSSGFPL*QGGGINPHDPPKG GKKRGEPEPTTGPSKRGGKQGF
4950	10447	A	5258	1	359	LFPKVNLSPVTPAKDTGLTAAPQEP KAPKASPVQHALPSSLSVPHTAILV TGAQLCGPAVNLSQIKDTACKSLLG LEKKHAEAPAAENPHGGPGDSSA PY**GDAPKGHAIRAVEVPD
4951	10448	A	5259	1	441	FFFLNRVLTITQAGVQWCDHGS LQ PRSLGLK*PSHFSLPSS*DYRCAPPH LANFYIFYKDRWGFTMLPRLVWEL LGSSDLSILDSQSAGITGVRHHTWA NFFNFLCVSGIN*RNFYNKFTSWGS HPNSQYYSGISWGQSTNILLGY
4952	10449	A	5260	1	553	FYFYFFFFPLFFFFKPQDDFLVPGDQ NQRPGGSMPLGTAFILFQMKTL SLV RRGINQDN*HWRQEDPLIPISPGFPS RIPPLKSEMSLPLSTDGSETRRTQSP FDEIYMAHDASGLRLPDSPPPAAP GRDPAPSGQRAPGKLRGQCQLKSE

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						RESRKEERQRSKPGEAAALGGVAC TFHLKSRS
4953	10450	A	5261	1486	1695	GKSCRPNYIFILFSSFLRRSFALVA QAGVQWCDLGLSQPPPGFK*FSCL SLPSSWDYRYPPLCPANFC
4954	10451	A	5262	1	334	RRFVSQETGNLYIAKVE*SDVGNYT CVVTNTVTNHKVLGPPTPLILRNDG VMGEYEPKIEVQFPETVPTAKGATV KLECFALGNPVTIWRADGKPIA RKARRHEGCEM
4955	10452	A	5263	78	313	KVTYIQKNVYSKCTAGWVFTQRAR VGSREPFPAAPSPGPHGGDPPSPQQL G*PLSPLPQPAPVRLPSPVMMSERIL PF
4956	10453	A	5264	3	320	IFSQENL*YSDGSDILGLLALQAEEN LGMVMIFTLVTAVQEKLEIVDQIK TSSSSSSSSSSSAEEAEKQLFHGTP VTIENVLNWESQGWRRQTFLGKILE KEKG
4957	10454	A	5265	3	941	APPRCLGDLWARARATMTDYGEE QRNELEALESIYPDSFTVDCTLIQPS *QLVFQNINGLS*YHILLQ*CFT*QG PC*VLSENPP\STITVTSEAGENDES IHIKLLSCVLAVQTTLKFTYSEKYPD EAPLYEIFLPGKILEDNDVSDILKLL \ALQAEENLGMVMIFTLVTAVHERI NVLVDHIIITRCEVEMKL*DKEAEE AVKQLFHGTPVTIENFLNWKA/RSF DAELLEIKKKRMKEEEHAGLDKK\S GKQLFETDHNLDTSIQFLEDAGNN VEVDESLEFQEMDDLEDEDDDPD YNPADPESDSAD
4958	10455	A	5266	1	332	LKKHKSTRVP*NVKSGK*NFSPPFKI RPWAQKRAKKKGAREKKAD*EKG EFGKLSSSSRFRPGKKV*G*PKGFOR NFEKKPVKSQGPVNMGVIPAFEKKP RIPPAKIPI
4959	10456	A	5267	3	375	SASPQTLQQSLPRSIAPKPLTVRLPM NQIVTSVTIAANMPSNIGAPLISSMG TTMDGSAPSTQVSPSVQTQQHQMQ LSSSSSSSSSQMQMQQQQLQQHQ MHQQIQQMQQQHFQHHMQ*HLQ Q
4960	10457	A	5268	1	360	KGAPKHGQAPLGDPPRAVGGQEH* GPARGRGPGPREPGSGQTSSPWVH VRPGGGKNDSGKARP*ILDPKSVSC IPAPSSHRPLSSPTNPFP*SSYEGSP RSPQPWTLQPQGPWPPSRQA
4961	10458	A	5269	1	181	KKKPQTWEKLV*GLF*KKRNPWG QRVPPVTPPLWGVKKRGGVFFRGL KPPLKPRENPPF
4962	10459	A	5270	10	108	SHINVPMNQ*VVS LGPGQVTKGW DQGLLMCE
4963	10460	A	5271	1	336	EFLGAVGFCRLWIPNFAVLAKPLYG VTK*GDTELFKWGSQQQ*AFHELK EKLMSAPALGLPDLTKPFTLYVSER EKMAIGVLIQMVGPWPRPVAYLSK

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						ELDGVSKARSEGCE
4964	10461	A	5272	1	118	TEVRH GKLDSSKWIPIRGN*NIYNP HCLSYKLEHGS DQEIPSDWYPFATV QFSVPDLC
4965	10462	A	5274	2	327	SCLVLVLLCVEYLFYPYLHFQSI CVFT GEVSFLQAAYS WVMGFFVFLFI LHI SYFL*LLWGLFISLHLWLSLT CEDLF LLFFSRCLIIYICFVLLFMSFLILWR LLVF
4966	10463	A	5275	171	331	LKTSFRTKTCT*MLTASLFVIAKTW KQPRCPSVGE*LSNL*YVQTM ECYS VLK
4967	10464	B	5276	83	332	MGKRDNRVAYMNP IAMARSRGPIQ SSGPTIQDYLNRPRTWEEVKEQLE KKKKGSKALAEFE EKMNENWKKE LEKHREKLLSGX*
4968	10465	A	5277	76	138	
4969	10466	A	5278	1	1050	
4970	10467	C	5279	146	433	MKKKSNERWDQVYKILKGKSLRPG FPRCATVRAIQHHGEAGQSGGLYEP NSNGEIKGSNPVFRANNTGLSESTK AYLGRSKRATRKEKERLQGF G*
4971	10468	A	5280	27	264	NPNHQSLLCRAFCGVLILPVLALL TRLSFGELTYNNHFIYIFKAFFKFI* VFKWTGDNMFFIKGDMDSLAFGGG G
4972	10469	A	5281	135	358	VHSPVL*LISTIPTSRLKFLKETGHGT PMEEIPEEELSEDVEQIDHADRELRR GQNLRCGIHRLP THIQVGQN
4973	10470	A	5282	15	196	KGKIVKLDIFI*NFSSAKDPVNY*K DNYRLRKMTANHISDKEFVSKTYK ECLKNLKKF
4974	10471	A	5283	307	383	YF*VSLATLCVYFLLDEGNILTATK VFTSMSLFNILRIPLFELPTVISAVVQ TKISLGR
4975	10472	A	5284	3	267	TIVRPYLLKKKTGTIVEERVNAPGW NEDDDVSVSDESELPSTTLKAFEK STMEQLVEKACFRDYHRLGL*TL SG SCCRS*P*SRRVQ
4976	10473	A	5285	1	260	TAVPSAASMTSTRAASASSVHVPVS ALGAGSAATAASEEMQTIPQATAA KYPRTIHPESSTSASRSLGT/ TISSHP VSHKCSFHKSG
4977	10474	A	5286	60	292	VTNFLIFHMRJISKYISIFLTVFFFVSQ IVLLFKHSYFSYLELWKMQRDSK NAT*KRAL*RFHEKS FHEGCMCIKS
4978	10475	A	5287	738	1152	KGRVWSWC SRKRTFC SFGSFS SSSDA LTSYITTAIPTAVGGASATAVPS AASMTSTRAASASSVHVPVSALGA GSAATAASEEMSDKELITCTRQLKR DGCFGQYTNQPGTGNMGKKQPRIT LCPLNKRKVVAVKPN
4979	10476	A	5288	3	555	RKRTFC SFGSFS SSSDALTSYITHCCQ SPPAAV*LASATAVPSAASMTSTRA ASASSVHVPVSALGAGSAATAASEE MYVPRVVTSAQQKAGRTITARITGR CDFASKNRISSSLAIMGVSPHELSC

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						CGKTSSQSTVQTHSLKQLPAKYPRTHSIPESSTLSLPRSLGTQISSHPVSHKCSFP
4980	10477	A	5289	94	323	VIGYRNIRCTILTSTITSSLSIL*LNH*PETRLSE*AGV*DKGLVVAQMMWLMDHIFKYTNFGIVSLVHGDFIRQ
4981	10478	A	5290	2	319	MVLVTLDCKYAVAALWGKVKVDEVDGEALGRMLMVVYPWTQRFWES*GDLSPPDADMGNPKVKVHGKVLGAVSNGQAHVDNLKGTFFATVSEMHCCKLHVAQEPEVL
4982	10479	A	5291	1	159	RDLQHFPSSVAM*DQTQNDIASTSNHESILQGIGQSQL*EEVQLME*APVDC
4983	10480	A	5292	187	282	LRSY*CLLLMISFTRNANLFR LHGTHTDTFKCLEYEKCFNCNSDLIVHHRINMDHNPHTSA*DSGLLLGMHF
4984	10481	A	5293	1	156	SGGVDEQMMREKEELMLWLQDYEKIKKAEREL*EQIKREMKKNQKRKREKK
4985	10482	A	5294	179	322	NKVGGLTLPNCKTYYKATIIKTVWYWRKKRQIGQ*NRIESPIDPHKY
4986	10483	A	5295	2	395	RDRESDRDGQRRERERRTRKWSRSRSHYRSPSRCRTKSKSSSFGRIDRDSYSPR*KGRWANDGWRCPRGNDRYRKNDPEKQENARKEKNDIHLADDPNSADKHRNDCPNWITEPINC GPDPRTRNPEKL
4987	10484	A	5296	3	228	HELPHPGGLGLKRGCVWLEVAEHVVLGKALLILLPYRFKRNLAMDDKTGMTRNPHFSHNNWIPTFFSTQYFWIIFKVRWPRLKDTTDLRILAPNCLADRLSRHRCNIWQFMQGIRPLVLNFGSCT*PSFQPQQLYTNLFQHPVFLDHL
4988	10485	A	5297	61	360	YVNSKCSNHRK*SLSSSSSERESSFVPQVELHGRDLG*LQLWLPFGFKFPGLTPLRNGDDGPRPQPANLGLLVKTGFSPVAHLGVNLGTLGDCPALP
4989	10486	A	5298	124	351	EREFRFVPQVELHDRDLGSLHPGTPGLRKFSGLTLPRSGDNGPGPPPVNLGFLEETGFSHVAHFGLNFGT*GDCP
4990	10487	A	5300	3	388	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQRQLHLNGTFPNTSDADMEPCVDGWVHDIISFSSTIVTE*DLVCDSQSLTSVAKCAFMTG*TADGFLGAHLSHRVRASSNVCMSGGSIVC
4991	10488	C	5301	47	269	MPPLIQSGMSSRTKTRTSSPCWNVHPAPEQYEAPDKDFMIVALDCSAAWPRAWVVTWSSWCPQQHHDIAVPVHA*
4992	10489	A	5302	1	253	MYTQ/HPEQYEAPDKDFMIVAL/DLSGLAEGLGGHVEQL/VARSNIMTL LFQCM/QAEFMPILGTNLNPEF/ISVCNNATWAIGEICMQW

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4993	10490	A	5304	229	2984	PCPCQNFLRCSTSFNFSLPCAMDWQ PDEQGLQQVLQLLKDSQSPNTATH RIVRDKLKQLNQFPDFNNYLIFVLT RLKSEDEPTRSLSGILKNNVKAHY QSFPPPVADFIKQECLNNIGDASSLI RATIGILITTASKGELQMWPELLPQ LCNLLNSEDYNTCEGAFGALQKICE DSSELLDSDALNRPLNIMIPKFLQFF KHCSPKIRSHAIGCVNQFIMDRAQA LMDNIDTFIEHLFALAVDDDPEVRK NVCRALVMLLEVRIDRLIPHMHSHIQ YMLQRTQDHDENVALEACEFWLTL AEQPICKEVLASHLVQLIPILVNGM KYSEIDIILLKGDVEEDEAVPDSEQD IKPRFHKSRVTLPHEAERPDGSED AEDDDDDDALSDWNLRKCSAAAL DVLANVFEELLPHLLPLLKGLLFH PEWVVKESGILVLGAIAEGCMQGM VPYLPHELPHLIQCLSDKKALVRSIA CWTLRSYAHWVVSQPPDMHLKPL MTELLKRILDGNKKVQEAACIAFAT LEEKACTELVPYLSYILDTLVFAFG KYQHKNLLILYDAIGTLADSVGHHL NQPEYIQKLMPLLIQKWNEKDED KDLFPLLECLSSVATALQSGFLPYC EPVYQCCVTLVQKTLAQAMMYTQ HPEQYEAPDKDFMIVALDLFSGLA GLGGHVEQLVARSNIMTLLFQCMQ DSMPEVRQSSFAFLGDFTKACSSHV KPCIAEFMPILGTNLNPEFISVCNNA TWAIGEICMQMGAEMQPYVQMVL NNLVEIINRPNTPKTLLTENTGRITSP SAIPAITIGRLGYVCPQEVAPMLQQF IRPWCTSLRNIQDNEEKDSAFRGIC MMIGVNPGGVVQDFILFCDAVASW VSPKDDLDRDMFYKILHGFKDQVGE DNWQQFSEQFPPLKERLAAFYGV
4994	10491	A	5305	47	411	
4995	10492	A	5306	20	1020	LSLTSRMEEAELVKGRQLQAITDKRK IQEEISQKRIRKLGEDKPKA/QPLKT KALREKWLPWNPASGKEQEEM KKQNQQDPAPRSQVPRTKYPSGLR KRSQDLEKAELQISTKEEAILKKLKS IERTTEDIIRSVKVEREERAEESEDI YANIPDLPKSYIPSRLRKEINEEKED DEQNRKALYAMEIKVEKDLKTGES TVLSSIPLPSDYFNVTGIKVYDEGQK SVYAVSSNHSAAYNGTDGLAPVEV EELLRQALERNKSKSPTEYHEPVYAN PFYRPTTPQRETVPGPNFQERITIK TNGLGIGVNESIHNMGNGLSEERGN NFNHISPI
4996	10493	A	5307	1	95	GTRTFLRTYLSEIARRHPEFYAPELL *FAKR
4997	10494	A	5308	1	338	GTSLSA*GLNIDGQLGLGHTEDI PYTPCRSLFG*PIQQVACGWHV TIMLTEHGQALLCGCNSIVQLAGPH GHLRRVGT*TIELRRENAVHIGAALMPH

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						VALTTSRSIFQCR
4998	10495	A	5309	3	472	VTEFAKTCVADESAENCCKSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPNLRLVRP EVDVMCTAFHDNEETFLKKLYEI ARRHPYFYAPELLFFAK/RLDELRD EGKASSAKQRLKCASLQKFGRAF KA\VARLSQRFP
4999	10496	A	5310	12835	13995	TIPIESDIFPSIFYLYLSSLAYADTYE ALSRFY*KKKLINLLLSLN*ATHFPK IMPVVQVELKAKFN*LFR\KCFLPST NPLLCRWR*YDEWNIATS*LIPAKC SLFYLLC*TVSCLAENT*LLFFRLLV RYTKKVPQVSTPTLVEVSRNLGKVS SKCCKHPEAKRMPCAEDYVSL*KHI IN***KNFPFRYC*CYLS*AEGSNVC VCMFCACVCACTCVYV*YWQSRPR G**FFFF*DGVSLLCCPGWSAVVPSR LTATSASQVQAILLPQPPK*LGLQV HATMPG*FFVFLVENFQLHLF*ISAL LPVL*LSVVLNQLCVLHEKTPVSDR VTKCCTESLVNRRPCFSALEVDETY VPKEFNAETTFHADICTLSEKERQI KKQT
5000	10497	A	5311	1	349	GTSKKLANKVVYNVGLCICLFDITK LEDAYVFPDGDGASHTKVHFRVCEC HPFLHEILTGKIKGCSPEGAHPLR* HPDFPLFSRPPAFLSPSQYILSPREIL VHPSILKFRTRRPY
5001	10498	A	5312	1	410	IEHGIVTNWDDMEKIWHHTFYNEL RVAPEEHPVLLTEAPLNPKANREK MT/QGSVPLPAFPP*SLQIMFETFNT AMYVAIQAVLSLYASGRITGIVMD SGDGVTHTVPIYEGYALPHAILRMD LAGRDLTDYLMKIL
5002	10499	A	5313	216	390	GSADARAPPVLSPVIFCPS*FLTGRP LQGVVMVGMGQKDSYVGDEAQSKR GILTLKYPIEHGIVTNWDDMEKIWH HTFYNELRVAPEEHPVLLTEAPLN KANREKMTQVRLGRRPCSSRPFP FLPILISDGSSPAGRHHGGHGPGLLR GRRGPEQAWHPDPEVPH
5003	10500	A	5314	4	1254	HAHAKLGTRAASSRTLFFRQLRRR VSLPVAMEEEIAALVIDNGSGMCK AGFAGGDA\PRA\VFPSIVGRPRHQG VMVG\MGQK\DSYVGDEAQSKRGI LTLKYPIEHGIVTNWDDMEKIWHH TFYNELRV\APEE\HPVL\TEAPLEP QGQTREKMTQ\IMFETFNT\PAMYR GPSRAVLSL*ASGR\TTGHCHGTLG DGVTHTVPIYGGLPHCSTPFLRLGP GLARDLTDYLMKILT*SEGYSFTTH GPSGKFVRDIKEKLCYVALDFEQE MATAASSSSLEKSYELPDGQVITIG NERFRCPEALFQPSFLGMESCIHET TFNSIMKCDVDIRKDLYANTVLSGG TTMYPGIADRMQKEITALAPSTMKI KIIAPPERKYSVWIGGSILASLSTFQ

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						QMWISKQEYDESGPSIVHRKCF
5004	10501	A	5315	279	418	VEHSISNKENFLGQGTGCHACNLNT LGGRGGRITWRSGV*DQLDQH
5005	10502	C	5316	274	530	MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE XQIXKQTALV*
5006	10503	A	5317	2	736	RLAKTYETTLEKCCAAADPHECYA KVFDEFKPLVEEPQNLKQNCSELF QLGEYKFQNALLVRYTKKVP/SVVL LLRLAKTYETTLEKCCAAAHPEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCKHPEA KRMPCAEDYLSVVLNQLCVLHEKT PVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLS
5007	10504	B	5318	120	1070	MPADLPSLAADFVESKDVCKNYAE AKDVFLGMFLYEYARRHPDYSVVL LLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNFHT ECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEV ENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDY SVVLLLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLKQNC CELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRKPRKSGQQML*
5008	10505	A	5319	2	668	
5009	10506	C	5320	246	365	MDDFAAFXXXCCXXDXKGDLLXR RKVKNLLLQVQLPLGF*
5010	10507	C	5321	261	656	MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE RQIKKQTALVELVKHKPKATKEQL KAVXDDFXAFVEKCKGDXXKGELL XRRXVXNLL*
5011	10508	C	5322	158	607	MLCQSVGSKCKHPEAKRMPCAED YLSVVLNQLCVLHEKTPVSDRVTK CCTESLVNRRPCFSALEVDETYVPK EFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVXDD FXAFVEKCKGDXXKGELLXRRXVX NLL*
5012	10509	C	5323	158	532	MLCQSVPCAEDYLSVVLNQLCVLH EKTVPVSDRVTKCCTESLVNRRPCFS ALEVDETYVPKEFNAETFTFHADIC TLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDDFAAFVEKCKKAD XKG*
5013	10510	A	5324	2	740	PADLPSLAADFVESKDVCKNYAEA KDVFLGMFLYEYARRHPDYSVLL LRLAKTYETTLEKCCAAADPHECY AKVFDEFKPLVEEPQNLKQNCSELF EQLGEYKFQNALLVRYTKKVPQVS TPTLVEVSRNLGK/VCCTESLVNRR

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						PCFSALEVDETYVPKEFNAETFTFH ADICTLSEKERQIKKQTALVELVKH KPKATKEQLKAVMDDFAAFVEKCC KADDKETCFAEEG*KLGAASQAAL GLY
5014	10511	A	5325	1	588	
5015	10512	A	5326	364	1356	TGDHAFQLWKSMMKHTFQVSTPTLV EVSRLGKVGSKCKHPEAKRMPC AEDYLSVVLNQLCVLHEKTPVSDR VTKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQTALVELVKHKPKATKEQLKAV MDDFAAFVEKCKADDEMPADLPS LAADFVESKDVCKNYAEAKDVFLG MFLYEYARRHPDYSVLLLLRLAKT YETTLKCCAAADPHECYAKVFDE FKPLVEEPQNLIKQNCLEQLGEY KFQNALLVRYTKKVPQVSTPTLVE VSRNLGKVGSKCKHPEAKRMPCA EDYLSVVLNQLCVLHEKTPVSDRV TKCTESLVNRRPCFSALEVDETYV PSVNSNSCRGLKKPRKSGQQML*TS *SKKNALSEDYLSVVLNQLCVLHE KTPVSDRVTKCTESLVKGDHAFQ LWKSMMKHTFPKSL/YAETFTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VLLLLRLAKTYETTLKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCELFEQLGEYKFQNALLVRYTKK VPQVSTPTLVE/VLKKPRKSGQQML* TS*SKKNALCRRLSIPWS*TSYVCC MRKRQ*VTESPIRNLGKVGSKCK HPEAKRMPCAEDYLSVVLNQLCVL HEKTPVSDRVTKCTESLVNRRPCF SALEVDETYVPKEFNAETFTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VLLLLRLAKTYETTLKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCELFEQLGEYKFQNALLVRYTKK VPQVSTPTLVEVSRNLGKVGSKCK HPEAKRMPCAEDYLSRGPEPVMCV A
5016	10513	A	5327	1468	1946	LHISWEGEPIDYSVLLLLRLAKTYE TTLEKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCLEQLGEYKF QNALLVRYTKKVPQVSTPTLVEVS RNLKVGSKCKHPEAKRMPCAED YLSVVLNQLCVLHEKQ*VTESNA AQNPW*TGDHAFQLWKSMMKHTFP KSLMLKHSPSMQIYENQDSISSKLK ECCEKPLLEKSHCIAEVNDEMPAD LPSLAADFVESKDVCKNYAEAKDV

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						FLGMFLYEYARRHPDYSVVLRLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCLEFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRN/LRKSGQLR*I*TSCGRASEFNQTKL*AF*AAWRVQIPECAISSLHQESTPSVNSNSCRGLKKPRKSGQHTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLGGTGRPCFSSSGKSMETYPKGFNAETFTFPGSFCT/LSWEGEPIDYSVVLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCLEFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPVC
5017	10514	A	5328	1	2063	MKKVKERDSFIMEDLGAELKSSAYSRGVFRRDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDVMCTAFHDNEETFLKKYLVEIARRHPYFYAPELLFFAKRYKAAFTCCQAADKAACLLPKLDELDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECHGDLLECADDRA DLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCLEFQGEYKFQNA AISSVTPKKVPQVSTQLLTPTLVEVSK/NTLGKVGSKCKHPESKKKCPVAENYLSVVLNQLCVLLHEKTPVSDRVTKIAAQEPLVNRRP/CFSALEVR*NIPFPKEVNA/ETFTFHADICTLS/EKERQIRKQTALVELVETQAPRQKEQLKA/VLWDDFAAFVKIAAKA/DDKETCFAEETISGNAGAKKAIFLVNDEFILMSLTLIQNHRITYSSLPPCLYDSKKLLFHYLASIYPFVPPQDACKGVSE L
5018	10515	A	5329	1	339	RRRRKKNEKRKRQRKIKDEKSRKNSLRVEMRETWRQREKQKEEDREKRGQQEKERRKREIEEKEST*CEQMEIGKTKKVNIHCRWQTQLKLKFHLFSLFSIKMSLSFSTRA
5019	10516	A	5330	2	189	ARGGDAGDAFDGFGFGDDPSD*LSCHIDVHRYLFSA LCDCYTFYFVHIRVFLSMRLADTA
5020	10517	A	5331	3	346	HELETFP*CHNMPLLFYRDRLSASDMLQVRKVMMDHVEYESIITLNNESQSTSSNNNEHPGGQERSLARA

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5021	10518	A	5332	2	442	VFMDADTLVLANIDDLFDREELSA APDPGWPD CFNSGVFVYQPSVETY NQLLHLASEQGGDQGILNTFFSSWA TTDIRKHLPIFYNLSSISYIYSLPAI*S EDVSGAISHLVPLGGDSQAMAQAV LVFLGKEPGRGTEWGNKGPR
5022	10519	A	5333	1	292	VLANIDDLTREEMSAAQTQGWPD C/FNSGVFVYQPSVET/YNQLLHLAS EQGSFDGGDQGILNTFFSSWATTDI RKHLPIFYNLSSISYIYSLPVLPE
5023	10520	A	5334	81	1163	VTNLRPRPPAHFVITMTDQAFVTL TTNDAYAKGALVLGSSLKQHRTR RLVVLATPQVSDSMRKVLETVFDE VIMVDVLDSGDSAHLTLMKRPELG VTLTKLHCWSLTQYSKCVFMDAD TL\VLANIDDLFDRE\ELSAAPDPG G\PD CFNSGVFVYQPSVETYNQLL HLAS\EQGSFDGG\DQGILNTFF*QL GQQQDIRKHLAFIYNLSNISIYSLP AFKVFGASAKVVHFLGRVKPWN TY\DPKTKSVK\SEAHDPNMTHPEFL ILWVGTSFTTNVLP LL\QQFGPWSK DT\CSYVN\VGRC LQGAISHLSLGEI PA\MAQPF\VSSEERKERWEQQQAD YMGADSF DN\KRKLD TYLQ
5024	10521	A	5335	1	241	GTSNSEHALDDRSTAQCRVQM QVV QQ*LQLAKDKERLQAMMTHLHV KSTEPKAAPQPLNLVSSVTL SKSAL EAYALET
5025	10522	A	5336	13	229	ACPRSPFPDRLGCCFP PPAVC*AP AGPHPDGTTSELECTPAPHPSCPEVS VQQKPEPSALYGTGF PFG LQS
5026	10523	A	5337	1	341	GLGSGTSSSSSVKSSISPKRVARWSFS SRVCPVCPSSALSV*DSRSP*ASKSS SNASGSPFCRVKLLSCELQSKADS FSSSSAVSRDRLSSSSMLSRGQL*Q ETSKEAQMPR
5027	10524	A	5338	3	168	
5028	10525	B	5339	978	1502	MSNLTLCISTKHTPGISRakeKKK GTSRLPTSLCQRRVGLTEEKSCSPEL QQKFRSETITEELVGLMNKFVEDT KKG VHQKEGW PSSAYGVTKIGVTV LSRIHARKLSEQRKGDKILLNACCP GWVRTDMAGPKATKSPEEGAETPV YLALLPPDAEGPHGQFVSEKRVEQ W*
5029	10526	A	5340	3	239	HEAKSSPNLVKAILQIQEATQIPRRI NKNKSTLRHRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLESESMGT
5030	10527	A	5341	3	322	HEAKSSPNLVKAILQIQEATQIPRRI NKNKSTLRHRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLSETMEAR KKWHNYQMIEKNCQPTILHPAKLS FK
5031	10528	A	5342	4	351	VGRGRQSHLSHSHPTDPKGQQASP GWNPGVRMLPGLKWLPQPPAASLS *VPSSPTQQT SAGHLLSMSHEALTW

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						VDRATGLAGNGEACVSGTQRHPGL SLAPPGCAPSPSSRAARA
5032	10529	A	5343	3	163	HEEQPEGLSPNLDRLFDRHCNQFS SRD*PIFLARCSHEYSGRHPRLADSI LL
5033	10530	A	5344	112	362	EREQRFTGLNDVHYLPIMYIVVGCA IFIT*V*RGWSSPTKCRSTDYCVNP STRLHAYMAPRHKLHSHCAERDPD QFTLLRHC
5034	10531	B	5345	85	206	XFSDPEVKKETRPALGSTVLLAPFL HEHEPPSAEVLPGSWRX*
5035	10532	A	5346	142	653	GFWHQRILGASDQAHLPLPHKQDG SADGARRVLACARGQGDLRLRLH LAAVPLQLPGGLRRRAVHVHGGGC QQDGGAESWS/PSPPSRGPRTLHR VEKVPGAPVTPLPVAFCNPDHGIE DPAFP*PAAGPR*LQEGPCGSRAS RAPPTSTRSCCTECLRNLSLILIC
5036	10533	A	5347	261	538	GSRRLLFSPRGPRTPAWKRSTGA PVTSPPIAFSCNPDHGIEDPAFP*PAA GPR*LQEGPCGSRASRAPPTSTRS CCTKCLRNFLILIC
5037	10534	A	5348	7	264	FQKISALPQRSYDTHNTPHDTPARV SYKHAGANHTHIHTPMNTVSTTIYP PHAYLHTHTQKTPPHIYSTHAP*I*L FISTYAHTKN
5038	10535	A	5349	208	713	SVKMMVRYSLDPENPTKSCSKSRGS\N LRVHFKNTRETAQAIGMHNRKAT\N KYLKDVTLQKQCVFRRYNGG\NGR CAQAKHWGWTQGR\WP*RVLNSL VIEHIQVNKAPKMRRRTYRAHGRIN PYMSSPCHIEMILTEKEQIVPKPEEE VAQKKKISQKKLKKQKLMARE
5039	10536	C	5350	286	591	MVRLFNLNPEKRQRKSWQIRGFQS SCFTLGLTVKLAQAIGMHIRKATE VSERWSLYRNSVYHSDGNNGGVG RRAQAKQWGLGHKVGPGKKECLN FLLHML*
5040	10537	A	5351	1	305	GTSIYNVLYEVPLPPGRSLKFSGVY GPIICQRPSTNELPLDFPVKEVFELL GVDNVYQLFTWALLQKYILLYVQR *CNVTKALELSNLLLFHICDIKLV
5041	10538	A	5352	15	234	LSCPDQVHPHSLVPYPEPRRATASV PETSGPPFPHRRPYATTPALGHNP HA*LSSSFAGSRYKLGEMLHI
5042	10539	A	5353	3	257	HEVKYKNPAQ*QWHRLGPDHAVPE EFRYHKQLIQSQLFLHYHLSQTFTL QESADLQNAFLNSGQCILNKPLKFA DLHSDFMKTI
5043	10540	A	5354	3	334	IIKFIWNPKRA*IAEAILSKKNIAGGI TLPDFRLYNKAIVI*TAWYWHKNR HIDQWNRILNPEIKSHTYSQRIFDKI DKNIH*GKDTLFNKWCWERWIAIC RRIKLDLSLV
5044	10541	A	5355	1	119	QKSRW*TPPNSYMKVNVPEKSRNG ETSLRTKIAVCQYYM
5045	10542	A	5356	3	349	HEPANADFAFRFYLIASETPGKNIF

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						FSPPRFPAAAYAMLSLGACSHSRSQL EGLGFNLTESESDARRRCRQ*VGT LDLTGHGLQTRGGQGPWPRARPSR GGDAAAGSARLPPR
5046	10543	A	5357	1	499	
5047	10544	B	5358	66	641	MASKINTKALQSPKRPRSPGSNSKV PEIEVTVEGPNNNNPQTSARPTQ TNGSNVPFKPRGREFSFEAWNAKIT DLKQKVENLNFNEKCGEALGLKQAV KVPFALFESFPEDFYVEGLPEGVPFR RPSTFGIPRLEKILRNKAKIKFIKKP EMFETAKESTSSKSPPRKINSSPNV NTTASGVEDLNIQ*
5048	10545	A	5359	2	306	ARGVCGGCRCLGFCGSVVGDLMY* NSFDCFKKVLRY*GFFGLYWGLIP* LIWFAPEQAIYLTDNVVRDKFT*R DGSDSLSAEVLAGGCALGSLVIVTN SL
5049	10546	A	5360	3	120	HEGKEPDIPLYETVQTVGPSHARTY TVASHSEGR*TIC
5050	10547	A	5361	2	366	SLPASDRPPISSPLATSGTIFSAISCF WDLPAFPLWLAPSCQPTMSSQIRQN YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART
5051	10548	A	5362	1	108	
5052	10549	A	5363	2	536	ARAARDWKNYSTDVEAAVNSLVN LYLQASYTYLSLGFYFDRDDVALE GVSHFFRELAEEKREGYERLLKMQ NQRGGRALFQDIKKPAEDEWGKTP DAMKAAAMALEKKLNQALLDLHAL GSARTDPHLACDFLEPHFIDEEVKLI KKMGDHLNLHRAGWPRRLGLGE YLFERLTLKHD
5053	10550	A	5364	3	331	HEQYPGSSISISLTLGCPDMPVIAR* TAAADESLVPTRLMLQLADYGPVI YSLVI*VCLTAAFTLAQQHSMKIY ADIIGSEDTTNEDYRSIALYFEREMR YLQAAKF
5054	10551	A	5365	3	52	HEQSWKAENEFTLADLKQLPELN PPVLMPRGNVGTPLRVFLELIRACR LPPRIITQLHFQIPKIGYSLRYCNVPF EYEDSDTAVQE*LT
5055	10552	A	5366	3	323	STFFFFFLRQSLALVAQAGLRTQW RNLGSLQAPPPGFTPFSCSLPSSWD YRRPPRLA\NFFFFFFFVFLAETGFH CVLARMVISIS*PRDQPASASQSAGIT GVSD
5056	10553	A	5367	3	337	HERHEDTLTLKERNRGNGILDDID DHNIIYHLPDA*SEEYEFKEQTTL LRASIPFSVGGSNQLIEAIGKMVRGR LYPWSVDVKVENPQHNDFMKLITML ITHMHDLDQDV
5057	10554	A	5368	16	313	SHSVTQAGVQCWHLHAQLIFLYF LVETGFHRVSQDGLYLLTS*SARLG LPKCWDYRRDDHAWPVQFFKCS PRPQAILDFAFTSHELCLGSMRLKLS

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5058	10555	A	5369	1665	1787	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5059	10556	A	5370	1431	1553	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5060	10557	A	5371	1740	1862	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5061	10558	A	5372	1173	1295	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5062	10559	A	5373	1027	1149	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5063	10560	A	5374	2250	2372	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
5064	10561	A	5375	934	1092	FFVFLVETGFHRVSQDGLDLLTS*S ARLSLPKCWDYRREPPCPRIYILTR SR
5065	10562	A	5376	2588	2824	VAGTIGACHHAQLIFVFLVETGFHH VGQDGLDLLTS*STHLGLPKCWDS RREPLRPASPVVFQRTSAPVMADLT PTVS
5066	10563	A	5377	935	1138	RRGFTMFHHVSQGGDLLTS*SARL GLPKCWDYRREPLCPAWKDY*CKL QDEVISQQGLKVSVVLH
5067	10564	B	5378	79	1551	MSEVTKNSLEKILPQLKCHFTWNLF KEDSVSRDLEDRCVNCQIEFLNTEFK ATMYNLLAYIKHLDGNNEAALECL RQAEELIQEHADQAEIRSLVTWGN YAWVYYHLGRLSDAQIYVDKVKQ TCKKFSNPYSIEYSELDCEEGWTQL KCGRNERAKVCFEKALEEKPNNE FSSGLAIAMYHLDNHPEKQFSTDVL KQAIELSPDNQYVKVLLGLKLQKM NKEAEGEQFVEEALEKSPCQTDVLR SAAKFYRRKGDLDKAIELFQRVLES TPNNGYLYHQIGCCYKAKVRQMQ NTGESEASGNKEMIEALKQYAMDY SNKALEKGLNPLNAYSDLAEFLETE CYQTPFNKEVPDAEKQQSHQRYCN LQKYNKSEDVAVQHGLEGLSISK KSTDKEEIKDQPQNVSENLLPQNA NYWYLQGLIHKQNGDLLQAAKCY EKELGRLLRDAPSGIGSIFLSASEL DGSEMGQGA VSSSPRELLSNSEQL N*
5068	10565	A	5379	925	1127	FFVFLVETGFHRVSQDGLDLLTL*S THLGLPKCWDYRREPLRPATFSSYQ RNNPDLILNDTIMPNIK
5069	10566	A	5380	438	815	TRPSFSFNPLTLFFFFLRRSLALSPRL ECGSAISAHCKLRLLGSSHSPTSASR VAGTTSARHAWLMFFVFLVETG FHLVSQDSL DLLTS*SAPLGLPKCW DYRHEPPRPAHLHFLNFFLFSYT
5070	10567	A	5381	7944	10115	KQCNYGHNLTCSNFFFFWRWSLA PSPRLECNGAISAHCKLRPPGFTPFS CLSLPSSWDYRRSPRAANFFVFLV ETGFHQVSQDGLDLLTL*SARLGLP KCWDYRREPPCPESALIF
5071	10568	A	5382	1	211	LKTSEKWRNRQDKSNKGSKKAER

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						RATHADRNREAARIRRKTYTNERK HYEHHRTAGKDQDERATEDSRE* RE
5072	10569	A	5383	2	373	ARECHHLCKINYMDLVKEFMTLNA SAPLRSSFSDTMIRLPALTYPLFPAL ATCAGYSDKA*SSISYVLHNSALWR ASGPTDHRDAPA*A*LESRRSTLRIC ELRTLYSLIKSTASNFDPIKLFS
5073	10570	A	5384	112	913	DFLSMPNRRGGVSLPPTPP*PPFSVT HTIFSVSFSFHWLKGSLRRQFSYCF YGMVLVPFSPHPPLSLSAPSKCLRIP PLPWGWVTAPRLRSHPSVTGRAVL ERKPSVRG*AGSLNTQARDTPPQLP ERPPEG*ALFPPFPYSMAAPPSQLKPT LKITAVRS*ASGGATGLGGWSPGLL P*EQGLRPTATLTQTSGIALNPRSLT PAPQLRLSCPPHFALTTRA VPGGPQ PLAWGPEPGTPPAQPRSPDSAQSH TVYRRESILFFIL
5074	10571	A	5385	2	345	SFWLLCGSSCSDLRSCQVLKCTRNI PYSLVPTASCEHLHGPCIYRPSVQS VLTCTAAQATNILSAQSLLSGPTTQ* WGLTYPCLLVGAADLTPTTPPPPT PAPPHLPSTPPP
5075	10572	B	5386	36	340	MFLDEYARRHPDYSVVLRLAKT YETTLEKCCAAADPHECYAKVFDE FKPLVEEPQNLKQNCLEFEQLGEY KFQNALLVRYTKKNALCRRLSIRGP EPVI*
5076	10573	A	5387	3	182	
5077	10574	C	5388	602	877	METTLRRKCCARLQILHGMAMPKV FRWNFKPLVGRSLRNLNPNKIVEAF WSQLGRSYKFGPMRYLVSFTPKES YPKCSNFPTLCRRVFKET*
5078	10575	A	5389	1	404	GTRNDKMEPGLEQGTIPRLDSVTSS ECFASSGFHEDRSLSDVEEQEDSDG FYKEPITMEDLISYSFQVAIGMESLS SRLCIHRDLEARNFHLSGNYCDTSL EF*IENYDIYL**FNIYSPTKLKPEDT RLKET
5079	10576	A	5390	110	424	LSLLQREREGHLNGSPSFMKCSGF YRLA*GVCV*VSFVL*Y*HILIYSML TVLILCIYFFNMLISGIYTDYAYFYIC YIYYCYIF*FILLCFYTLMTIFFGLI
5080	10577	A	5391	2	361	ARETVKRIQYPIPLEGRLGLKPLIES LI*DGLLELCMSPTYTPILLVK*SDW *Y*LVEDLQAINQTVQTTHPVVPNP YTILSKIPYDHQWFTEIDLKDAFWA CPLAEDS*DIFTFEWARA
5081	10578	A	5392	3	335	QSQSWWRQKGVSRAGAGPIHPQGL LFGFS*GDLGPLGTLGEQGLIGQRG EPGLEGDSGPMGPDGLKGVRGDPG PDGEHGEKGQEGLMGEDGPPGPPG AAGVRGLHGKSGY
5082	10579	A	5393	61	497	
5083	10580	A	5394	16	951	RRPKIRDKFWGVS/KKLAHSEASPI SGASKRAKKQINVYVGKSS/QGK

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						MVVVWVKLDRDTVFALVNYIFFKG KWERPFVVKDTEEDFHVDQATT KVPMMKRLGMFNIQHCKKLSSWV LLMKYLGNAIAIFFLPDEGLQHL NELTHD\IVTKFLE\NEDRRSASLH PKLSITGTYDLK\TVLGQ\LGITKVFS NGAD\LSGVTEEAPLKLSKAVH*GC A*PSTEERGLKLAGGHVF*EGHYPC FIPPRGSSFNKPFVFLNGFEQN/SPSF PLFMGEKWWNPTPKITGLSLLNPS PSLGPLPGMTLKKGLSWK
5084	10581	A	5395	2	306	GFDHVAQAGLEPLGSSDLPPSASQS AGITGMSHHTQPAYILKISFITLPFIIR SLS*VPFVFSIMYKSSFNFSPCGESVF STNLLNNEYLLIDWWLHFIY
5085	10582	A	5396	1	375	
5086	10583	A	5397	162	426	
5087	10584	A	5398	140	426	
5088	10585	A	5399	158	705	PSEKNKNNLLLGVVYVRHLPNLLD ETQIFSFSQFG\PVTRFRLSR\NKRT GN\SKGYAFLEFESEDVCQNSCLKQ WNNYLFGGKTLG/QCHFMPPEKVH K\NSFKDWDFPFKQPSYPSVKRV*S ESDTNTKA/DGMEERFKKKERLLRK KLAKKGIDYDFPSLILQKTESISKTN RQTSTKGQVFT
5089	10586	A	5400	2	388	FLFFFEMESRSVAQAGVQWCDLG SLQPPPPGLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGQAGLELLAPS DPPA
5090	10587	C	5401	197	415	MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF*
5091	10588	A	5402	671	986	KGVLFFFFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5092	10589	A	5403	65	921	
5093	10590	A	5404	213	442	
5094	10591	A	5405	1	1506	
5095	10592	A	5406	1	286	DRLIYIPFPDEKSLVPILKANLGKSP VPKDLDFLDLVPWGCGRLP NRGCAHSLHSPAGHACYSLTLDR GFLQKSKPKAVKLPRFSFG
5096	10593	A	5407	2	158	
5097	10594	A	5408	1	9064	MLARAARGTGALLRGSLLASGRA PRRASSGLPRNTVVLFPQQEAWV VERMGRFHRILEPGLNILIPVLDRI YVQSLKEIVINVPEQSAVTLDNVTL QIDGVLYLRIMDPYKASYGVEDPEY AVTQLAQTMRSELGKLSLDKVFR ERESLNASIVDAINQAADCWGIRCL RYEIKDIHVPPRVKESMQMQVEAE RRKRATVLESEGTRESAINVAEGKK

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						QAQILASEAEKAEQINQAAGEASAV LAKAKAKAEAIRILAAALTQHNGD AAASLTVAEQYVSFAFSKLAKDSNTI LLPSNPGDVTSMVAQAMGVYGALT KAPVPGTPDSLSSGSSRDVQGTDA LDEELDRVKMTWSPVPNFQLLNIPS NWGQPHAPGQTSTEV PADGDGATD GPLCLAHASLCCQVAGAAAAALPG AIAGGAVGWARIPRLRLSLSTGMQ KASVLLFLAWVCFLFYAGIALFTSG FLLTRLELTNHSSCQEPGPGSLPW GSQKGPGACWMASRFSRVVLVLID ALRFDAQPQSHVPREPPVSLPFL GKLSSLQRILEIQPHHARLYRSQVDP PTTTMQRLKALTGTSLPTFIDAGSN FASHAIVEDNLIKQLTSAGRRVVF GDDTWKDLFPGAFSKAFFPSFNVR DLDTVDNGILEHLYPTMDSGEWDV LIAHFLGVDHCGHKHGHHPPEMAK KLSQMDQVIQGLVERLENDTLLVV AGDHGMMTNGDHGGDSELEVSAA LFLYSPTAVFPSTPPEEPEVIPQVSLV PTLALLGLPIFGNIGEVMAELFSG GEDSQPHSSALAQASALHLNAQQV SRFLHTYSAATQDLQAKELHQLQN LFSKASADYQWLLQSPKGAEATLP TVIAELQQFLRGARAMCIESWARFS LVRMAGGTALLAASFCILLASQW AISPGFFCPLLLTPVAWGLVGAIAY AGLLGTELKLDLVLLGAVAAVSSF LPFLWKA WAGWGSKRPLATLFPI GPVLLLLLFR LAVFFSDSFVVAEAR ATPFLLGSFILLVVLHWEQQLP PKLLTMPRLGTSATTNPPRHNGAY ALRLGIGLLLCTRLAGLFHRCPEETP VCHSSPWLSPLASMVGGRAKNLW YGACVAALVALLAAVRLWLRRYG NLKSPEPPMLFVRWGLPLMALGTA AYWALASGADEAPRLRVLVSGAS MVLPRAVAGLAASGLALLWKPVT VLVKAGAGAPRTRTVLTPFSGPPTS QADLDYVVPQIYRHMQEERGRLE RTKSQGPLTVAA YQLGSVYSAAMV TALTLAFLPLLHAERISLVFLLLF LQSFLLLHLLAAGIPVTPGKYLSDD SLKDNSDSQGLRKRQQPPGNEADA RVRPEEEEEPLMEMRLRDAPQHFI AALLQLGLKYLFILGIQILACALAAS ILRRHLMVWKVFAPKFIFEAVGFIV SSVGLLLGIALVMRVDGAVLLSSAS TERHCQQTTRGRKPTLVSVLVLDSE QRKDGRRLRSALVSSYRFLETSPAGA ELFRPASATMSRQTTSVGSSCLDLW REKNDRLVRQAKVAQNSGLTLRRQ QLAQDALEGLRGLLHSLQGLPAAV PVLPLELTVTCNFILRASLAQGFTE DQAQDIQRSLERVLETQEQQGPRLE QGLRELWDSVLRASCLLPELLSALH

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						RLVGLQAALWLSADRLGDLALLLE TLNGSQSGASKDLLLLKTWSPPAE ELDAPLTLQDAQGLKDVLLTAFAY RQGLQELITGNPDKALSSLHEAASG LCPRPVLVQVYTALGSCHRKMGNP QRALLYLVAALKEGSAWGPPLLEA SRLYQQLGDTTAELESLELLVEALN VPCSSKAPQFLIEVELLLPPDLASP LHCQTQSQTKHILASRCLQTGRAGD AAHYLDLLALLLDSSEPRVGPCMP EVFLEAAVALIQAGRAQDALTLCEE LLSRTSSLLPKMSRLWEDARKGTKE LPYCPLWVSATHLLQGQAWVQLG AQKVAISEFSRCELELLFRATPEEKEQ GAAFNCEQGCKSDAALQQLRAAAL ISRGLEWVASGQDTKALQDFLLSV QMCPVSAKRLRPSFESSLPLPLPLPL PPRGSGASVVRPTPRCRPRPARLAP LERTSGPGQVFRPTPPGRRPGALGR QSAVRPTTRRKPLVPGESRPREPEA PAGPEEDIKVQRLGNLPKITIKQWH NWNSDPMGLTIEFLLLTLLSKGDD LSTAILKQKNRPNRLIVDEAINEDNS VVLSQPKMDELQLFRGDTVLLKG KKRREAVCIVLSDDTCSDEKIRMNR VVRNNLRVRLGDVISIQPCPDVKYG KRIHVLPIDDTVEGITGNLFEVYLKP YFLEAYRPIRKGDIFLVRGGMRAVE FKVVETDPSPYCIVAPDTVHCEGEP IKREDEEESLNEVGYYDDIGGCRKQL AQIKEMVELPLRHPALFKAIGVKPP RGILLYGPPGTGKTLIARAVANETG AFFFLINGPEIMSKLAGESNLRKA FEEAEKNAPAIIFIDELDAIAPKREKT HGEVERRIVSLLTLMDGLKQRAH VIVMAATNRPN SIDPALRRFGRFDR EVDIGIPDATGRLEILOHTKNMKLA DDVDLEQVANETHGHV GADLAAL CSEAAALQAIKKMDLIDLEDETIDA EVMNSLAVTMDDFRVRTTPVPQW ALSQSNPSALRETVVEVPQVTWEDI GGLEDVKRELQELVQYPVEHPDKF LKFGMTPSKGVLFYGPFGCGKTLL AKAIANECQANFISIKGPELLTMWF GESEANVREIFDKARQAAPCVLFFD ELDSIAKARGGNIGDGGGAADR VIN QILTEM DGMSTKKNVFIIGATNRPDI IDPAILRPGRLDQLIYIPLPDEKSRVA ILKANLRKSPVAKAGARSWADVVD LGVPGLKMTNGFSGS*P*QEILPACF AKLAI\RESNREVKIKAKNREEGKT NPIKPMGRYE*WIDPVPEIR\RD SLL KEAQSFCA PFLFSNDIRKY\EMFA QTLSQ/ESRGFGSFRFP SGNQGGAGP SQGSGGGTGGSVYTEDNDDDLYG
5098	10595	A	5409	96	299	
5099	10596	A	5410	174	324	
5100	10597	A	5411	74	242	

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5101	10598	A	5412	129	899	AAPGLGRGGGAAAGGGAVCPGTE RPCAMAYAYLFKYIIIIGRTTGVG*N PCPNALQFTD/KRGFQPSAMTLTIGV EFGA\RMITIDGKQIKL\QIWDTAGQ ESFRS\ITRSYYRGAAGALLVYDITR\ *DTFNH\LTW\LEDARQHSNSNMV IMLIG\NKSD\LESRREVKK/EKGEA FA\REHGLIFM\ETSAKTGFQCRKEG ILFNTAKEILLKKFPRKGVFLTFN*W RANGH\IKLGPQPAAYPIATHAGQS GGQQAGGGCC
5102	10599	A	5413	1	408	MQLKRANPGPRRAPVRETVMLLLC WGVPGRPYKVDTESALLYQGPHN TLFGYSVVLHSHGANR\WGAPTAN WLANASVINPGAIYRCRIGKNPGQT CEQLQLGSPNGEPCGKTCLEERDNQ WLGVTLSRQPGENG
5103	10600	C	5414	1	1026	MGLGIYLDQYTRQKGQDPVAELKQ LIPLVVSLSAPNLEMPLLKKKTNP TFLKSLSGGLNLFNPFVETVTEE VKVHPRNNTGGYNPEEEDEETASE NCFPWNVGDLMEVASEVHIRRVQ KKEYVEENKIPRNPTYKGCCEGPLQE NYKPLLNKIKEDTNKWKNIPCSWIG RTDVTKMAILPKHDRVAEQRVVGA LVKQRASQCPRCGRSGPPGTAT ASPSPGRRPFGAVIAPRFP SHALSSW YAGCNAEKSEVNAPFGTQGMRFIS AASYKDWVQVLQQKDVSRNMGTK ARMMP LGSSGGCHTIRTEVTQDSE GQLAAVTTTGYTVVGLEPPKVS*
5104	10601	A	5415	1	681	
5105	10602	A	5416	1	779	MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEEK VPETTTTFWAPGVEAPGDDAERRR REASGPATRHSP\PTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSS\TVQPVAAAATPSY ALIGSSLWPVNERGRQESRTCIIDQ SAWHVGRAEIRKLLPYCSTQGGGLK YSDVTSGMVKDPPDVL\DRQKCLD ALAALRHAKWSSEIRF
5106	10603	A	5417	1	1274	MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGPPLGLLGV RPGMPPQPQGPAPLRPDSSDDRYV MTKHATIPTTEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTL\LSRIAE NLPKQLAFISPEKYDIKCAVSEAAII LNSC\VEPKMQVTITLTSPHIREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLQSCV\IIR ILRDLCQRVP\TWS\DFPSWAMELLV EKAISSAS\SPQSPGDALRRVFECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PD\QQR\EDITSSAQFA\LRLLAF

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						RQIHKVLGMDPLPQMS\QRFN\IHNNH QDR\RRDSGDGVDGFEAEGKKDKKD YDNF
5107	10604	A	5418	144	522	VDLLRAAGRQWQGPLRPRPSGRR* SARRA/LGKTTYCTDPAKFISVLWT YLATMLHVELPHMNLLSTMDLIEH YGKLAFNLDYYTEVLDLS*LLDHL AS/VPFLTAYRQVTEKLVQLIEDYIL RCFIHP
5108	10605	A	5419	1	2437	MAVPGEAEEEEATVYLVVSGIPSVLR SAHLRSYFSQFREERGGGFLCFHYR HRPERAPPQAAPNSALIPTDPAEAG QLLSQTSATDVRPLSTRDSTPIQTRT CCCVISVRGLAQAQRLIRMYSGRR WLDHSGTWLPGRCLIRRLRLPTEAS GLGSFPFKTRKELQSWKAENEAFTL ADLKQLPENPPVLMPRGNVGTPL RVFLELIRACRLPPRIITQLQLQFPKT GSSRRYGNVPFEYEDSETVEQEELV YTAEGEEIPQGTYLADIPASPCGEPE EEVGKEEEEESHSEDDDDRGEEWE RHEALHEDVTGQERTTEQLFEEIE LKWEKGGSGLVFYTDAQFWQEEE GDFDEQTADDWDVDMSVYYDRDG GDKDARDSVQMRLEQRLRDGQED GSVIERQVGTFERHTKGIGRKVMER QGWAEGQGLGCRCSGVPEALDSDG QHPRCKRGLGYHGEKLQPFQGLKR PRRNLGLISTIYDEPLPQDQTESLL RRQPPTSMKFRDMAFAVIGPPGSG KTTYCLGMSEFLRALGRRVAVVNL DPANGLPYECAVDVGELVGLGDV MDALRLGPNGLLYCMEYLEANL DWLRAKLDPLRGHYFLFDCPGQVE LCTHHGALRSIFSQMAQWDLRLTA VHLVD\SHYCTDPAKFISVLCTSLAT MLHVELPHINLLSKMDLIEHYGKLA FNL\DYYTEVLDLSYLL*PPGLLTLS SATTRPASIEEA/MCKLIEDYNLVSF IPLNIQDKESIQRVLQAVDKANGYC FGAQEQRSLEAMMSAAMGADFHS STLGIQEKYLAPSNQSVEQEAMQL
5109	10606	A	5420	2	78	
5110	10607	A	5421	94	253	
5111	10608	A	5422	2	318	
5112	10609	A	5423	460	672	
5113	10610	A	5424	357	795	
5114	10611	A	5425	310	478	
5115	10612	A	5426	1	399	
5116	10613	A	5427	2	390	
5117	10614	A	5428	3	392	GGKIIVGDATEKDASKKSDSNPLTE ILKCPTKVLLRNMVGAGEVDEDL EVETKEEKEKYGVGKCV\FEIPG APDDEAVRIFLEFERVESAIKAVVD LNGRYFGGRVVKACFYNLDFRVL DLAEQV
5118	10615	A	5429	837	1005	

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5119	10616	A	5430	174	247	
5120	10617	A	5431	1	360	
5121	10618	A	5432	1	382	
5122	10619	A	5433	338	442	
5123	10620	A	5434	1	140	
5124	10621	A	5435	3	339	PINFESVGPTYRGSSCLAVVPEFLG MSVAFVPDWLRGKAENVQETIQR/L LE*NDQLIRCI/LEYQNKARGNECVQ YQHVLRNLI/YLATIADAQSQPALS KAMGIIFQKQ
5125	10622	A	5437	157	371	
5126	10623	A	5438	150	284	
5127	10624	A	5439	84	901	ARKSVRMASRMTRRDPLTNKVAL VTASTDGIGFAIARRLAQDRAHVVV SSRKQQNVDQAVATLQGEGLSVT GTVCHVGKAEDRGAAWWPPAVKL HGGIDILVSNAAVNPFFGSIMDVTE EV\WDKTLD\NVKGPKP*MTKAVV PEMEKRGGGSVVIVSSIAAFSPSPG FSPYNVSKTALLGLAQTLPIELAPR NIRVNCLAPG\LIKTSFSRMLWMD KEKEESMKETLR\IRRLGEPEDCAGI VSFLCEDASYITGETVVVGGGTPS RL
5128	10625	A	5440	2	468	
5129	10626	A	5441	63	219	
5130	10627	A	5442	3	558	
5131	10628	A	5443	7	909	DQCEVCRNSEVRPAACPGHSGSPA QGPPRPFRMKAAVLTAVLFLTGSQ ARHFWQQDEPPQSPWDRVKDLAT VYVDVLKDSGRDYVSQFEGSALGK QLNLKLLDNWDSVTSTFSKLREQ GPVTQEFWDNLEKETEGLRQEMSK DLEEVKAKVQPYLDDFQKKWQEE MELYRQKVEPLRAELQEGARQKLH ELQEKLSPGGEEMRDRARA/HVDAL RTHLAPYSGELRQRLGAR/LGALRE NGGARMGQYHA/QATEHLSTLSEK AKPALEDLRQGLLPVLESFKVSFLS ALEEYTKKLNTQ
5132	10629	A	5444	3	195	
5133	10630	A	5445	189	263	PPGSHLGHPANAPSH*GPYPGLHS
5134	10631	A	5446	1905	2052	
5135	10632	A	5447	1903	2050	
5136	10633	A	5448	1	115	
5137	10634	A	5449	1	402	GKTSKLEFSIYLAPHSTTAAIEPYNSI LTHTTLEHYDWAFMAYNGAIYDI CRRNLDIGRTTYTNLNTLIGQIESSIT ASLRFDGALNGDLT*FQTNLVPYPR IHFPLATYAPVISAEEKAYHEQLSVA EITNAC
5138	10635	B	5450	81	319	XVVEPYNSILTHTTLEHSDCAFMV DNEAIYDICRRNLDIERPTYTNLNR IGQIVSSITASLRFDGALNVDLTFEQ TNL*
5139	10636	A	5451	1	422	GKSKLEFSIYPAPQVSTAVVEPYN SILTHTTLEHSDCAFMVDNEAIYDI

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						CRRNLDIERATYTNLNRIGQIVSSIT ASLRFDGALNVDLTEFQTNLVPYPR MHLPLGTYAPVICA EK/A YHETA FV QKTTCLG*PSQQMW
5140	10637	A	5452	771	1640	ALQLHPHHPHPWSTLIVPFMVDN EAIYDICRRNLDIERPTYTNLNRVIR A/QMGPSITASLRFDGALNVDLTEF QTNPGAPTPIHLP/LWPTYAPVHLL AGGKPYHGTAFL*AGGFTNGLVLE ARPTQMGGNVDPWHGVNYMGLL AWLYRGDVGFPKIDNGWPLPTIKN QAQHSSFVDW/CGPTGLSRFGHSTY QPSTVVPGLT WAKV\QRAV\CML\ SNTTAIAEA*ARLDHKFDLMYAKR AFVHWYVVGEGMKEGEFSEAREDM AALEKDYEEVGVDSVEGEGEEGE EY
5141	10638	A	5453	89	435	
5142	10639	A	5454	2	287	TNEIEPEEN*HTKARNFRRFVTAINN TPRNIREG/GDHL LHHWIAL LADCPI TAHMYEDVALIKDHTLDNSLIRELQ TLQEFNITLETALVKGIDI
5143	10640	B	5455	218	3940	MSGGGGGGSAPS RFADYFVICGL DTETGLEPDELSALCQYIQASKARD GASPFISSTTEGENFEQTPLRRTFKS KVLARYPENVEWNPFDQDAVGML CMPKGLAFKTQADPREPQFHAFIT REDGSRTFGFALTFYEEVTSKQICSA MQTLYHMHNAEYDVLHAPPADDR DQSSMEDGEDTPVTKLQRFNSYDIS RDTLYVSKCICLITPMSFMKACRSV LQQLHQA VTSPPQPPPLPLESYIYNVL YEVPLPPPGRSLKFSGVYGPICQRP STNELPLFDFPVKEVFELLGVENVF QLFTCALLEFQILLYSQHYQRLMTV AETITALMFPFQWQHVVYPILPASL LHFLDAPVPYLMGLHSNGLDDRSK LELPQEANLCFVDIDNHFIELPEDLP QFPNKLEFVQEVSEILMAFGIPPEGN LHCSESASKLRRLRASELVSDKRNG NIAGSPLHSYELLKENETIARLQALV KRTGVSLEKLEVREDPSSNKDLKV QCDEEELRIYQLNIQIREVFANRFTQ MFADYEVFVIQPSQDKESWFTNRE QMQNFDKASFLSDQPEPYLPFLSRF LETQMFASFIDNKIMCHDDDDKDP VLRVFDSDRVDKIRLLNVRTPTLRTS MYQKCTTVDEAEKAIELRLAKIDHT AIHPHLLDMKIGQGKYEPGFFPKLQ SDVLSTGPASNKWTKR NAPAQWRR KDRQKQHT EHLRLDNDQREKYIQE ARTMGSTIRQPKLSNLSPSVIAQTN WK FVEGLLKECRNKTKRMLVEKM GREAVELGHGEVNITGVEENTLIAS LCDLLERIWSHGLQVKQGSALWS HLLHYQDNRQRKLTSGSLSTSGILL DSERRKSDASSLMPPLRISLIQDMR HIQNIGEIKTDVGKARAWVRLSME

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						KKLLSRHLKQLLSDHELTKKLYKR YAFRLCDDEKEQFLYHLLSFNAVD YFCFTNVFTTILIPYHILIVPSKKLGG SMFTANPWICISGELGETQIMQIPRN VLEMTFECQNLGKLTTVQIGHDNS GLYAKWLVEYVMVRNEITGHTYKF PCGRWLKGMDGSLERILVGELL TSQPEVDERPCRTPLQQSPSVIRRL VTISPNKPKLNTGQIQESIGEA VNG IVKHFHKPEKERGSLTLLCGECGL VSALEQAFQHGFKSPRLFKNVFIWD FLEKAQTYETLEKNEVVPEENWH TRARNFCRFVTAINTPRNIGQGWO VSDAGVLGEPEITSYTTGICPAG*
5144	10641	A	5456	238	406	
5145	10642	A	5457	2	204	
5146	10643	A	5458	1	431	
5147	10644	A	5459	1	225	
5148	10645	A	5460	3	321	
5149	10646	A	5461	1	1257	MSHRKFSAPRHGSLGFLPRKRSSRH RGKVKSF PKDDPSKPVHLTAFLGY KAGMTHIVREVDRPGSKVNKKEVV EAVTIVETPPMVVVGIVGYVETPRG LRTFKTVFAEHISDECKRRFYKNWH KSKKKAFTKYCKKWQDEDGKKQL EKDFSSMKKYCQVIRVIAHTQMRL LPLRQKKAHLMGDQVERGALWPE KADWARERLEQQVPVNQVF/GQD EMIDVIGVTQGGKAYKGVTSRWH TQESCPKDPTEGLRKIVACIRAWH PARVAFSVARA/GQ/KGYHHRTEIN K\KIYKIGQGYLIKGGKLIKNNAST DYDL/SLDKSINPSGWAFVHLW*K* PNDFVML/KG/CVVGTKKRVLT LR KSFAGCRRKRRGFGEELTLSSIDTTS KF\GHGRFQTMEKKAFMGVPLKKD RIAKEEGA
5150	10647	A	5462	114	456	
5151	10648	A	5463	3	76	
5152	10649	A	5464	2	951	CWNSGEVRWPLPPPPPRFVARRKM ADLEEQLSDEEKVRIF/LKFFIHAPPG EINEGFNDVRLLLNNDNLLREGAA HAFAQYNLDQFTPLKIEGYEDQVLI TEHGRLGEMGKFLDPKNRICFKF* SL*GRRATDPKDPCAEVNAVESWR TSVETALRAYVKEHYPEWESGTVY GQKNRWDSQTHIACIESHQFQAKNF WNGRWSEWKFTITPSTTQVVGIL KIQVHYEDGNVQLVSHKDIQDSL TVSNEVQTAKEFIKIVEAAENEYQT AISENYQTMSDTTFKALRRQLPVTR TKIDWNKILSYKIGKEMQNA
5153	10650	A	5465	3	553	
5154	10651	B	5466	26	384	MHHEALSEALPGDNVGFNVKNVSV KDVRRGNAVAGDSKNDPPMEAAGF TAQVILNHPGQISAGYALYWIAIVD MVPKGPMCVESFSDYPPLGRFAVR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DMRQTVAVGVKAVDKKAAGLAS*
5155	10652	A	5467	1	1254	
5156	10653	A	5468	1	1386	
5157	10654	A	5469	33	1653	KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKFEK EAAEMGKGSFKYA WVLDKLAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD\CAVLIVAA GVGEFEAG\SKNGQTREHALLAYT LGVKQ\LIV\GVNKM DSTPEPPYSQK RYEEIVKEVSTYIKKIGYY\PDTLAF EPISGWNGDDMLEPSANMPWFKG WKVTRKDG\NASIGTTLLEALDCVL PPTRP\DKPLR\LPLQDVYKIGGIG\ TVPVGRVETGVLPKPG\MGVTFAPS QRLQREVKICPKMHHEAFE*SSFLG DNVGFNVKNVSCQGCSVRGNV*H GDSK\NDPPMEA/SLGFTAQVI\LNH PGPNKAPG*CPWYWDCHTAH\IAC KVCLSLKEKI*F/DRSW*KSLEDGP*I LGSLGDAGHWLIWVPGQAPCVFEK LLKTIPPLGRFA\VRDNEDRQLCGW VSIKSSWTKKAAGSWAKVTK\SAQ KSSERLKWNIPNTCHPTLYQVWEE RSQELFGSIGHLSLSSKRLVNDNNA S
5158	10655	A	5470	2	4966	
5159	10656	A	5471	2	4821	RWPRRARLLRRGRGGGGVESLPHF GAPVPRARLQLTARRGHAGLRARM REAAAALVPPPAFAVTPAAAMEEPP PPPPPPPPPEPETESEPECCLAARQE GTLGDSACKSPESDLED FSDETNTE NLYGTSPSTPRQMKRMSTKHQRN NVGRPASRSNLKEKMNAPNQPPHK DTGKTVENVEEYSYKQEKKIRAAL RTTERDHKKNVQCSFMLDSVGGSL PKKSIPDVDLNKPYSLGCSNAKLP VSVPMPIARPARQTSRTDCPADRLK FFETLRLLLKLTSVSKKKDREQRGQ ENTSGFWLNRSNELIWLELQAWHA GRTINDQDFFLYTARQAIPDIINEILT FKVDYGSFAFVRDRAGFNGTSVEG QCKATPGTKIVGYSTHHEHLQRQR VSFEQVKRIMELLEYIEALYPSLQAL QKDYEKYAAKDFQDRVQALCLWL NITKDLNQLRIMGTVLGKLNLSDI GWPVFEIPSPRPSKGNEPEYEGDDT EGELKELESSTDESEEEQISDPRVPEI RQPIDNSFDIQRDCISKLERLESE DDSLGWGAPDWSTEAGFSRHCLTSI YRPFVDKALKQMGLRKLILRLHLK MDGSLQARIALVKNDRPVEFSEFP DPMWGS DYVQLSRTPPSSEKCSA VSWEELKAMDLPSEFPAFLVLCRVL LNVIHECLKLRLEQRPAGEPSLLSIK QLVRECKEVLKGGLLMKQYYQFM LQEVLEDLEKPCDNIDAFEDDLHKM LMVYFDYMRSWIQMLQQLPQASHS

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LKNLLEEEWNFTKEITHYIRGGEAQ AGKLFCDIAGMLVLKSTGSFLEFGLQ ESCAEFWTSADDSSASDEIIRSVIEIS RALKELFHEARERASKALGFAKML RKDLEIAAEFRLSAPVRDLLDVLS KQYVKVQIPGLENLQMFVPTLAE EKSIIQLLNAAAGKDCSKDSDDVL IDAYLLLTKHGDRARDESDSWGTV EAQPVKVVPQVETVDTLRSMQVDN LLLVVMQSAHLTIQRKAFQQSIEGL MTLCQEQTSSQPVIKALQQLKND ALELCNRISNAIDRVDMFTSEFDA EVDESESVTLQYYREAMIQGYNF GFEYHKEVVRLMSGEFRQKIGDKYI SFARKWMNYVLTKCESGRGTRPR WATQGFDFLQAIEPAFISALPEDDFL SLQALMNECIGHVIGKPHSPVTGLY LAIHRNSPRPMKVPRCHSDPPNPHLI IPTPEGFRGSSVPENDRLASIAAELQ FRSLSRHSSPTEERDEPAYPRGDSSG STRRSWELRTLISQSKDTASKLGPIE AIQKSVRLFEEKRYREMRRKNIIGQ VCDTPKSYDNVMHVGLRKVTFKW QRGNKIGEGQYGVYTCISVDTGEL MAMKEIRFQPNHKTIKETADELKI FEGIKHPNLVRYFGVELHREEMYIF MEYCDEGTLEEVSRGLQEHVIRLY SKQITIAINVLEHGIVHRDIKANIF LTSSGLIKLGDFGCSVKLNNAQTM PGEVNSTLGTAAAYMAPEVITRAKG EGHGRAADIWSLGCVVIEMVTGKR PWHEYEHNFQIMYKVGGMGHKPPIP ERLSPEGKDFLSHCLESDPKMRWT ASQLLDHSFVKVCTDEE
5160	10657	A	5472	3	425	
5161	10658	A	5473	1	234	
5162	10659	A	5474	3	260	
5163	10660	A	5475	3255	3467	LNKNLGLIFFFFFFFFFETASRSVTR LEYSGSILAHCELRLPGSRHSPVVS TWEAEAGELPEPRRQRLR
5164	10661	A	5476	1	4497	
5165	10662	A	5477	2	891	
5166	10663	A	5478	1	9786	
5167	10664	A	5479	27	13959	VPFSVAAAEEPAQPARAARPRPGRS PGAAPPQLAMDPPRPALLALLALPA LLLLLLAGARAEEMELENVSLVCPK DATRFKHLRKYTYNYEAESSGVP GTADRSATRINCKVELEVPQLCSFI LKTSQCILKEVYGFNPEGKALLKKT KNSEEFAAAMSRVELKLAIEGKQV FLYPEKDEPTYILNIKRGIIISALLVPP ETEEAKQVFLDVTYGNCSHTFTV KTRKGNVATEISTERDLGQCDRFKP IRTGISPLALIKGMTRPLSTLISSQS CQYTLDAKRKHVAEAIKCEQHLFL PFSYKNKYGMVAQVTQTLKLEDTP KINSRFFGEGTKKMGLAFESTKSTS PPKQAEAVLKTQVELKKLTISEQNI

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QRANLFNKLVTLELRGLSDEAVTSL PQLIEVSSPITLQALVQCGQPQCSTH ILQWLKRVHANPLLIDVVTYLVALI PEPSAQQLRIFNMARDQRSRATLY ALSHAVNNYHKTNPTGTQELLDIA NYLMEQIQDDCTGDEDYTYLILRVI GNMGQTMEQLTPELKSSILKCVQST KPSLMIQAAIQALRKMEPKDKDQ EVLQTFLLDDASPGDKRLAAYLML MRSPSQADINKIVQILPWEQNEQVK NFVASHIANILNSEELDIQDLKKLVK EVLKESQLPTVMDFRKFSRNYQLY KVSIPSLDPASAKIEGNLIFDPNNY LPKESMLKTTTLTAFGFASADLIEIGL EGKGFEPTEALFGKQGFPPDSVKN ALYWVNGQVPDGVSKVLVDHFGY TKDDKHEQDMVNGIMLSVEKLIKD LKSKEVPEARAYLRILGEELGFASL HDLQLLGKLLLMGARTLQGIQMI GEVIRKGSKNDFFLHYIFMENAFEL PTGAGLQLQISSSGVIAPGAKAGVK LEVANMQAELVAKPSVSEFVTNM GIIIPDFARSGVQMNTNFFHESGLEA HVALKPGKLFKIIPSPKRPVKLLSGG NTLHLVSTTKTEVIPPLIENRQSWSV CKQVFPGLNYCTSGAYSNASSTD SYPLTGDTRLELELRPTGEIEQYSV SATYELQREDRALVDTLKFVTQAE GAKQTEATMTFKYNRQSMTLSEV QIPDFDVDLGTILRVNDESTEGKTS YRLTLDIQNKKITEVALMGHLSCDT KEERKIKGVISIPRLQAEARSEILAH WSPAKLLLQMDSSATAYGSTVSKR VAWHYDEEKIEFEWNTGTNVDTKK MTSNFPVDLSDYPKSLHMYANRLL DHRVPQTDMTFRHVGSKLIVAMSS WLQKASGSLPYTQTLQDHLNSLKE FNLQNMGLPDFHIPENFLKSDGRV KYTLNKNLSLKIEIPLPFGGKSSRDLK MLETVRTPALHFKSVGFHLPSPREFQ VPTFTIPKLYQLQVPLLGVLDLSTN VYSNLYNWSASYSGGNTSTDHFSL RARYHMKADSVVDLLSYNVQGS ETTYDHKNFTLSCDGLRHKFLDS NIKFSHVEKLGNNPVSKGLLIFDASS SWGPMQMSASVHLDSSKKKQHLFVKE VKIDGQFRVSSFYAKGTYGLSCQRD PNTGRLNGESNLRFNSSYLQGTNQI TGRYEDGTLSTSTSDLQSGIHKNTA SLKYENYELTLKSDTNGKYKNFAT SNKMDMTFSKQNALRSEYQADYE SLRFFSLLSGSLNSHGLELNADILGT DKINSGAHKATLRIGQDGISTSATT NLKCSLLVLENELNAELGLSGASM KLTTNGRFREHNAKFSLDGKAALT ELSLGSAYQAMILGVDSKNIFNFKV SQEGLKLSNDMMGSYAEMKFDHT NSLNIAGLSLDFSSKLDNIYSSDKFY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KQTVNLQLQPYSLVTTLNSDLKYN ALDLTNNGLRLEPLKLHVAGNLK GAYQNNKHIYAISSAALSASYKA DTVAKVQGVESHRLNTDIAGLAS AIDMSTNYNSDSLHFSNVFRSVMAP FTMTIDAHTNGNGKLALWGEHTGQ LYSKFLLKAEPLAFTFSHDYKGSTS HHLVSRKSISAALHKKVSALLTPAE QTGTWKLKTQFNNNEYSQDLDAY NTKDKIGVELTGRTLADLTLLDSPI KVPLLLSEPINIIDALEMRDAVEKPQ EFTIVAFVKYDKNQDVHSINLPFFET LQEYFERNRQTIIVLENVQRNLKH INIDQFVRKYRAALGKLPQQANDY LNSFNWERQVSHAKEKLTALTKKY RITENDIQIALDDAKINFNEKLSQLQ TYMIQFDQYIKDSYDLHDLKIAIANI IDEIIEKLKSLDEHYHIRVNLVKTIH DLHLFIENIDFNKSGSSTASWQNV TKYQIRIQIQEKLQQLKRHIQNIDIQ HLAGKLKQHIEAIDVRVLLDQLGTT ISFERINDVLEHVKHVFVINLIGDFEV AEKINAFRAKVHELIERVEVDQIQ VLMDKLVELAHQYKLLKETIQKLSN VLQQVKIKDYFEKLVGFIDDAVKK LNELSFKTFIEDVNKFLDMLIKKLS FDYHQFVDETNDKIREVTQRLNGEI QALELPQKAEALKLFLEETKATVA VYLESQDTKITLIINWLQEALSSAS LAHMKAKFRETLEDTRDRMYQMDI QQELQRYLSLVGQVYSTLVTYISD WWTLAAKNLTDFAEQYSIQDWAK RMKALVEQGFTVPEIKTILGTMPAF EVSLQALQKATFQTPDFIVPLTDLRI PSVQINFKDLKNIKIPSRFSTPEFTIL NTFHIPSFTIDFVEMKVKIIRTIDQML NSELQWPVPDIYLRDLKVEDIPLARI TLPDFRLPEIAIPEFIPTLNLNDFQVP DLHIPEFQLPHISHTIEVPTFGKLYSI LKIQSPLFTLDANADIGNGTTSANE AGIAASITAKGESKLEVLNFDQAN AQLSNPKINPLALKESVKFSSKYLR TEHGSEMLFFGNAIEGKSNTVASLH TEKNTLELSNGVIVKINNQLTLDN TKYFHKLNIPKLDSSQADLRNEIKT LLKAGHIAWTSSGKGSWKWACPRF SDEGTHESQISFTIEGPLTSFGLSNKI NSKHLRVNQNLVYESGSLNFSKLEI QSQVDSQHVGHSVLTAKGMALFGE GKAEFTGRHDAHLNGKVIGTLKNS LFFSAQPFEITASTNNEGKLVRFPL RLTGKIDFLNNYALFLSPSAQQASW QVSARFNQYKYNQNFSAAGNNENIM EAHVGINGEANLDFLNIPLTIPEMRL PYTIITTPPLKDFSLWEKTGLKEFLK TTKQSFDSLVAQYKKNKHRHSIT NPLAVLCEFISQSIKSFDRHFEKNRN NALDFVTKSYNETKIKFDKYKAES

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HDELPRTFQIPGYTVPVVNVEVSPF TIEMSAFGYVFPKAVSMPSFSILGSD VRVPSYTLILPSLELPVLHVPRNLKL SLPDFKELCTISHIFIPAMGNITYDFS FKSSVITLNTNAELFNQSDIVAHLLS SSSSVIDALQYKLEGTTTLTRKRGL KLATALSLSNKFVEGSHNSTVSLTT KNMEVSVATTTKAQIPILRMNFKQE LNGNTKSKPTVSSSMEFKYDFNSSM LYSTAKGAVDHKLSLESLSYFSIES STKGDVKGSVLSREYSGTIASEANT YLNSKSTRSSVKLQGTSKIDDIWNL EVKENFAGEATLQRIYSLWEHSTKN HLQLEGLFFTNGEHTSKATLELSPW QMSALVQVHASQPSSFHDFPDLGQ EVALNANTKNQKIRWKNEVRIHSG SFQSQVELSNDQEKALHDIAGSLEG HLRFLKNILPVYDKSLWDFLKL DV TTSIGRRQHRLRVSTAFVYTKNPNGY SFSIPVKVLADKFIIPGLKLN DLNSV LVMPTFHVPFTDLQVPCKLDFREI QIYKKLRTSSFALNPLTLPEVKFPEV DVLTKYSQPEDSLIPFEITVPESQLT VSQFTLPKSVSDGIAALDLNAVANK IADFELPTIIVPEQTIEIPSIKFSVPAGI AIPSFQALTARFEVDSPVYNATWSA SLKNKADYVETVLDSTCSSTVQFLE YELNVLGTHKIEDGTLASKTKGTFA HRDFSAEYEEDGKYEGLQEWEGKA HLNIKSPAFTDLHLRYQKDKKGIST SAASPAVGTVGMDMDEDDDFSKW NFYYSPQSSPKKL TIFKTEL RVRES DEETQIKVNWEEEAASGLLTSLKDN VPKATGVLYDYVNKYHWEHTGLT LREVSSKLRRNLQDHAEWVYQGAI REIDDIDERFQKGASGTTGT YQEWK DKAQNLYQELLTQEQASFQGLKD NVFDGLVRVTQEFHMKVKHLIDSLI DFLNFPRFQFPKPGIYTREELCTMF IREVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISMREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFGPSGVGWTVK YYEGEEKIVSLIKNLLVALKDFHSE YIVSASNFTSQLSSQVEQFLHRNIQ EYLSILTDPDGKGKEKIAELSATAQ EIKSQANATKKIISDYHQQFRYKLO DFSDQLSDYYEKFIAESKRLNDLSI QN\YHTFLDYTSREFNWKKLAIQPQ SLNPYMKLAPGELYHPLIFLKEIFN LFFFSNLNFSHRHRKNCKLPILIKPY SEPALQ
5168	10665	A	5480	2	316	
5169	10666	A	5481	2	401	
5170	10667	A	5482	126	415	

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5171	10668	A	5483	3	499	
5172	10669	A	5484	1	241	
5173	10670	A	5485	12	308	
5174	10671	B	5486	394	565	MSAEERLRSSGVLSQKVIAHSLGFD KHGNRLGRGKGYDAYLKRCLQH QEVKPYTLALAFKEQICLQVPVNEN DMK*
5175	10672	B	5487	674	807	MSAEERLRSSGVLSQKVIAHSEYQK SKRISIFLSMQDEIETEEIHKDIFQRGK ICFLPSVRVPEQSHGYGLGFDKHGN RLGRGKGYDAYLKRCLQHQEVK PYTLALAFKEQICLQVPVNENDIK*
5176	10673	A	5488	113	339	
5177	10674	A	5490	2	388	FLFFFEMESRSVAQAGVQWCDLG SLQPPPPGLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVQGAGLELLAPS DPPA
5178	10675	C	5491	197	415	MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF*
5179	10676	A	5492	768	1081	KGVLFFFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5180	10677	A	5494	305	477	
5181	10678	A	5495	1	903	
5182	10679	A	5496	111	295	KPATSVPVIVCVCSSAKPELPLCPAT YTEHHAGQPHWWYHAAR/DLVSW K*QISQRGEINPH
5183	10680	A	5497	1	505	
5184	10681	A	5498	3	345	
5185	10682	A	5499	1	1416	
5186	10683	A	5500	618	707	
5187	10684	C	5501	1729	2511	MDIASTNTSNKSDTNMEQVPATND TIKRLESKLLKNQAKQQSESGRLSL GASRGSSVESLPPTSEGKRMSADMS EIEARIAATTGNGQPRRSIQDLTVT GTEPGQVSSRSSSPSRMITTSGPTS EKPTRSHPWTPDDSTDINGSDNSIP MAYLTLDHQLQPLAPCPNSKESMA VFEQHCKMAQEYMKVQTEIALLLQ RKQELVAELDQDEKDQQNTSRLVQ EHKKLLDENKSLSTYYQQCKKQLE VIRSQQQKRQGT*
5188	10685	A	5502	1	3489	
5189	10686	A	5503	1	246	
5190	10687	A	5504	40	124	NVPQFTAKAPCKHEKCLNTNSPDLF EAC*DNIDQTAVSLTAPKTGKRK*R NKVQLS**PQFTAKAPCKHEKCLNT NSPDLFEAC
5191	10688	A	5505	156	1001	GIQQFGQYCLNMLQINQLLSKIKLA NPKEKTAMYLVELARFNRVQPQY KLLD*RGPAHSMFVSQSLGEQT WESEGSSIKKAQQA VGNKALTESTL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PKPI*KPPKSNVNNNPGCITPTVELN GLAMKRGRACHPQAIRSKAIPK**S *LQLSSHV*SEVS\FPIPKIFYVQLTV GNNEFFGEGKTRQAARHNAAMKA LQALQNEPI/LRKISSGMVNQERIW MMTK/HANKSEISLVFEIALKRNM VSFEVIKESGPPHMKSFVTRVSVGE FSAEGEGNSKK
5192	10689	A	5506	175	411	
5193	10690	A	5507	198	381	
5194	10691	A	5508	137	346	
5195	10692	A	5510	3	136	
5196	10693	A	5511	2	673	
5197	10694	A	5512	1	257	
5198	10695	A	5513	1	712	PRKT/PPAPH\DGDRKELPRTKLLPP API\STD*SQHADRGTEP/GPIRPSIEP GPPVQFGTSDKDSDLRLVVGDSLIA EKELPASVTEAIPVSRDWQLLGSGA ASAEPQSKNLD SGHCVPEHSSSGQR LYPEVFYGSAGPSSSQISGGAMDFH LAFSGGQGRHLEKGPPDGQRSLGPE GTRSLGCPHPAEGVPLAPYPRGLYI DYKY/MKGERGGRRGGVLGLGPHFP SSPFPWSPVPGAVC
5199	10696	A	5514	2	322	
5200	10697	A	5515	1	6470	MSDRSGPTAKGKDGGKYSSLNLF TYKGKSLEIQKPA\VAPRHGLOSLG KVAIARR/MRPPANLPSLKAENKGN DPNVSLVPKDG TGWASKQE QSDPK SSDASTAQPPESQPLPASQTPASNQP KRPPAAPENTPLVPSGVKSWAQAS VTHGAHGDGGRASSLLSRFSREEFP TLQAAGDQDKAAKERESAEQSSGP GPSLRPQNSTTW RDGGGRGPDELE GPDSKLHHGHDP RGG LQPSGPPQFP PYRGMMPFMYPPYLPFP PPYGPQG PYRYPTPDGPSRFRVAGPRGSGPP MRLVEPVGRPSILKEDNLKEFDQLD QENDDGWAGAHEEVDYTEKLKFS DEEDGRDSDEEGAEGHRDSQSASG EERPEADGKKGN SPNSEPTPKTA WAETSRPPETEPGPPAPKPLPPGDY PDRGGPPCKPPAPEDEDEAWRQRR KQSSSEISLAVERARRRREEEERM QEERRAACAEKLKRLDEKFGAPDK RLKAEPAPPAAPSTPAPPPAVPKE LPAPPAPPASAPTPEPEEPAQAP PAQSTPTPGVAAAPTLVSGGGSTSS TSSGSFEASPVEPQLPSKEGPEPPEE VPPPTTPPVKVEPKGDGIGPTRQPP SQGLGYPKYQKSLP PRFQRQQEQ LLKQQQHQWQQHQQGSAPTPVP PSPPQPVTLGAVPAPQAPPPPKALY PGALGRPPMPPMNFDP RWM MIPP YVDPRLQGRPPLEFYPPGVHPSGL VPRERSDSLGLSSEPFDRHAPAMLR ERGTPVDPKLA WVGDVFTATPAE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PRPLTSPRLRQAADDDKGMRSCTPP VPPPPPYLASYPGFENGAPGPPISR FPLEEPGPRPLPWPPGSDEVAKIQT PPKKEPPKEETAQLTGPEAGRKLPA SRSGAGPPPPRRRESRTETRWGPRPG SSRGIPPEEPGAPPRAGPIKKPPPP TKVEELPPKPLEQGDTPKPPKPDPL KITKGKLGPKETPPNGNLSPAPRL RRDYSYERVGPTSCRGRGRGEYFA RGRGFRGTYGGRGRGG/RSEFRSYR EFRGDDGRGGGTGGPNHPPAPRGR HASETRSEGSEYEEIPKRCRQSGSET GSETHESDLAPSDKEATPKEGTLT Q/VPLAPPPPGAPP/SPAPARFTC/RG GRRVFTPR/GVPSRRGRGGGR/PPPQ VCPGWSPPAKSLAPKKPPTGPLPPS KEPLKEKLIPGPLSPVARGGSNGGS NVGMEDGERPRRRRHGRAQQQDK PPRFRRLKQERENAARGSEGKPSLT LPASAPGPEEALTTVTVAPAPPRAA AKSPDLNQNDSQANEWETASESS DFTSERRGDKEAPPPVLLTPKAVGT PGGGGGGA VPGISAMSRGDL SQRA KDLSKRSFSSQRP GMERQNR RP GP GKAGSSGSSSGGGGGGPGGRTGPG RGDKRSWSPKNSRSPPEERPPGLP LPPPPSSSAVFRLDQVIHSNPA GIQ QALAQ LSSRQGSVTAPGGHPRHKP GPPQAPQGSPRPTRYEPQRVNSG LSSDPHFEEPGPMVRGVGGTPRDSA GVSFPFPKRREPRPKPELLQEESLP PPHSSGFLGSKPEGPGPQAESRD TG TEALTPHIWNRLHTATSRKSYRPTS MEPWMEPLSPFEDVAGTEMSQSDS GVDLSGDSQVSSGPCSQRSSPDGGL KGAAEGPPKRP GGSSPLNAVPCGP PGSEPPRRPPAPHDGDRKELPREQP LPPGPIGTERSQRTDRGTEPGPIRPS HRP GPPVQFGTSDKSDRLVVGDS LKAEKELTASVTEAIPVSRDWELLP SAAASAEPQSKNLD SGHCVPPESSS GQRLYPEVFYGSAGPSSSQISGGA MDSQLHPNSGG/FRPGTPSLHPYRS QPLYLPPGPAPPSALLSGVALKGQF LDFSTMQATELGKLPAGGVLYPPPS FLYSPAFCPSPLPDTSLQLVRQDLPS PSDFYSTPLQPGGQSGFLPSGAPAQ QMLLPMVDSQLPVV\NFGSLPPAPP PAPPPLSLLPVGPALQPPSFVVRPQS SPSTGVLP*LARPPVYFGRTELHP VNIKPF RDF\QKLSSNLGGPGSSRTP PTGRRPSSLRFSGLNSRLQSQRLS NLTSGVF\RNQAASTFYQAGLPHPD ALRWIPKPWERTG\RP\RDGPSRR\A AEEP\GSRGDKEP\GLPPPR
5201	10698	A	5516	2	119	
5202	10699	A	5517	1	325	FFFFF*DRVSLLLPKLECNGTISAHC NLRLPGSSD SPASASSSFTIHVAPLP

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QLRHY*IFYDGTRSLYAG*YSQNLLI YSAPRQPQYHFKDMNKILDSIQRSY TKI
5203	10700	A	5518	228	481	QFFRNTIFF*DRVSLLLPKLECNSAIS AHHNLCPLPGSSDSPASASRVAGITG TCHHTRLLAFVFLVETGFYHVSQSG LELLTSGD
5204	10701	A	5519	175	431	LIVKMPFLK*SWKIF*MSK**VMLIH *GFVFLFVCFF*DRVSLLLPRLECN GPISAHRLHLPDSSDSPASAYIKGF VRQLSHEE
5205	10702	A	5520	257	453	TKGGGYTQRTAIQFILFIYLFYI*DG VSLLLPRLE*NGAISAHCNHLPGSS DSQKTKKNFCTQ
5206	10703	A	5521	277	1230	ISFHLSTFGAPSF F F F F F F E M E F S L L L P R LECN GAISAHRNLRLPGSSDSPASAS PVGWDYRHVHPRSANFV F F F S R D G VSPCWSGLVSNRPQMIPPSRPPKV LDTGLATMPGLCLANFCGRNRVSL MCPWSPELKQSTCLSLPKCWDYR RAAVPGLFILFFLRHRCPTLTQDEV QWCDHSSLQSTPEIKHPPASASQSS WDQRHAPLHLANFYFYF*FFETES\ HSVT\RLLECSGAILAHCNLCPLGSSY SPAPAS*VAGTTGAH/RRLANFFVFL VEMGFHHVRQVDARSLDLVICLPR PPKVLGLQDVSHHRPAYF
5207	10704	A	5522	1	467	FFFLF*EGVSLLLPRLECSGAISA/HC NLHLPGSSDSPASASQEDGITGVRY HAWLIL/VFLVEIGFHHVGQADLKP *PQVIHPPLFFFLRQSFALVAQAGV QWCDLSSLQTPPPRVQGILLAQPE YL VAGFTGMRHHTRLFFFFAFLVET GFHPC
5208	10705	A	5523	293	681	QGTILIGLCPFDITPAIVDILLAFWHV R\CPRPTVSCFCKKVLLV*NFFFFF FFFETESCSVTRLECSGVILAHCNL RLPGSSDSHASASRVAETTGVRRHA WPIFVFLVETRFHHVGQAGLELLTS GD
5209	10706	A	5524	274	321	
5210	10707	A	5525	2	733	
5211	10708	A	5527	1	3555	MHYVLNSSSMETFVGEQNYEGSSR LCVCKRTREADDPSARDSVCEGVR ARFNICGINQIVLKCPIWGCENPAQ MGCPPVGKADRCGLLAN SATCEKG MFCHADLVGITPTVFPSHPRCKTTA SAKLACQQQDVLDRQSLSSIDKNPS ERGQSQLSNPTDDSWKGRPYANQK LFASLLIKCVVQLELIQTIDNIVFYPA TSKKEDAHEMVAAQQDITLDADIHI ETEDQGMKYMSSQHFLKLLDCLQ ESHFSKAFNSNYEQRTVLWRAGF KGKSKPNLLKQETSSLACCLRILFR MYVDENRRDSWEEIQRLLTVCS ALAYFITVNSESHREAWTSLLLLLL TKTLKINDEKFAHASMYYPYLCEI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MQFDLIPELRAVLRKFFLRIGVVYKI WIPEEPSQARCRAILPGFECEAERRQ ERVVPATVRGWGSLLRFCIPTSSYN KCLLNMYCVPDPIAMELSDANLQT LTEYLKKTLDPDPAIRRPAEKFLESV EGNQNYPLLLLTLEKSQDNVIKVC ASVTFKNYIKRNWRIVEDPNKICE ADRVAIKANIVHMLSSPEQIQKQL SDAISHIGREDFPQKWPDLLTEMVN RFQSGDFHVGVLRTAHSFLKRYR HEFKSNELWTEIKLVDAFALPLTN LFKICDNaALYAQKYDEEFQRYLPR FVTAIWNLLVTTGQEVKYDLLVSN AIQFLASVCERPHYKNLFEDQNTLT SICEKVIVPNMEFRAADEEAFEDNS EEYIRRDLEGSIDIDTRRRACDLVR GLCKFFEGPVTGIFSGYVNSMLQEY AKNPSVNWKKHDAIYLVTSLSK AQTQKHGITQANELVNLTEFFVNHI LPDLKSANAIMRSFSLQEAIPYIPT LITQLTQKLLAVSKNPSKPHFNHYM FEAICLSIRITCKANPAAVVNFEAL FLVFTEILQNDV/PSESVDQYRKQIFI LLFQRLQNSKTTKFIKSK*NHLDVL QK**KK\MFGMVLEKIIPEIQKVS NVEKKICAVGITKLLTECPMMDTE YTKLWTPLLQSLIGLFELPEDDTIPD EEHFIDIEDTPGYQTAFSQAFAAGK KEHDPVGQMVNNPKIHLAQLSHKL STACPRSCGSSPVEDGVCIGAPRSP TASVCFPSLVGSINGPAPAPPPPTVR TTSSGWHCGGACARKARRGPSGRS ALSRLDRSGPS
5212	10709	A	5528	1	4611	
5213	10710	A	5529	58	3051	CQLRSAAGVPSSSVSPRDPAMEL SDANLQTLTEYLKKTLDPDPAIRRP AEKFLESVEGNQNYPLLLLTLEKS QDNVIKVCASVTFKNYIKRNWRIV EDEPNKICEADRVAIKANIVHMLLS SPEQIQKQLSDAISIGREDFPQKW PDLALTEM\VNRFQSGDFHVGVLRT AHSFLKRYRHEFK\SNELWTE\K LVDAFALPLTYLFAKATIELCSTH ANDASALRILFSSLILISKLFYSLNFQ DLPEFFEDNMETWMNMFHTLLTLD NKLLQTDDEEEAGLLELLKSQICDN AALYAQKYDEEFQRYLPRFVTAIW NLLVTTGQEVKYDLLVSNAIQFLAS VCERPHYKNLFEDQNTLTSICEKVI VPNMEFRAADEEAFEDNSEEYIRRD LEGSIDIDTRRRACDLVRGLCKFFE GPVTGIFSGYVNSMLQEYAKNPSV NWKKHDAIYLVTSLSKAAQTQKH GITQANELVNLTEFFVNHLPLDKSA NVNEFPVLKADGIKYMIFRNQVPK EHLLVSIPLLINHLQAGSIVVHTYAA HALERLFTMRGPNNATLFTAEEIAP FVEILLTNLFKALTLPSSSENEYIMK

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- tho- d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AIMRSFSLQEAIIPIYIPTLITQLTQK LLAVSKNPSKPHFNHYMFEAICLSIR ITCKANPAAVVNFEEALFLVFTEILQ NDVQEFIPYVFQVMSLLLETHKNDI PSSYMA LFPHLLQPVLWERTGNIPA LVRLQAFLEGRSNTIASAAADKIP GLLGVFQKLIASKANDHQGFYLLNS IIEHMPPEVDQYRKQIFILLFQRLQ NSKTTKFIKSFLVFINLYCIKYGALA LQEIFDGIQPKMFGMVLEKHIPEIQK VSGNVEKKICAVGITNLLTECPPMM DTEYTKLWTPLLQSLIGLFELPEDD TIPDEEHFIDIEDTPGYQTAFSQLAF AGKKEHDPVGMVNNPKIHLAQSL HMLSTACPGRVPSMVSTSLNAEAL QYLQGYLQAASVTLL
5214	10711	A	5530	1	396	
5215	10712	A	5531	1	1095	
5216	10713	A	5532	1	1077	
5217	10714	A	5533	1	986	
5218	10715	B	5534	214	975	MEVKT KARELRDECTSLSSRFQLE ERVLVMENQMNQMKQEEKFREKRI KRNEQSLQEIWDYVVKRPNLRVIGVP ESDGENGT KLENTLQDIIQENFPNL ARKANIQIQETQRMPPQRYSSRRATP RHIIVRFTKVEMKETMLRAAREKG RVTHKGKPIRLTADLSAETLQAKRE WGPINFILKEKNFQPRISYPAKLSFIS EGEIKSFTDKQMLRDFVTTTPALKE LLKEALNMERNNQYQHCKNMPNC KDHPG*
5219	10716	A	5535	3	1135	
5220	10717	A	5536	1	1023	
5221	10718	A	5537	2	2747	LHLWGQGTKQKQDSSNLCRLKCP LTALKRAVVLPARSWRSENGQTAS SKGKLTTRKDIYTENPSVHHHHQRP KVDKTTKMGKKQNRKTGNSKKQS ASPPPKERSASPPPKERSSSPATEQS WREN/DLFDDELRAEGFKRSNYSE LWEDIQTKGKEVENFEKNLEECITRI TNEKCLKELMELKTKARELCEEC RSLRSRCDQLEERVSA MEDEVKMN EMNEMKREGKFREKRIKRNEQSLQ EIWDYVVKRPNLRLTGVPESDGENG TKLENTLQDIIQENFPNLARQANVQI QEIQRTPPQRYSSRRATPRHIIVRFTK VEMKEKILRAAREKGRVTLKGKPIR LTADLSAETLQARREWGPIFINILKE KNFQPRISCPAKLSFISEGEIKYFTDK QMLRDFVTTKPALQELLKEALNME RNNRSPSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKKEVEN FEKNLEECITRITNEKCLKELMELK TKARELREECRSLRSRCDQLEERVS AMEDEMNEKREGKFREKRIKRNE QSLQEIWDYVVKRPNLRLIGVPESDV ENGKLENTLQDIIQENFPNLARQA NVQIQEIQRTPHRFSSRRATRNLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RFTKVEMKEKMLRAAREKGRVTH KGKPIRLTADLLAETLQARREWGPI FNILKEKNFQPRISYPAKLSFISEGEI KYFTEKQMLRDFVTTSPALEELLKE ALNMERNNRRTTRQKVNKDIQELNS ALHQADLIDISRTLHPKSTEYTFSSA PHHTYSKIDHIVGSKALLSKCKRTEI ITKCLSDHSAIKLELRIKKLTQNCCTT TWKLNNLLNDYVWVQNEMKAEIK MFFENNENKDDTTYQNLWDTFKAV CRGKFIALNAHKRKQKRSKTDLTLS QLKELEKEEKHIQKLAEGKK
5222	10719	A	5538	99	432	
5223	10720	A	5539	100	732	
5224	10721	A	5540	242	1300	NPRRSGHSLEAKLRDSSSYSELLRDIL QKHEAVHMEALDELYEALAETLM AKESTQGHRSYLLPSGGSVTLSEST AIISHGTTGLVTWDATLYLAEWAIE NPAAFTNRTVLELGSGAGLTGLAIC KDVPPPGIHLQRTCHSRVLEQLRGN VPS\NGLSLEADITAKLDSRVTVVAQ LDWDVATVHQLSAFQPDVVIAADV LYCPEAIMSLVGVLRRLAACREDQ RAPEVYVAFTVRNPETCQLFTTELA PSTCEGVLSLSHLTDKDIRTHRGQA TLELLQTAARPPGSRASTIHPSLPMP RASAPAPPEHSPSWQPCAQMHPQQ PLPAHRDTPNPVPHVGVQPVNYRA NKQAST
5225	10722	A	5541	3	167	
5226	10723	A	5542	2	378	
5227	10724	A	5543	3	359	
5228	10725	A	5544	15	347	
5229	10726	B	5545	141	371	DFGYFYGSSYVAAPDSSRTPGLSRS RDGLLVAKLDLNLCCQQVNDVWNF KMTGRYEMYARELAEAVKSNSYST IVKE*
5230	10727	A	5546	1	1154	MAGAEWKSLEECLEKHLPLPDLOE VKRVLYGKELRKLDLPREAFEAAS REDFELQGYAFEAEEQLRRPRIVH VGLVQNRIPLPANAPVAEQVSALHR RIKAIVEVAAMCGVNIICFQEAWTM PFAFCTREKLPWTEFAESAEDGPTT RFCQKLAKNHDMVVVSPILERDSE HGDVLWNTAVVISNSGAVLGKTRK NHIPRVGDFNESTYYMEGNLGHVP FQTQFGRIAVNICYGRHHPLNWLM YSINGAEIIFNPSATIGALSESLWPIE ARNAAIANHCFTCAINRVGTEHFP NEFTSGDGKKAHQDFGYFYGSSYV AAPDSSRTPGLSRSRDGLLVAKLDL NLCCQQVNDVWKFKITGRYEMYAR ELAEAVKSNSYSTIVKE
5231	10728	A	5547	424	604	
5232	10729	A	5548	52	318	
5233	10730	A	5549	3	148	
5234	10731	A	5550	258	458	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5235	10732	A	5551	1	217	
5236	10733	A	5552	246	361	
5237	10734	C	5553	69	254	MDHLYNXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXEIQXXXXXERERNKN PFPAGDDIISRGVGGQ*
5238	10735	A	5554	32	169	NPVPPYPLCPALVFFLLLIYLLIY*PS PLLRMSAPAGKGFLFLSL
5239	10736	A	5555	417	490	
5240	10737	A	5556	2	121	
5241	10738	A	5557	69	398	
5242	10739	A	5558	2	732	GRVPSQCGWIRMRSRSCREDQKPG MDDQRDLISNNEQLSMLGRPGAP ESKCSRGCPLHSAFSILVTLVVQA INAYFLYH*HGRDLKLTVPQNLQ LENL\RMKLP\KPPKPVSKMRMATP LL\MQALPMGALPQGPMPQATKYG NMTEDHVMHLLQNADPLKVYPPL KGSFPENLRHLKNTMETIDWKVFES WMHHWLLFEMSRHSLEQKPTDAPP KESLELEDPSGLGVTKQDLGPVPM
5243	10740	A	5559	2	359	
5244	10741	A	5560	2444	2755	DYYYFFEMESCSVAQAGVQWRDL GSLQPPPPSSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVQQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS
5245	10742	A	5561	1724	1941	AHLLYEWIFFFFFFFEMESHSAQA GVLWRDLSSLQAPPPGSQSDSPAS ASWVAGITGACHHARHEWNFKC
5246	10743	A	5562	2	362	
5247	10744	A	5563	138	236	
5248	10745	A	5564	1	278	
5249	10746	A	5565	80	591	RGCKREGLSMSSLIRRVISTAKAPG A\IGPPTVQAVLV\DRTHLHFRDQIG HGPLPSWTSLCPGGVAGRSLNKL KNMGEIPESLPGCDFATNVVKTTCSS GLDINDLQLLFNEILQTVFSRSNFPA RAAYPSWLLLQKGSRIEIAVAIQ GPLTTAFILSGDPCCVWDC
5250	10747	A	5566	141	340	
5251	10748	A	5567	209	386	
5252	10749	A	5568	1	346	
5253	10750	A	5569	160	391	
5254	10751	A	5570	101	332	
5255	10752	A	5571	500	752	
5256	10753	A	5572	2	82	
5257	10754	A	5573	3	165	
5258	10755	A	5574	1	219	
5259	10756	A	5575	1	327	
5260	10757	A	5576	2	160	
5261	10758	A	5577	1	189	QQLRHPDLHLQRRSQAQQHQGGQ DS*AQMLCRVPTVPSTTCGRTVSLP LPPKTQGHPHDLDP
5262	10759	A	5578	2	224	
5263	10760	A	5579	1	1392	
5264	10761	A	5580	1	1272	PGCGRPRAFSLNIAIDIEKRGFTSHF VRQTPSPSPNNL*YLIYRRYRQFHA

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						LQSKLEERFGPDSKSSALACTLPTLP GRRPLPSCCCRAAVRIPALNAYMK VPVGLATLARGRALPPWDPLQGS CLWSLSTQSQSPVSPDLCAWSLVR* PRQALGARVLDVRIFFYQSPYDSEQ VPQALRRLRPTRKV*VTSPWAST WPEPAAPRAEVTAPTLARLSHCNF KAGDVIFLLSRINKDWLEVSSEVRM EVRKLVFVKILKDFPEEDDPTNWL CYYYEDTISTIKSVAWEGGACPAFL PSLRPLPTSPSHGSLSHSKAPSGSQ MSHNAVTSHQRPGWPGQPHSPFP PTLKDLELTR*GAGNGAGELDTLD AEGDLVRLLSDEEDVALMVRQARGL PSQKRLFPWKLHITQKDNYRVYNT MP
5265	10762	A	5581	437	728	
5266	10763	A	5582	570	1648	TQPGTGWARLSTCSLGPSTMAVA QQLRAESDFEQLPDDVAISANIADIE EKRGFTSHFVFVIEVKTGGSKYLI YRRYRQFHALQSKLEERFGPDSKSS ALACTLPTLPKVVYGVKQEIEM RIPALNAYMKSLLSLPVWVLMDED VRIFFYQSPYDSEQVPQALRRLRPR TRKVKSVPQGNVDRMAAPRAEA LFDFTGNSKLELNFKAGDVIFLLSRI NKDWLEGTVRGATGIFPLSFVKILK DFPEEDDPTNWLRCYYYEDTISTIK DIAVEEDLSSTPLLKDLELTRREFQ REDIALNYRDAEGDLVRLLSDEEDV ALMVRQARGLPSQKRLFPWKLHIT QKDNYRVYNTMP
5267	10764	A	5583	1705	2233	
5268	10765	A	5584	1	354	
5269	10766	A	5585	270	390	
5270	10767	A	5586	3	132	
5271	10768	A	5587	234	362	
5272	10769	A	5588	1	402	
5273	10770	A	5589	2	509	
5274	10771	A	5590	3	1607	SPRPGIPRCFHLVISTEHRRVMTEFG LSWVFLVAIFKGVQCEVQLVESGG DLVQPGGSLRLSCAASGFTSSYAM HWVRQAPGKGLKYVSGISSNGRRT YYANSVKGRFTISRDNKNTLYLQ MGSRAEDMAVYYCARGGDHIVP AAVAPFHMDVWGQGTTVTVSSASP TSPKVFPLSLCSTQPDGNVVIACLP PGLLPPGATQCDLERKRTGRDRQK LPTQPGCLRGPVHHEQPADPAGHT VPSRQVRDMPREALHESQPGCDCA LPSSLNSTYIPISLNSTYIPISLMLPPPT VTAPTGPSKDLFLGSKATFTCTLP LRDASGVTFTWDALKVGKSAVQGP P*RRDLGCYCYSVSSVLPGCAEAH GTHGEGPSLWHCWYPESKDPA*PP TLFKIRGNTTFPGPRFHLLPPSEGAG PWNELVTLATCLGIGLSAPRMLLVC

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						WVAGGHRSLREKYLTWASRQKP SQGTTTFAVTSILRVAEDWKKGD TFSCMVGHEALPLAFTQKTIDRLAG KPTHVNVSVVMAEVDGTCY
5275	10772	A	5592	2	315	
5276	10773	A	5593	245	455	
5277	10774	A	5594	1	2863	MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEESNQATGTSRWDG VSKKAPRHLSVPCTRPREARQEA DSTRLSAESGETDQDAGDVGPDP PDSYYGLLGTLPQEQALSHICSLP VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAAVVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTITLTHEQQ LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRFLYVTFNKSIAK QAERVFPNSVICKTFHSMAYGHIGR KYQSKKKLNLFKLTPFMVNSVLAE GKGGFIRAKLVCKTLENFFASADEE LTIDHVPWCKNSQGGQRMVEQSE KLNGVLEASRLWDMRKLGECTEE AHQMTHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTLVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVKDKFIRRW VHKEGFSGFKRYVTAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLQPLPALR\VEPFS\ EDEWNLLYVAVTRAKKRLIMTKS LENILTLAGEYFLQAE LTSNVLKTG VVR\CCVG\QCENNAIPVDTVLTMKK L\PIY*ATGK\ENKGGYLCHSCAEQ RIGPLAFLTASPEQVRAMERTVENI VLPRHEALLFLVF
5278	10775	A	5595	3	613	
5279	10776	A	5596	2	1419	PPHLLSSPFVAAPRARATAGFTLS ASAMQEIAHLQAGQCGNQIGAKFW EVISDEHGIDPTGTYHGDSDLQLERI NVYYNEATG\GNYVPRAVLVDLEP GTMDSVRSFGPGQIFRPNFVFGQS GAGNNWAKGHYTEGAELVDAVLD VVRKEAESCDLQGFQLTHSLGGG TGSGMGTLISKIREFPDRIMNTFS VVPS\PKCQDTVVEPYNATLSVHQL VENTDETYCIDNEALYDICFRTLKL TTPTYGDLNHLVSA TMSGVTTCLRF PGQLNADLRKLAVNMVFPRLHFF

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						MPAFAPLTSRGSQQYRGLTVPELTQ QMFDANKMMAACDPRHGRYLTV AVFRGRMSMKEVDEQMLSVQSKN SSYFVEWIPNNVKTA VCDIPPRGLK MAVTFIGNSTAIQELFKRISEQFTAM FRRKAFLHWYTGEQMDMEFTEAE SNMNDLVSEYQQYQDATAEQGEFE EEAEEVA
5280	10777	A	5603	1	384	
5281	10778	A	5604	185	700	
5282	10779	A	5605	1	414	
5283	10780	A	5606	3	138	
5284	10781	A	5607	1	433	NNPDFKAGV\MALPTL\LQIQRHDD YLVMLKAIRILVQERLTQDAVAKA NQTKGLPVALDKHILGFDTGDAV LNEAAQILRLHIEELRELQTKINEA IVAVQAIHFVHVWVWVSKCHILGGGS PENWVCSRDLPLLIATFFFNKV
5285	10782	A	5608	1	459	
5286	10783	A	5609	118	375	VAVVQIIFLPVFIAEKYKDLVPDnsk TADNATKNAEPLINLDVNNPDFKA GVMALANLLQIQRHDDYLVMLKIA IRILVQERLTQD
5287	10784	A	5610	344	513	
5288	10785	A	5611	3	116	
5289	10786	A	5612	3	869	HEVFSRPRPGEPNREAGTMFRRRLT VLDYHNPAFGNCKDETEFRNFIVW LEDQKIRHYKIEDRG\NLNRNIHSSDW PK\FFEKYLRDVNCPFKIQDRQEI DWLLGFAVRPEYG\DNAEKYKDLV P\DNSK\TADNAPKNAEPWINLDVN NPDK\AGVMALG*PAFRFQRHDD\ FLVNA*RQFRIWVQERLTQDA\VA KAKSNKKRALPVALAQTHILGFD\T GDASSLMKLEILRIACTYEELREL DQKSTKAIVAVQAIYC*SQRQDHRL GKSLEDEHFEDLQLSPLL
5290	10787	A	5613	298	403	
5291	10788	A	5614	3	611	
5292	10789	A	5615	192	340	
5293	10790	A	5616	187	361	
5294	10791	A	5617	187	385	
5295	10792	A	5618	2	340	
5296	10793	A	5619	1	702	EKYIQLVRQRALEGALGNTIYKSQ TAKGTPQETEGTSSGSKSNVRSGR VPSGRMV\IHSHFPAEVT*E*TRVH WIWQS*CQGESWKQVPVFLCHSGS* RNALL\CLRHDVDALLWQPHSSKQ DDMWEHIATFNALGYVQASKRDK KFFACAPNYSYAALCECLRRVFIYR QPAPMSTVLNKKGRQA\VGQVAK QQVASLETNDPNLGIQATNERLFV LTTKNLFLIKVNTEN
5297	10794	A	5620	3	357	
5298	10795	A	5621	1	1926	
5299	10796	A	5622	1	362	LQTSDEETGFSCLFYVCAATSFVL VCIINNWSCKAD*DTRWTFRIKIGR

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						T/SVVVDLLYWRDINITGVVFGATLFL LLSLTVFSIVSVTAYIALALLSVTISF TIYKGVSHAIPKSDEGHPF
5300	10797	A	5623	247	533	KSFPGWQTYFSCGWVGCGLGRGS QNASPPASPLPQLPPG*RRSWPLRG TACRSWSALSGWAAGLYHPPRMPP LMWEAGAGSPGELRGTRIRER
5301	10798	A	5624	128	667	
5302	10799	A	5625	12	3756	VPRLSRPSPSQSSPTPTTARGSETRP RRRRQQLQHHLHPPAMEDLDQSPL VSSSDSPRPQPAFKYQFVREPEDEE EEEEEEEEDEDEDLEELVLERKPA AGLSAAPVPTAPAAGAPLMDFGND FVPPAPRGPLPAAPPVAPERQPSWD PSPVSSTVPAPSPLSAAAVSPSKLPE DDEPPARPPPPPPASVSPQAEPVWTP PAPAPAAPPSTPAAPKRRGSSGSVD ETLFALPAASEPVIRSSAENMDLKE QPGNTISAGQEDFPSVLLETAASLPS LSPLSAASFKEHEYLGNLSTVLPT GTLQENVSEASKEVSEKAKTLLIDR DLTEFSELEYSEMGSFSVSPKAESA VIVANPREEIIIVKNKDEEEKLVSNNI LHNQQELPTALTKLVKEDEVVSSEK AKDSFNEKRVAVEAPMREEYADFK PFERVWEVKDSKEDSDMLAAGGKI ESNLESKVDKKCFADSLEQTNHEK DSESSNDDTSFPSTPEGIKDRSGAYI TCAPFNPAATESIATNIFLLGDPTSE NKTDEKKIEEKKAQIVTEKNTSTKT SNPFLVAAQDSETDYVTTDNLT TEEVVANMPEGLTPDLVQEACESEL NEVTGTKIAYETKMDLVQTSEVMQ ESLYPAAQLCPSFESEATPSPVLPD IVMEAPLNSAVPSAGASVIQSSSPL EASSVNYESIKHEPENPPPYEEAMS VSLKKVSGIKEEIKEPENINAALQET EAPYISACDLIKETKLSAEPAPDFSD YSEMAKVEQVPDHSSELVEDSSPDS EPVDLFSDDSIPDVPQKQDETVMV KESLTETSFESMIEYENKEKLSALPP EGGKPYLESFKLSLDNTKDTLLPDE VSTLSKKEKIPLQMEELSTAVYSND DLFISKEAQIRETETFSDDSSPIIIDEF PTLISSKTDSFSKLAREYTDLEVSHK SEIANAPDGAGSLPCTELPHDLSLK NIQPKVEEKISFSDDFSNGSATS LLPPDVSAATQAEIESIVKPKVLV KEAEKKLPSDTEKEDRSPSAIFS SKTSVVVDLLYWRDIKKTGVVFGA/ SAVFLLSLTVF\SIVSVTAYIALAL LSVT\ISFRIYKGVIAIQKS\DEGHP FRAISGNL/ESCLYLRELGSGRYSNS\ ALGSMWNCTVKGNFRAPSFSSWM DLVDSL/RSFAVLMWVFTYVGCGLG LMVLDTTGFWALNF/ISSSGSWLIYE RHQAQ\IDH\YGLANKNVKDAMA KIQAQIPG\LKRKAE

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5303	10800	A	5626	2	436	RRQFEERQQEMEHVYELLENKMQL LQESRLAKNEAARMAALVEAEKE CNLELSEKLKGVTKNWEDVPGDQV KPDQYTEALAQRDK*VPSVFLRL SFAHSQGIQQLSCSLSRT/RQ*ELHY F*DFMGPQPKTFFSGLNFQWYPL
5304	10801	A	5627	3	309	
5305	10802	B	5628	454	645	MTCKKENFSLKLLIYFLEERMQQK YEASREDIYKRNTTELKVEVESLKRE LQDKKQPSGLKPWA*
5306	10803	A	5629	1	294	
5307	10804	A	5630	14	228	
5308	10805	A	5631	201	350	
5309	10806	A	5632	262	626	PSARPHCFGLEAMHARSLPCWNCS SRLLILAFS/WGSE/CCTRKPRIIDV VYNASNNELVRTKTLVKNCIVLIDS TPYR\QWYESH\YALPLGRKKGAKL TPEEEELNKKRSKKIQKKYDERKE NAKISSLLEEQQGKLLACIASRPK QCGRADGYVLEGKELEFYLRK\KA RKRQINPCFVFTHGNRGVYCFVPTF MLPEYMTVFS\AIFPCPAKLIWGGGL QPLALTSASYPETGSPHC
5310	10807	A	5633	3	452	
5311	10808	A	5634	26	477	NSTDSETHHGARLLPDKTNVKAA WGKVGAHAGHEYGAELERMFLSF PTVTKTYFPHFDLASHG\SAQVKG/HT GKKVADALTNAV\ANVDDMPN\AL SALS\DLHAHKL\RVDPVNFKLLSHCL AGGPWAAHLPRPSSTPGGATPSLEQ SSWASC
5312	10809	A	5635	1	147	
5313	10810	A	5636	1	503	AAAAARAAGTAGPWRSAARLPALP ASSLGAAAMAASAKRKQEEKHLK MLRDMTGLPHNRKCFDCDQRGPTY VNMTVGSFVCTSCSGSLRG*NPPHR VKSISMTTFTQ\QEI\FLQKHGNEVC PPEQAKVVASVHASISGSSASSTSS TPEVRPLKSLLGDSAPTLHLN
5314	10811	A	5637	272	360	
5315	10812	A	5638	1	1934	WRRRRRLSRLCRLVWPVSPRTTAP GPRRAQYSQAAAAGSGAGGARRR RAAAAAARAAGTAGPRRSAARLPA LPASSLGAAAMAASAKRKQEEKHL KMLRDMTGLPHNRKCFDCDQRGPT YVNMTVGSFVCTSCSGSLRGLNPPH K/VGKSISMTTFTQ\QEI\FLQKHGNE VCKQIWLGLFDDR\SSAIPDFRDPQK VKEFLQEKYEKKRWYVPPEQAKVV ASVHASISGSSASSTSS\TPEVKPLKS LLGDSAPTLHLNKGTPSQSPVVGRS QGQQQEKKQFDLLSDLGSDIFAAPA PQSTATANFANFAHFNSHAAQNSA NADFANF\DAFGQSSGSSNFGGFPTA SHSPFQ\PTTGGSAASV\NANFAHFD NFPKSSSADFGTFNTSQSHQTASAV SKVSTNKAGLQTADKYAALANLDN

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						IFSAGQGGDQGSFGTTGKAPVGSV VSVPSQSSASSDKYAALAE LDSVFS SAATSSNAYTSTSNASSNVFGTVPV VASAQTQPASSSVAPFGRTPSTNPF VAAAGPSVASSTNPFQTNARGATA ATFGTASMSMPTGFGTPAPYSLPTS FSGSFQQPAFPAQAAFPQQTAFSQQ PNGAGFAAFGQTKPVVTPFGQVAA AGVSSNPFMTGAPTQGFTGSSSTN PFL
5316	10813	A	5639	1	307	
5317	10814	A	5640	957	3132	GEEEPLWQGSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHAEKQAR *PLGPWCRRKKKGAEEEKPKRRR QEKQAACPFYNHEQMGLLRDEALA EVKDMEQLLALGKEARACPYYGSR LAIPAAQLVLPYQMLLHAATRQA AGIRLQDQVVIIDEAHNLIDTITGMH SVEVSGSQLCQAHSQQLQYVERYG KRLKAKNLMYLKQILYLLEKFVAV LGGNIKQNPNTQSLSTGTTELKTIN DFLFQSQIDNINLFKVCVPSAPQMK HGHCRNLNPKLVTQISNSDCPRVQRY CEKSMISRKLFGFTERYGAVFSSRE QPKLAGFQQFLQSLQPRTEALAAP ADESQASTLRPASPLMHIQGFALAAL TTANQDGRVILSRQGSLSQSTLKFL LLNPAVHFAQVVKECRAVVIAGGT MQPVSDFRQQLACAGVEAERVVE FSCGHVIPPNDILPLVICSGISNPLE FTFQKRELPMMDDEVGRILCNLCG VVPGGVVCFFPSYEYLRQVHAHWE KGGLLGRLAARKKIFQEPKSAHQV EQVLLAYSRCIQACGQERGQVTGA LLSVVGGKMSEGINFSDNLGRCV VMVGMPFPNIRSAELQEKMAYLDQ TLPRAPGQAPPKALVENLCMKAV NQSIGRAIRHQKDFASVVLLDQRYA RPPVLAKLPAWIRARVEVKATFGPA IAAVQKFLQVYGTSPLNLHLSKLQD TFYPNTSNTYAKGR
5318	10815	A	5641	1	1668	
5319	10816	A	5642	947	2782	GEEEPLWQGSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHAEKQAR/ KKKGAEEEKPKRRRQEKQAACPFY NHEQMGLLRDEALAEVKDMEQLL ALGKEARACPYYGSR/LAIPAAQLV VLPYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGSQL CQAHSQQLQYVERYGKRLKAKNL MYLKQILYLLEKFVAVLGGNIKQNP NTQSLSTGTTELKTINDFLFQSQIDN INLFKVQRYCEKSMISRKLFGFTER YGAVFSSREQPKLAGFQQFLQSLQ RTTEALAAPADESQASTLRPASPLM HIQGFALAALTTANQDGRVILSRQGS LSQSTLKFLLLNPAVHFAQVVKECR AVVIAGGTMQPVSDFRQQLACAG

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						VEAER\VVEF/SCGHVIPPDNILPLVI CSGISNQPLEFTFQKRELPMIFQEP KSAHQVEQVLLAYSRCIQACGQER GQVTGALLLSVVGKMSSEGINFSD NLGRCVVMVGMPPFNIRSAELQEK MAYLDQTLPRAPGQAPPKALVEN LCMKAVNQSIGRAIRHQKDFASVV LLDQRYARPPVLAKLPAWIRARVE VKATFGPAIAAVQKFHREKSASS
5320	10817	A	5643	1143	3233	GEEEPLWQGCAGLPWLPAEPLCK* RREKPRFCAAYQRPLRGHAQKQAR\ KKKGAEEEKPKRRRQEKQAACPFY NHEQMGLLRDEALAEVKDMEQLL ALGKEARACPPYRSRLAIPAAQLV VLSYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGSQ LCQAHSQLLQYMERYGKRLKAKN LMYLKQILYLLEKFVAVLGGNIQ NPNTQSLSQTGTTELKTINDFLFQSQI DNINLFKVQRYCEKSMISRKLFGFT ERYGAVFSSREQPKLAGFQQFLQSL QPRTEALAAPADESQASVPQPASP LMHIEGFLAALTANQDGRVILSRQ GSLSQSTLKFLLNPAVHFAQVVKE CRAVVIAGGTMQPVSDFRQQLLAC AGVEAERVVEFSCVFGPSLALTIGH VIPPDNILPLVICSGISNQPLEFTFQK RELPMMDDEVGRILCNLCGVVPGG VVCFFPSYELRQVHAHWKGGLL GRLAARKKIFQEPKSAHQVEQVLL AYSRCIQACGQERGQVTGALLSV VGGKMSSEGINFSDNLGRCVVMVG MPFPNIRSAELQEKMAYLDQTLPR PGQAPPKALVENLCMKAVNQSIG RAIRHQKDFASIVLLDQRYARPPVL AKLPAWIRARVEVKATFGPAIAAV QKVSPTFFFLRASPPRDHISHCLLSA QFHREKSASS
5321	10818	A	5644	3	744	
5322	10819	A	5645	40	126	
5323	10820	C	5646	187	366	MDERDSHCPYLLSSETTAKGTGLAE SAGKEDPVELDSSLEARVRRRRPST SMPLTSAPC*
5324	10821	A	5647	1	382	TADCAKPVPLAVVSLDSRYGQWES RSSIHA\VTN*ASSSSSSSSSSSF\SR\ YPRFIEFIHFDIQSTGQ/RITSR*HPPR/ DLRDALF*LNSLIPLVRTSSKSAARR RP\GEAPRGTA VPGADPAGGTRPR
5325	10822	A	5648	3	684	QGPRAALGALFPCWAPGKYVHGV RAKHPRATARAPRGSP/LPPHRVSE KTIRVVVFHRRPAGPADPAPGPSRG HRGGAG/EPPTYSTPLMSLHRARLE SSSTGSSFPADSAKPVPLAVVSLDSR *GQWESRSSIHA\VTN*ASSSSSSSS SS\FSR\YPRFIEFIHFDIQSTGQ/RIT SRQHPPR/DLRDALF*LNSRIPLVRTS SKSAARRRP\GEAPRGTAAPGADPA GGP

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5326	10823	A	5649	2	331	
5327	10824	A	5650	3	340	
5328	10825	A	5651	1	94	
5329	10826	A	5652	2	496	ASMGCSPLLSLLSLLVGAWLKLGH*TAGHAGGAGKGDGALRPGGREG EAPLPASGMRLQPPAGEVALGAQG ASPPCAFNFLWNLSIQAQLRRVRG QGCSWRWLVLAAQAEELLGDPALV PTRRQPVGRAAPAPAASSLCCADPA GREVTQVVVVQVVVNSSS
5330	10827	A	5653	3	997	
5331	10828	A	5654	3	131	
5332	10829	A	5655	112	289	
5333	10830	A	5656	35	5228	LDPLGRMVMGIFANCIFCLKVKYLP QQQKKKLQTDIKENGKFSFSLNPQ CTHIILDNADVLSQYQLNSIQKNHV HIANPDIWKSIREKRLLDVKNYDP YKPLDITPPPDQKASSEVKTEGLCP DSATEEEDTVELTEFGMQNVEIPHL PQDFEVAKYNTLEKVGMEGGQEA VVVELQCSRDSRDCPFLISSHFLDD GMETRRQFAIKKTSEDASEYFENYI EELKKQGFLREHFTPEATQLASEQ LQALLLEEVMNSSTLSQEVSDLVE MIWAEALGHLEHMLLKPVNRISLN DYSKAEGILLVKAALKNGETAEQ LQKMMTEFYRLIPHKGTMPKEVNL GLLAKKADLCQLIRDMVNV CETNL SKPNPPSLAKYRALRCKIEHVEQNT EEFLVRKEVLQNHHSKSPVDVLQI FRVGRVNETTEFLSKLGNVRPLLHG SPVQNI VGILCRGLLLPKVVEDRGV QRTDVGNL GSGIYFSDSLSTS IKYSH PGETDGTRLLICDVALGKCMDLH EKDFSLTEAPPGYDSVHGVSQ TASV TTDFEDDEFVYKTNQVKMKYIIF SMPGDQIKDFHPSDHTLEEYRPEF SNFSKVEDYQLPDAKTSSSTKAGLQ DASGNLVPLEDVHIKGRIIDTVAQVI VFQTYTNKSHVPIEAKYIFPLDDKA AVCGFEAFINGKHI VGEIKEEEAQ QEYLEAVTQGHGAYLMSQDAPDVF TVSVGNLPPKAKVLIKITYITEL SILG TVGVFFMPATVAPWQQDKALNEN LQDTVEKICIKEIGTKQSFSLTMSIE MPYVIEFIFSDTHELKQKRTDCKAVI STMEGSSLDSSGFSLHIGLSAAYLPR MWVEKHPEKESEACMLVFQPDLD VDLPDLANESEVIICLDCSSMEGVT FLQAKEIALHALSLVGEKQKVNIIF GTGYKELFSYPKHITSNTAAAEFIM SATPTMGNTDFWKT LRYLSLLYPA RGSRNILLVSDGHLQDESLTLQLVK RSRPHTRLAFACGIGSTANRHVLRIL SQCGAGVFEYFNAKSKHSWRKQIE DQMTRLCSPSCHSVSVKWQQLNPD APEALQAPAQVPSLFRNDRLLVYGF IPHCTQATLCALIQEKEFCTMVSTTE

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						LQKTTGTMIHKLAARALIRDYEDGI LHENETSEHEMKKQTLKSLIKLSKE NSLITQFTSFVAVEKRDENESFPDI PKVSELIKEDVDLPYMSWQGE QEAVRNQSLLASSEWPELRLSKRK HRKIPFSKRKMELSQPEVSEDFEED ALGVLPFTSNLERGRVEKLLDLS WTESCKPTATEPLFKKVSPWETSTS SFFPILAPAVGSYLTPTTRAHSPASL SFASYRQVASFGSAAPPRQFDASQF SQGPVPGTCADWIPQSASCPTGPPQ NPPSAPYCGIVFSGSSLSSAQAPLQ HPGGFTTRPSAGTFPELDSPLHFSL PTDPDPIRGFGSYHPSAYSPPHFQPS AASLTANLRLPMASALPEALCSQSR TTPVDLCLLEESVGSLEGRCPVF QSSDTESEDELSEVLQDSCFLQIKCDT KDDSI PCFLEVKEEDEIVCTQHWQD AVPWTELLSLQTEGFWKLTPELG LILNLNTNGLHSLKQKGIQSLGVK GRECLLDLIA TMLVLQFIRTRLEKE GIVFKSLMKMDDPSISRNPWAFEAI KQASEWVRRTEGQYPSICPRLELGN DWDSATKQLLGLQPISTVSPHRLV HYSQG
5334	10831	A	5657	10	82	
5335	10832	C	5658	189	396	MVHPAGPLASQXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXELWLHHLSSS *
5336	10833	C	5659	54	485	MXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXRPEDFATYYCQ QNYISPLTFGGGTVKVEIXRTVAAPS VFIFPPSX*
5337	10834	A	5660	5	417	
5338	10835	A	5661	3	398	
5339	10836	C	5662	12	451	MXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXFSYYCQ QSYVSPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQ*
5340	10837	A	5663	3	679	AWWNSETPAQLLFLLLWLPTYTSG EIVLTQAPGTLSPGERATLSCRAS QTIGSTYLAWYQQRPGQAPRFLIYG ASSRATGIPDSSSSSSSSSSSSSSSS SSSSSSSSSQYYTSPFTFGGGTKV EIRRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDYSLSSST LTLSKADYEKHKVYAACEVTHQG
5341	10838	B	5664	94	321	XDRVTTTCQATQDIGNYLNWYQHK PGKAPNLLIYDASNLETGVPSRFSG RSGTHFTFTISSLPEDIATYYCQQ

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						YX*
5342	10839	A	5665	3	764	AWLESISPTMRVPAQLLGLLLWIP GSVADIMMTQTPLSLSVSPGQSASIS CKSSQSLLHSDGKTHVYWYLQKPG QSPQLLIYEVSSRFSGVDPDRFSGSGS GTDFTLKITRVEAEDVGVIYCQQY NSYLLFTFGPGTKVDIKRTVAA\PSV FIFPP\SDEQLKSGTASVVCLLNNFL FPARRAKVQWEGGINALQSGNSQEC VTE\QDSKGSTYSLASSTLTVSKADY EKHKVYACEVTHQGLSSPVTKSFN RGE
5343	10840	A	5666	1	534	RRPRREPWKPQRSFSSSCYS/ELPDT TGEIVLTQSPGTLSPGERATLSCR ASQSVSNYYLAWYQQKPGQAPRL IYDTSSRATGIPDRFSGSASGTDFTL TISRLEPEDFAVYYCQQYGSSPPMY TFGQGTKLEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKV QW
5344	10841	A	5667	184	621	LHECISVLFPISDTTGEIVLTQSPATL SLSPGERATLSCRASQSVNNYYLA WYQQKPGQPPRLIYDASNRITGIP ARF\SGSGSGTEFTFHHSAAACSLKDF CSLFTVQQLINWASDSPLGQGTRL GD/IKRTVAAPSVFIFPPSDE
5345	10842	A	5668	156	364	
5346	10843	A	5669	2	2143	SSDGSWWTGFQWREWQAGRSVN SWDNPKEVRASSKDKSRGSIQEA MRMQSSAKLLCSAWTLAYSIAVRT LSSDSEGQPLVIHRQTGSGEDLQQ TPTDLQLRVLTIRKTNKQKGHPHQ NPISRRQEITKIRAELKKIETQKPFK KINESRSWFFKINKIDRLLARLIKK KIEKNQIDAINKDKGNITNPTEIQT TIREYYKHL YANKLEHLEEMDKFL DIYTLPRLNQEEVESVNRPIGSEIE AIINSLPTKKSPGPDRFTAELYQRYK EELVPFLKLQFQIEKEGILPNSFYEA SIILISKPGRDTTKENFRPISLMNID AKILNKILANQIQHHKLIHHHQV GFIPGMQGWFNILKSINVIHHINRTK DKNHMIISIEAEKAFDKIQPFMLKT LNKLGIDGTLYLTKIIRAIYDKPTA NIILNGQKLEAFPFTGTGRCPLSP LLFNIVLEALARAIQKEKEIGIQLG KEDVKLSLFADDMIVYLENPIVSAQ NLLKLISNFSEVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLNEIK EDTNKWKNI PCSWIGRINIVKMAIL PKTLNQKFSYWFRVKNHYIHQRTFP LKETEFNTIATLYNGASP/RTAPKST GTNGHQASGLPRF*RIAFCSALVKS KRKLYQGYLPGQTDREEGVSWCP GGP
5347	10844	A	5670	1	2781	
5348	10845	A	5671	1	2988	

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5349	10846	A	5672	1	3516	
5350	10847	A	5673	1	2850	
5351	10848	A	5674	1	2850	
5352	10849	A	5675	1	3087	
5353	10850	A	5676	1	3111	
5354	10851	A	5677	1	2742	
5355	10852	A	5678	1	3474	
5356	10853	B	5679	1	3264	MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQADLIDIYRTLHPKSTEYTF FFSAPHHTYSKTDHIVGSKALLSKC KRTEIITNCLSDHSAIKLELRIKNLTQ NRSTTWKLNNQLLNDYWAHNEMK AEIKMFFETNENKDDTTYQNLWDTF KAVCRGKFIALNAHKRKQERSKIDT LTSQLEKEKQEQTHSKASRRQEIT KIRAELEIETQKILQKINESRSWFF ERINKIDRPLARLIKKKREKNQIDAI KNDKGDITDPTIEIQTIREYYKHL YTNKLENLEEMDKFLDTYTLPRLN QEEVESLNRPIGPEIVAINSLPTKK SPGPDGFTAKFYQRYKEELVPFLK LFQSIEKEGILPNSFYEASIIIPKGR DTTKKENFRPISLMNIDAKILNKILA KRIQQHIKKLIHHDQVGFIPGMQGW FNIHKSINVIQHINRPKDKNHMISID AEKAFDKIQPFMLKTLNKLIGDGT YFKIISAIYDKPTANIILNGQKVEAFP LKTGTRQGCPLSPLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPVSAQNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNALITKSI LSQKNKAGGITLPDFKLYYKATVT KTAWYWYQNRDIDQWNRTEPSEIT PHIYNLIFDKPEKNKQWGKDSLLN KWCWENWLAICRKLKLDPFLTPYT KINSRWIKDLNVRPKTIKTLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKQTTIRVNRQ PTKWEKIFATYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKKHMKKCSSSLAIREMQIK TTMRYHLTPVRMAIKKSGNNRTW EYNILCSLVPLLCSLWLHLDHHL KEDRTKHLTASDNLEKTELSRWKE RALLYEHRVLRPAIDSQHSAPRRI QGHLVCGSDLTGFMDDVAVIDVS PF*
5357	10854	A	5680	1	3780	
5358	10855	A	5681	1	3290	MGELITPLSTLDRSTRQKVNKDTQE LNSALHQGDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHILGSKALLSKCKR TEIITNYLSHSAIKLELRIKNLTQN RSTTWKLNNLLLNDYWIHNEMKAE

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						IKMFFETNENKDTTYQNLWDAFKA VCRGKFIALNAHKRQERSKIDTLT SQLKELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDTIKND KGDIATNPTEIJTTIREYYKHLNAN KLENLEEMDKFLDTYTLPRLNQEE VESLNRPTGAEIVAIINSLPTKKSPG PDGFTAESYQRYKEELVPFLLKLFQ SIEKEGILPNSFYEASIIIPKPGRDTT KKENFRLISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIQMGQWFNI RKSINVIQHINRAKDKNHMIIISIDAE KAFDKIQQPFMLKTLNKLIGIDGTYF KIIRAIYDKPTANIILNGQKLEAFPLK TGTRQGCPLSPLLNFIVLEVLAIR QEKEIKGIQSGKEEVKLSLFADDMI VYLENPIVSDQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNI PCSW VGRISIVKMAILPKVIYRFSAIPIKLP MTFFTELEKTTLKFIWNQKRARIAK AILSQKNKAGGITLPDFKLYYKATV TKTARYWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKNKQWGKDSL NKWCWENWLAICRKLKLDPLTPY TKINSRWIKDLNIRPKTIKTLEENLG STIQDIGMGKDFMSKTPKAMATKD KIDIWDLIKLSFCTAKETTIRVNGQ PTKWEKIFATYSSDKGLISRICNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAACKHMKKCSSSLAIRQMCIK TTMRYHLTP/VKFRSTSHQSP*REAR GPGPLANAGSPGLRQIPETCHLKHP LGMLLLSHHSALSATHNPTPCKLQS SVMFTTSAAMLSDPWGLRKGLGRE MFSCKTTEGNQLEAGAAEQSLYAL PKPSDLQT
5359	10856	A	5682	1	3780	
5360	10857	A	5683	1	2877	
5361	10858	A	5684	1	3126	
5362	10859	A	5685	3	3244	
5363	10860	A	5686	1540	3288	SSSLHPWDARLVQYTQINKCNPAY KQSQRQKPHYYYQLEAFPLKTGTRQ QPFMLKT/LYSIVLEVLAIRQKKE IKGIQLGKEEVKLSLFADDMIVYLE NPIVSAQNLLKLISNFSKVSGYKINV QKSQAFLYTKNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWKNI PCSWVGRIN IVKMAILPKVIYRFNAIPIKLPMTFFT ELEKTTLKFIWNQKRARIAKSILSQK NKVGGITLPDFKLYYKATVTKTAW YWYQNRVIDQWNRKEPSEITPHTY NYLIFDKPEKNKQWGKDSL FNKWC WENWLAICRKLKLDPLTPYTKINS RWIKDLNVRPKTIKTLEENLGITIQD

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						IGMGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRVNRQPTT WEKIFTTYSSDKGLISRIYNELKQIY KKKTNNPIKKWVKDMNRHFSKEDI YAAKKHMKKCSSSLAIREMQIKTT MRYHLPVRMAIHKSGNNRCWRG CGEIGTLLHCWWDCCLVQPLWKS VWRFLRDLELEIPFDPAIPLLGIYPND YKSCCYKDTCT
5364	10861	A	5687	1182	3406	YQSLAETQPKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQVGFIP GMQGWFNIRKSINVTQHINRAKDK NHMIISIDA EKA FDKIQQPFMLKTLN KLGIDGTYFKIIRAIYDNPTANIILNG QKLEAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVK LSLFADNMIVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYTNNR QTESQIMS QLPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDTNK WKNIPCSGVEGRINIVKMAILP/KELE KTTLKFIWNQKRAHIAKSILNQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEITQHIYSYLI FDKPEKNKQWGKDSL FNKWCWEN WLAICRKLKLD PFLTPYTKINSRWI KDLNVRPKTIKTLEENLGITIQDIGM GKDFMSKTPKAMATKDKIDKWDL VKLKS FCTAKETTIRVNRQPTKWEK IFATYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDMNRHFSKEDIYAA KKHMKKCSSSLAIREMQIKTTMRY HLPVRMAIHKSGNNRCWRGCGE TGTLHCWWDCCLAQPLWKS VWR FLRDLELEIPFDPAIPLLGIYPNDYKS CCYKDTCTRMFIAALFTIAKTWNQP KCPTIIDWIKKMWHIYTMEYYAAIK NDEFVSFVGTWMKLEIILSKLSQEQ KTTHRIFSLIGGN
5365	10862	A	5688	1	7578	
5366	10863	A	5689	16775	19999	KMIKGISPPIPQKYKTTIREYYKHL YANKLENLEEMDKFLDTYTLPRNLQ EEVESLNRSITGSEIEA INSLPTKKSP GPDGFTA E FYQRYKEELVPFLLKLF QSIEKEGILPNSFYESSILIPKGRDT TKKENFRPISPISLMNIDAKILNKILA KRIQQHIKKLMHHDQVGFIPGMQ GFNIRKSINVIQHINRAKDKNHMIIS IDAEKA FDKIQQPFMLKTLNKL GIDGTYFKIIRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVK LSLFA DMIVYVENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTNNRQ TE SQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNKWK NIPCSWVGRINTVKMAILPKVIYRF NAIPIKLPMPPFFTELEKTTLKFIWNQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KRARIAKSILRQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNYLIFHKPEKNKQ WGKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSR WIKDLNVRPKTI KLEENLGITIQDIGMGKDFMSKTP KAMATKDKIDK WDLIKLSFCTAK ETTITVNRQPTKWEKIFATYSSDKG LISRIYNELKQIYK\KKTNNPIKKWA RDMNRHFSKEDIYAAKKHMKKCSS SLAIREMQIKTTMRYHLPVRMAII KKSGNNRSWYFEKINKIDRLRLI KKKREKNQIDA KNDKG DITTDPTI QTTTREYYKHL YANKLENLEEMDK FLDTYNLPRLKQEEVESLNRPIRGSE IVAIINSLPTKKSPGPDGFTAIFYHR YKEELVPLLLKLFQSIEKEVLPNSF YEASIIIPKPDRTAKKENFRPISLM NIDAKILNKILANRIQQHIKKLIHHD QVGFIPGMQGWFNIRKSVNVIQHIN RTKDKNHMII SIDA EKSFDKIQQHF MLKTLNKL GIDGSYLKIIRATYDKP TANIILNGQKLEAFPLKTGTRHGCP LSPLLFNIVLEVLARAIRQEKEIKGIQ LGKEEVKLSLFIDDMIVYLENPIISA QNLLKLISNFSSLRIQNQCTKITSILV HQ
5367	10864	A	5690	78	308	
5368	10865	A	5691	1	611	GASLGGFLAQKFAEYTHKSPRVHSL ILCNSFSDTSIFNQWTANSFWLMP AFMLKKIVLGNFSSGPVDPMMADA IDFMVDRLES LGQSELASRLTLNCQ NSYVEPHKIRDIPVTIM\DVFDQSAL STEAKEEMVQA\YPNA\RAHLKTG GNFPYLCRSAEGNLMVQIHLLOFH GTKYAAIDPSMVSAEELEVQKGS GISQEEQ
5369	10866	A	5692	3	301	
5370	10867	A	5693	75	361	
5371	10868	A	5694	3	356	
5372	10869	A	5695	1	583	SPLAAKSPPSLHLE/AFKNITSSSPE RHIFGEDRVVSEQPQVGTLEERNV VEALTGSAASRLRGGTSSRRLSSTP LPKAKRSLESEMYLEGLGRSHIASP SPCPDRMPLPSPTESRHSSSIPPVSSP PEQKVGLYRRQTELQDKSEFSDVD KLAFKDNEEFESSFECVDQKQIEEQ KEEEKIREQQVKERRQR
5373	10870	A	5696	306	4412	RLMMAQSNMFTVADVLSQDELRLK KLYQTFKDRGILDTLKTQLRNQLIH ELMHPVLSGELQPRISVEGSSLLIG ASNSLVADHLQRCGYEYSLSVFFPE SGLAKEKVFTMQDLLQLIKINPTSSL YKSLVSGSDKENQKGFMLHFLKEL AEYHQAKESCNMETQTSSTFNRRDS LAEKLQLIDDQFADAYPQRIKFESL EIKLNEYKREIEEQLRAEMCQKLKF FKDTEIAKIKMEAKKKYEKELTMF

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QNDFEKACQAKSEALVLRKSTLE RIHKHQEIETKEIYAQRQLLLKDMD LLRGREAELKORVEAFELNQLQE EKHKSITEALRRQEQNIKSFEETYDR KLKNELLNFHRLHGVCLALGILI*L WQVLEFGGSSPQECFYFLLEPKGQL VTAGKGK*NCENVPFGIANPDIMLL AVGSQDCA*SLSTKVLTLVGGGQM VQVDWK*PSDYHLGLSLLCAV*I*F TPLLFSVETN*KVIAFSK*PYDNTT LHFV*LSFGTQFIGSRKGFTGHFMFR GYIPGFSIEDFEVYKLSCLAPSGAPV P*ISSCTDNSLSRKMPPEELIFSHSDS\ RYQLELKDDYIIRTNRLIEDERKNK EKA VHLQEELIAINSKKEELNQSVN RVKELELELESVKAQSLAITKQNHM LNEKVKEMSDYSLLKEEKLELLAQ NKLLKQQLSESRNENLRLLNRLAQP APELAVFQKELRKA EKAIVVEHEEF ESCRQALHKQLQDEIEHSAQLKAQI LGYKASVKS LTTQVADLKLQKQT QTALENEVYCNPKQSVIDRSVNGLI NGNVVPCNGEISGDFLNNPFKQENV LARMVASRITNYPTAWVEGSSPDS DLEFVANTKARVKELQQEAEERLEK AFRSYHRRVIKNSAKSPLAAKSPPS LHLLEAFKNITSSSPERHIFGEDRVV SEQPQVGT LKEERN DVVEALTGSE ASRLRGGTSSRRLSSTPLPKAKRSL ECEMYLEGLGRSHIASPSPCPDRMP LPSPTESRHSLSIPPVSSPPEQKVGLY RRQTELQDKSEFSDVDKLAFKDNE EFESSFEFNSFNYENTLTSKYVAKW LCWELHRILLGKGAPSYFGFSSRAP VSCPHTALPFFVLVLLLRTHGTIVPH AAAGNMMPRQLEMGG LSPAGDMSH VDAAAAAVPLSYQHPSVDQKQIEE QKEEEKIREQQVKERRQREERRQSN LQEVLERERRELEKLYQERKMIEES LKIKIKKELEMENELEMSNQEIKDK SAHSENPLEKYMKIIQQEQDQESAD KVPVPWAGQSVGGGHPGLPWLNFL GRESVFSIEDKKSSK K MVQEGSLVD TLQSSDKVERHCIDPLWRTQQQGTI LEAETGSPDIEPASAFDLRLPLSL
5374	10871	A	5697	3	721	
5375	10872	A	5698	3	265	
5376	10873	A	5699	2	216	
5377	10874	A	5700	3	268	
5378	10875	A	5701	2	465	
5379	10876	A	5702	1	196	
5380	10877	A	5703	2	213	
5381	10878	A	5704	1	438	LQTWGPKQVC/SFFRRGGFEERVLL KNIRENGITGALLPCLDESRFENLGV SSLGERKKLLSYIQLRVQIHVDTMK\ VGYLAGCLVHALGEKQPELQISERD VLCVQIAGLCHDLGHGPF SHMFDG RFIPLARPEVKWTVCIHTVNSQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5382	10879	A	5705	2	1925	
5383	10880	A	5706	330	590	
5384	10881	A	5707	3	139	
5385	10882	A	5708	2	126	
5386	10883	A	5709	1	157	
5387	10884	A	5710	85	489	EKPLRWDSHLSCMLCWQAGFEAEQ KVGSSSRKLAISHALLEMLTPPPAG AMIPPPPSLPGPPRPGMMP\APHMG G\PPMMPMMGPPPPGMMPVGPAPG MRPPMGGHMPMMMPGPPVTRPPARP MMVPTRPGMTRPDR
5388	10885	A	5711	235	874	VVRRSGFLFCLFVLFSSMNSASVD GHLSGCRLFLFLSPLFRFYCDYCDT/ YLSPHDSPSVRQTHCSGK\KHIENV KDYYQK\WMEK\QSQSL\DKTTAA FQQGKIPPTPFSAPPP\AGA\MIPPPK /SFPGPSPLV*MPKHPHMGPPFW M\PMMPGSFLLGDGWPVGPASGEL RP\PMG\GHYCQLIAWGPPMDVGPS CPFH*WCPLGPGMTRPDR
5389	10886	A	5712	2	406	FRSPADPPVHCDKE*VLEVQREDED YHDSAKEKDEEDDSITRLLEFELEA YLSHNDYDGIKKLLQQLFLKAPVN TAELTNFLIQQNHIGSVIKHTDVS*D SIDDMDEDEAFGFISLLNLPDRKGT QCGEQIQE
5390	10887	A	5713	3	379	AVERGVPHFPDSPVQRDEEEKEVD TEDDDDDSDQEKDDEDNALDEEV NIEF\EAYSLSYNDYDGIKKLLPQLFI AAPVNTAKLPDLLIQQNHIGSAIKQ TDVSEDSNDDMDEEEASYSIDRLYN
5391	10888	B	5714	65	188	MWGFRIPADALIQRDEEEKEVLNE DEDDDDSDKEKDEEDRX*
5392	10889	A	5715	3	365	
5393	10890	A	5716	3	356	
5394	10891	A	5717	1	168	
5395	10892	A	5718	281	422	
5396	10893	A	5719	1	107	
5397	10894	A	5720	3	291	
5398	10895	A	5721	1	1260	WRTAAFWAFTVFLGDIILLTDVVIH EDQWIGETVLQSTFSSQLNLGSYS SIQPEEYSSVVCEVVLQDLLAYVSS KHSYLRDLPPRQPQRVNSIDFV\EL EHLQPDVLVHGSKELLDFITLITEG S/VYSYRGQKQ\KKVMLTV\DQAQG QHYALVLWGSWGQPGYPQLQRKK GYIWEFKYLFVQCNYTLENLELHTT PWSSCECLFDDDIRAITFKAKFQKS APSFVKISDLATHLEDKCSGVVLIK AQISELAFPITASQKIALNAHSSLKSI FSSLPNIVYTGCACGLELETDENRI YKQCFSCLPFTMKKIYYPALMTAI DGRHDVCIRVESKLIEKILLNISADC LNRVIVPSSEITYGMVVADLFHSL AVSAEPCVLKIQSLFVLDENSYPLQ QDFSLLDFYPDIVKHGANARL
5399	10896	A	5722	122	390	TFCVRSGLLDFAFPEPWRWGKWK

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						NWPESLEVWVLVLA VPLTHCDLGI LCCEDISQVLHVSQQI*PTRPGKR*L LGCAEVVLSSSASPG
5400	10897	A	5723	605	902	
5401	10898	A	5724	116	470	
5402	10899	A	5725	1	9786	
5403	10900	A	5726	10996	13825	MLTLRTRRS DGKMKSGFILGLSRAR SSFPMTKKRATPGHCRDPLEGHLRF LKNILPVYDKSLWDFLKL DVTTSIG RRQHRLRVSTAFVYTKNPNGYSFSIP VKVLADKFITPGLKLN DLNSVLVM PTFHVPFTDLQVPSCKLDFREIQIYK KLRTSSFALNLP TLPEVKFPEVDVLT KYSQPEDSLIPFFEITVPESQLTVSQF TLPKSVSDGIAALDLNAVANKIADF ELPTIIVPEQTIEIPSIKFSVPAGIVIPS FQALTARFEVDSPVYNATWSASLK NKADYVETSLDSTCSSTVQFLEYEL NVLGTHKIEDGTLASKTKGTLAHR DFSAEYEEDGKFEG LQEWEGKAHL NIKSPAFTDLHLRYQKDKKGISTA ASPAVGTVGMDMDEDDDFSKWNF YYSPQSSPDKKLTIFKTEL RVRESDE ETQIKVNWEEEAASGLL TSLKDNVP KATGVLYDYVNKYHWEHTGLTLR EVSSKLRRNLQNNAEWVYQGAIRQ IDDIDVRFQKAASGTTGT YQEWKD KAQNL YQELLTQEGQASFQGLKDN VFDGLVRVTQKFHMKVKH LIDSLID FLNFRPFQFPGKPGIYTREELCTMFI REVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISM YREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFDPSIVGWT VKY YELEEKIVSLIKNLLVALKDFHSEYI VSASNFTSQLSSQVEQFLHRNIQEY LSILTDPDGKGKEKIAELSATAQEII KSQAIATKKIISDYHQQFRYKLQDF SDQLSDYYEKFIAESKRLIDLSIQNY HTFLIYITELLKKLQSTTVMNPYMK LAPGELTIIL
5404	10901	A	5727	3	182	
5405	10902	A	5728	2	221	
5406	10903	A	5729	577	722	
5407	10904	A	5730	3	176	
5408	10905	A	5731	1	496	LLGVAPSRAFQEEILR/DRASFHE/RP NLFALKHPTSKAECTAEKCYRVTK GRGIFPSGSPFKSVTLEDGKTFIPGQ GNNA YVFPGV ALGV IAGGIRHIPDEI FLLTAEQIAQEVFEQHLSQGRLYPP LSTIRDVSLRIA IKVLDYAYKHNLD S YTPWKEAMNVQTV
5409	10906	A	5732	228	448	
5410	10907	A	5733	3	1877	EGEDRGLPRTMGAALGTGTRLAPW

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PGRACGALPRWTPTAPAQGCHSKP GPARPVPLKKRGYDVTRNPHLNKG MAFTLEERLQLGIHGLIPPCFLSQDV QLLRIMRYYERQQSDLDKYIILMTL QDRNEKLFYRVLTSDEVKFMPIVYT PTVGLACQHYGLTFRPRGRLFITIHD KGHLATMLNSWPEDNIKAVVVDG ERILGLGDLGCYGMGIPVGKLALYT ACGGVNPQQCLPVLLDVGTNNEEL LRDPLYIGLKHQRVHGKAYDDLDD EFMQAVTDKFGINCLIQFEDFANAN AFRLLNKYRNKYCMFNDDIQGTAS VAVAGILAAALRITNNKLSNHVVFVQ GAGEAAMGIAHLLVMALEKEGVPK AEATRKIWMVDSKGLIVKGRSHLN HEKEMFAQDHPESNSLDEVVRLVK PTAIIGVAAIAEA\FTEQILRNMAF RRAPIIFALSNPPRKAECTA\EKCYR VTEGPRGFFASGSPF*GVLIWEMGK TFIPGGRGNNAIYVFPGVATG\IA GGIRHIP\DEIFLLDSRAKLPQEVSEQ HL\SQGRLYPPLSTIRDVSLRIAIVL DYAYKHNLV\SYYPEPKDKEAFCKI PGSYTPDYDSFYT/VDSYIWAQGKA MNVQTV
5411	10908	A	5734	14	304	
5412	10909	A	5735	3	413	
5413	10910	A	5736	2	328	
5414	10911	A	5737	3	472	VTEFAKTCVADESAENCDSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLOHKDDNPRLPRLVRP EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDELRD EGKASSAKQRLKCASLQKFGERAF KA\VARLSQRFP
5415	10912	A	5738	1	2975	MKWVTFISLLFLFSSAYSRGVFRRT PLGPASSLPQSFLKCLEQVRKIQGD GAALQEKLCA TYKLCHPEELVLLG HSLGIPWAPLSSCPSQALQLAGCLS QLHSGFLYQGLLQALEGISPELGPT LDTLQLDVADFATTIWQQMEELGM APALQPTQGAMPAFASAFQRRAGG VLVASHLQSFLEVSYRVLRLHAQPG GGGDAHKSEVAHRFKDLGEENFKA LVLIAFAQYLQCCPFEDHVKL VNEV TEFAKTCVADESA*/ENCDSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLOHKDDNPRLPRLVRP EVDVMCTAFHDNEETFLKKYLYEI AR\RHPTCIA\ELLFFAKRYKAAFT ECCQAADKAACL\LPKLDEL\RDEG KASSAKQRLKCASLQKFGKRSFSK HGAVARL\SQEVFPKLEFCQEVSVQV *WTGL*PKFPHGNC\CHGRSCFECC WMDR/RRDLWPKYILWKIQDFDLP S*TGRDCC\EKPLVWGKIPTCICRK WEN*WRLPGLDFAFH*ACLIFVWK VKGCFGQNYCLRAKDVFPACFLY

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						\DYARRAS*FTLFVPAEEDLPRTYET TLEECCAAADPHECYAKVFDEFKPL VEEPQNLIKQNCLEFEQLGEYKFQN A\LLVRYT\KKVPQVSTPTLVEVSRN LGKVGSKCKHPEAKRMPCAEDYL SVVLNHLCLVHEKTPVSDTVTKCC TESFVNTPPCFSALEVDETYVPKHF NAETFTFHAHISTLSQKERQIKKQT ALVDLVKHKPKATKEQLKAVMDD FAAFVEKCKADDKETCFEEGKK LVAASQAALGLTPLGPASSLPQSFL LKCLEQVRKIQQDGAALQEKLCAT YKLCHPEELVLLGHSGLIPWAPLSS CPSQALQLAGCLSQLHSGFLYQGL LQALEGISPELGPTLDTLQLDVADF ATTIWQQMEELGMAPALQPTQGA MPAFASAFQRRAGGVLVASHLQSF LEVSYRVLRLHAQP
5416	10913	A	5739	132	918	
5417	10914	A	5740	59	335	
5418	10915	A	5741	219	642	KGWFLGAFHKLKTMKHLTMTMG C/VF*VKSQGVNDN\EEGFFSARGHR PLDDKKREEAP\SLRPAPPISGRWAI RASSQPKQLATSKGK*ERKSPWIAG KVVFSRLDPDLG\VVCCSLQGCSVC QGGFFLTTRGKGPFFQELVV
5419	10916	A	5742	1	359	
5420	10917	A	5743	1	322	
5421	10918	A	5744	2	862	FVDGKLHGRGSTDDKGPVAGWINA LEAYQKTGQEIPVNV\RFCLEGMEE SGSEGLDELIFARKDTFFKDVDYVC ISDNYWLGKKKPCITYGLRGICYFFI EVECSNKDLHSGVYGGSVHEAMTD LILLMEEHKL\YDDIDFDIEEFAKDV GAQILLHSHKSHLHLDLLPVVVRLL GQALFHTAHFPDNIPSSSKDILMHR WRYP\SLH\GIEGAFSGGAKTVIP RKVVVGKFSIRLV\PNMTPEVVGEQA CGAGTRESMSSLGYP\RAEDDSGLS ALPSQPQPFILYAT
5422	10919	A	5745	455	601	SLAICGSCPFLKTFTITGVFLSSL*YD PSKPALTGRMILSQFVLLNKK
5423	10920	A	5746	25	458	
5424	10921	A	5747	3	396	
5425	10922	A	5748	2	797	AGPAALGGAGLCRAADAGLCSAGC GFVKVVKNKAYFKRYQVKFRRR\R KGKTDYYARKRL\VIQDKNKYNTP KYRMIV\RV\TNRDIICQIAY\RIEGD MIVCAA*CTPNLPKYGV\KVGLTNY AAAY\CT\GLLL\ARRL\LNRF\MDN \YEGQV\EVTG\DEYNVESIDWSAQ GAF\TCY\LDAGLAR\TT\TG\NKVFG\ ALKGM\LMGGLSIPHSSKRFLGLSI PHSTK*ILGYDSENKEFN\AEVRRKHI MGQKFADDLHCLIEEDENASKK
5426	10923	A	5749	172	333	
5427	10924	A	5750	2	282	SLSREVQRQMHLVFFSKNKLKAGY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LMSVESSE/CFLEEVG/SQALVAGSY MPPSTVLQQIDS/VANADIINAARKF VS/GQKSMAAGGNLGHHTPLVDEL
5428	10925	A	5751	813	998	
5429	10926	A	5752	1	1418	MKLLTRAGSFSRFYSLKVAPKVKA TAAPAGAPPQPDLEFTKLPNGLVI ASLENYSPVSRIGLFIKAGSRYEDFS NLGTTLLRLTSSLTTKGASSFKITR GIEAVGGKLSVTATRENMAITVEC LRGDVDILMEFLNVTTAPEFRRWE VADLQPQLKIDKAVAFQNPQTHVIE NLHAAAYQNALANPLYCPDYRIGK VTSEELHYFVQNHFTSARMALIGLG VSHPVLKQVAEQFLNMRGGLGLSG AKANYRGGEIREQNGDSLVAHAFV AESAVAGSAEANAFAVQLHGPRVL GHHVKSQGGQPPAHLHQAVAKA/T QQP\FDVSAFNASYSDS\GLFG\YTIS QGHQLAGDCIK\AA\YNQVKTI\QG NLSNTDV\QAAQEPS*KAGIP*WSV ESSE\CFLEEVVRPRALVAGSYMPP VHSSFQQI/DSPKRGWGGAKMPDII NGGKRSFVSGPEVQWAASLENLGT LHLFV
5430	10927	A	5753	150	355	
5431	10928	A	5754	2	388	FLFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDSPALASSVWITDV RHHLWLIFVFLVETGFRHVQGASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVQGAGLELLAPS DPPA
5432	10929	C	5755	197	415	MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF*
5433	10930	A	5756	764	1079	KGVLFFFFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA
5434	10931	A	5757	213	383	
5435	10932	A	5758	1	981	
5436	10933	A	5759	124	354	
5437	10934	A	5760	2	646	CGGIHGNHTFKMALNQFSDMSFAEI KHKYLWSEPQNCSATKSNYLRGTG PYPPSVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALESAIAIATGKMLS LAEQQLVDCAQDFNNHGCQGGGPS QAFEYILYNKGIMGEDTYPY\QGKD GYCK\FQPGKAIGFVKDV\ANITIYD EEAMVEAVALYNPVSAFEVTQDF MMYRTGIYSSTSCHKTPDK
5438	10935	A	5761	1	218	
5439	10936	A	5762	272	364	
5440	10937	A	5763	1	1956	
5441	10938	A	5764	105	533	
5442	10939	A	5765	292	568	
5443	10940	A	5766	1	279	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5444	10941	A	5767	3	352	
5445	10942	A	5768	375	485	TPGLK*FSHDLLNCWDYRCETVH LAEIAQVSEKQI
5446	10943	A	5769	3	221	
5447	10944	A	5770	793	1039	SFSFTFKMLSGRRETFFFGGRFFWF VVVFFFLAGRGSFALVAQAGVQ WRDLRSLQPPPRGFRRFFCLSLPGA CGPRYLGG
5448	10945	C	5771	33	334	MSDSGKSSPVAHSILWIWGRDSDA YRDKQHILWPKRADCTESYPRVPA GGELPTYFLPPENKGLRIHELNSDD YSTEEEAQTPDCSITDFTRRHTLSYL V*
5449	10946	A	5772	194	593	
5450	10947	A	5773	1	877	
5451	10948	A	5774	2	352	
5452	10949	A	5775	3	726	EQEVDDYDPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKVGSKCKKHPEA KRMPCAEDYLS\VVNLNQLCVLH/EK TPVSDRVTKCCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKVGSKCKKHPEA KRMPCAEDYLSRGPEPVMCVA
5453	10950	A	5776	4274	5255	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLOHKDDNPNLPR LVRPEVDMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFJETGYNLSQK FKIDKFFNVFRYVYVMVVIDFVLV SNIILPKFNHLCCTHTHTHTLTLFST YLKNDRDKTIMCKLSLIG*LAESEF GGSGENVVDYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV
5454	10951	A	5777	15	218	
5455	10952	A	5778	141	318	
5456	10953	A	5779	1	290	TMSLNRLQEFGTSLVTLDAIPHILPE GDELLEENQEGCFS*SFLFATNATL GPRLWSPWLASGLSLPEACASPKH AAQGPHQKPPRLQPPQHSVCQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
5457	10954	A	5780	2	643	GTRLFEQLGEYKFNALLIRYTKKV PQVSTPTLVEVSRNLGKVGSKCK HPESKKECPVQEDYLSRGSWNQLL CVCIEKTPVKLTESPKC\CTESLG*T GRPLLFSALGKFDWKHYGFPRSF NCLKTFHLSMAGFMAHFFEEGRRT NSRKTNWHLFELVETQGPRQQRQ LKA\VMGGFAAFVEKCKKADKET CFAEEGKKLVAASQAALGL
5458	10955	A	5781	1	135	
5459	10956	A	5782	1	330	
5460	10957	A	5783	247	434	
5461	10958	A	5784	140	2569	SGSPVLDPSEPQPLAAMHVIKRDGR QERVMFDKITSRIQKLCYGLNMDF VDPAQITMKVIQGLYSGVTTVELDT LAAETAATLTTHKPDYAILAARIAV SNLHKETKKVFSVDMEDLYNYINP HNGKHSPMVAKSTLDIVLANKDRL NSAIIYDRDFSINYFGFKTLERSYLL KINGKVAERPQHMLMRVSVGIHKE DIDAAIETYNLLSERWFTHASPTLFN AGTNRPQLSSCFLLSMKDDSIIEGY DTLKQCALISKSAGGIGVAVSCIRA TGSYIAGTNGNSNGLVPMLRVYNN TARYVDQGGNKRPGAFIYLEPWH LDIFEFLDLKNTGKEEQRRDLFF ALWIPDLFMKRVETNQDWSLMCPN ECPGLDEVWGEEFEKLYASYEKQG RVRKVVKAAQQLWYAIIESQTETGTP YMLYKDSCNRKSNQNLGTIKCSN LCTEIVEYTSKDEVAVCNLAALN MYVTSEHTYDFKKLAEVTKVVVRN LNKIIDINYYPVPEACLSNKRHRPIGI GVQGLADAFILMRYPFESAQAQLLN KQIFETIYYGALEASCDLAKEQGPY ETYEGSPVSKGILQYDMWNVTPTD LWDWKVLKEKIAKYGIRNSLLIAP MPTASTAQILGNNESEPYTSNIYTR RVLSGEFQIVNPHLLKDLTERGLWH EEMKNQIIACNGSIQSIPEIPDDLKQL YKTVWEISQKTVLKMAAERGAFIG QSQSLNIHIAEPNYGKLTSMHFYGW KQGLKTGMYYLRTRPAANPIQFTL NKEKLDKEKVSKEEEKERNTAA MVCSLENRDECLMCGS
5462	10959	A	5785	1	161	
5463	10960	A	5786	2	170	
5464	10961	C	5787	219	398	MSQESVILFYSVGMSLFLFLFRVVT NFTFFPLAVICIRASHLLACPLPSLS LPHQPTH*
5465	10962	A	5788	2	472	
5466	10963	A	5789	3720	5308	PLLPLSPPHLTEVEGQGRMVGTEE TWSNCSGAFKPKCSPQPICLV LAP TRELAQQVQQVADDYGKCSRLKST CIYGGAPKGPQIRDLERGVEICISTP GRIDFLESCKTNLSRCTYLVLDL DKMLDMGSEPQIL*IGDPIRPDRQTL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MWSATWPKEVRQLAEDFLRDYTOI NVGNLELSANHNILQIVDVCMESEK DHKLIQLMEEIMAEKENKTIIFVETK RRCDDLTRRMRRDGWPAMCIHGD KSQPERDWVLNEFRSGKAPILIATD VASRGLDVEDVKFVINYDYPNSSD YVHRIGRTARSTNKGTA YTFTPGN LKQARELIKVLEEANQAINPKLMQL VDHRGGGGGGGGKGGRSRYRTTSSA NNPNLMYQDECRRRLRGVKDGG RDSASYRDRSETDRAGYANGSGYG SPNSAFGAQAGQYTYGQGTYGAAA YGTSSYTAQEY GAGTYGASSTTSTG RSSQSSSQQFSGIGRSGQPQPLMS QQFAQPPGATNMIGYMGQTAYQYP PPPPPPPSRK
5467	10964	A	5790	1	307	
5468	10965	A	5791	2821	5781	
5469	10966	A	5792	1	981	
5470	10967	A	5793	99	1023	NHKDGEKTEQKNGKL*KSECLSKN KAGGITLPDFKLYYKATVTKTAWY WYQNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKKWGNDSLFNKWC WENWLAICRKLKLDPF LTPYTKINS RWIQDLNIRPKNIKTLEEILGNTIQDI GMGKDFKSKTPKAMAIAKIDKW DLIKLKSFCTEKETTIRVNRQPTWE KIFAIYSSEKGLISRIYNELQQIYKKK TNNPIQKRVKDMNRHFSKEDIYAA KKT*KNAHHMKKCSSSPAIREIQI KTTMRYHLIPRMVVIKKSGNKG CW RGCGEIGTVLH
5471	10968	A	5794	3	1218	
5472	10969	B	5795	1	1098	MIDKGDIIIDPSEIQTIREYYNYLY TNKLENLEEMDKFLDTYTLPRLNQ EEVESLNRPTTGSEIEAIMNSLPTKK VQDQMDSQPNSTRVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADDMIV YLENPIVSARNLLKLIGNFSKVS KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLKRDVKDLFK ENYKPLLKEIKEDTNKWSIPCSWV GRINIMKMAILPKVIYRFNAIPNKLP MPFFTELEKTTLKFIWNQKRAHIAK SILSQKNKAGGITLPDFKLYYKATV TKTAWY WYQNRDIDQWNRTEPSEI MPHIYNHLIFDKPDKNKKWGKDSL FNKWCWENWQPYVES*
5473	10970	A	5796	1	1245	
5474	10971	A	5797	1	969	MIVYLENPIVSAQNLLKLIGNFSRVS GYKINVQKSQAFLYTNNRQTENQII SELPFTIASKRIKYLGIQLTRDVKDL FKENYKTLLKEIKEDTKKWKNI PCS WVGRINIVKIAILPKVIYRFSAIPIKL PMTFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGIMLPDFKLYYKAT VTKTAWY WYQNRDIDQWNRTEPS EIMLHIYKHLIFDKPDKNKQWGKDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LFNKWCWENWLAICRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKTEEN LGNTIQDIGTGKDFMSKTPKAMAT KAKIDKWDL/LRFCTAK*TTIRV
5475	10972	B	5798	1	1383	MGDFNTPLSTLDRSKRQKVKKDIQ ELNSALHQVDLIDIYRTPYPKSTEYT FFSAQHHTYSKTDHIVGSKELLSKC KRTEIITNCLSDHSAIKLELRICKLTQ NRSTTWKLNLLNLDYWVHNEMK AEIKMFFETNENKDTTYQNLRTLK AVCRGKFVALNAHQKQKISKIDTL TSQLKELEKQEQTTHSKASRRQEITKI RAELKEIETQKTLOKINDSRSWAIR QEKEIKGIQLGKEEVQLSLFADDMI VHLENPIVSAQNLLKLIGNFSKVS YKINVKKSQAFLYTNNRQTESQIMS EFPFTIASKRIKYLGIQLTRDVKDLF KENYKTLLNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAISIK LPMFTFFTEL GKPTLKLWVWQKRVRI AKSILSQKNKAGGIMLPDFKLYYKA TVTKTAWYWYQNRDIDQWNRTEP SEIMPHITTI*
5476	10973	A	5799	1	1272	MIISMDAEKAFDKIQQCFMLKTLNK LGIDGTYLKKIRAIYDKPTVNIILNG QKLEALPLKTGTRQGCPLSPLLFNIV LQALARAIRQEKEIKGIQLGKEEVK LSLFADDMIVYLENPIVKAQNLLKL ISNFSKVSQYKISMQKSQAFLYTNN RQIESQIMSELPFTIASKRIKYLGIQL TRDVKDLFKENYKPLLNEIKEDKN KWKNIPCSWVGRINIVKMAILPKFI WRQKRAHIAKSILSQKNKAGGIKLP DFKLYYKATVTKTAWYWYQNRDI DQWNRTEPSEIMLHIHNYLIFDKPD KNKKWRKDSL FNKWCWENWLAK CRKLKLHPFLT PYTKINSRWIKDLH VRPKTIKTEENLGITIQDKGMGKD FMSKTPEALATKANIDKSDLIKLS SCK\ETTIRVNRQPTWEKIFAIYSS
5477	10974	A	5800	1	1398	
5478	10975	A	5801	564	2444	LTNQKKSRTRWIHSRILPEVQGGAV LEVLARAIRQEKEVKGIGLKEEV KLSLFADDMIVYLENPIISAQNLLKL IGNFSKVSQYKINVQKSQAFLYTNN RETESQIMSELPFTTASRIKYLGIQ LTRDVKELFKETYNPLLNEIKEDTT KWKNIPCSWVGRINIVKIAILPKVICI FNAIPIKLPMFTFFTELEKTTLKFIRNQ KRARIAKSILSQKNKAGDVTLPDFK LYYKATVTKTVWYWYQNRDIDQW NRTEPSEIILHIYHNLIFDTPDKNKK WGKDSL FNKLCWENWLAICRKLKL DPFFTPYTKINSRWIKDLHVRPKTIK TEENLGNTIQDIGIGKDFMTKTQK AMATNAEIHKWDLIKLKHFTAKE TTIRVNRQPTKWENIFAIYSSDKRLI SRIYKELKHIIYKRKTNNPINKWAKD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPVRMAIHKK SGNNRCWRGCGENHSQQTITRTKIQ TLHVLNHRWELNNENTWTQEGEH HTLGPVVGWGRGEGQQCISPYSMG KASIPHAVLVVFFGLCQONAPNLDW SLVSLWWCLLGFTNFFCKEPDCKY VRLFRPLGIVFATPPLPPPPSSSTS S
5479	10976	A	5802	1	2430	
5480	10977	A	5803	2022	4573	
5481	10978	A	5804	1169	3077	VHCRFWILALCQMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQNLLIL QLISNFSKVSGYKINVQKSQAFLYT NNRQTESQMRSELPFTVATKRIKYL GIQLTRDVKDLFKENYKLLLNEIKE DTNKWKNIPRSWVGGRINLVKMAI LPKVIYRFNAIPIKLPMFTFTELEKTT LKFIWNQKRALIAKSSLSQKNKTGG ITLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNLIFDK PDKNKK\WGKDSL FNK WFWENCL AICRKLKLDPFL\TNYTKINSRWIKD LNFRPKTIKTLEDNLGNTIQDIGMG KDFMSLP/KTPEAMATKAKIDKWD LIKALKSFCTAKETTIRVNRQPTKWE KIFAIYSSDKGLISRIYNELKQIYKK K\TNNPIKKWAKD\TNRHFSKEDIYA ANRHMRCSSSLVIREMQIKTTMR YHLTPVRTAIKKSGDNRCWRGCGE IGTLLHCWWDCCLVQPLWKS VWR FLRDLELEIPFDPAIPLLGIPKDYKS CCYKDTCTCMFIAALFTIAKTWNQP KCPTMIDWIKKMWHIYTM EYYAAI KNDEFVSFVG TWMKLEIHL SKLSQE QKTKHCIFSLIGGN
5482	10979	A	5806	133	358	
5483	10980	A	5807	3	164	
5484	10981	A	5808	1573	1720	
5485	10982	A	5809	1573	1720	
5486	10983	A	5810	1	4860	
5487	10984	A	5811	2	2887	VRVIKSEDDVLVVCPTILTEDGMQA QHLGATLALYRLVKGQSVHQLLPP TYRDVWLEWSDAEKKREELNKME TNKPRDLFIKLLNKLKQQQQQQQ QHSENKRENSDPEESWENLV SDE DFSALSLESANVEDLEPVRNLFRL QSTPKYQKLLKERQQLPVFKHRDSI VETLKRHRVVVVAGETGSGKSTQV PHFLLLEDLLLNEWEASKNIVCTQP RRISAVSLANRV CDELGCENGPGG RNSLCGYQ\RMESRACESTRLLYCT TGVFA*GKLQEDGLSK*CVSMFIVD EV\HER\SVQSDFLIHLKEILQKRSD LHLILMSATVDSEKFSTYFTHCPILR ISGRSYPVEVFHLEDIIETGTFVLEK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DSEYCQKFLEEEEEVTINVTSKAGGI KKYQEYIPVQTGAHADLNPFYQKY SSRTQHAILYMNPHKINLDLILELLA YLDKSPQFRNIEGAVLIFLPLGLAHIQ QLYDLLSNDRRFYSERYKVIALHSI LSTQDQAAAF TLPPPGVRKIVLATNI AETGITIPDVVFVIDTGRTKENKYHE SSQMSSLVETFVSKASALQRQGRA GRVRDGF CFRMYTRERFEGFMDYS VPEILRVPLEELCLHIMKCNLGSPED FLSKALDPPQLQVISNAMNLLRKIG ACELNEPKLTPLGQH LAALPVNVKI GKMLIFGAIFGCLDPVATLA VMTE KSPFTTPIGRKDEADLAKSALAMAD SDHLTIYNAYLGWKKARQEGGYRS EITYCRRNFLNRTSLLTLEDVKQELI KLVKAAGFSSSTTSTSWEGNRASQT LSFQEIALLKAVLVAGLYDNV GKII YTKSVDVTEKLACIVETAQGKAQV HPSSVNRDLQTHGWLLYQEKIRYA RVYLRETTLITPPFVLLFGGDIEVQH RERLLSIDGWYFQAPVKIAVIFKQL RVLIDSVLRKKLENPKMSLENDKIL QITELIKTENN
5488	10985	A	5812	1	132	
5489	10986	A	5813	383	667	
5490	10987	A	5814	2444	2755	DYYYYFEMESCSVAQAGVQWRDL GSLQPPPP\SSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVQGQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS
5491	10988	A	5815	1724	1941	AHLLYEWIFFFFFFFFEMESHVAQA GVLWRDLSSLQAPPPGVSQSDSPAS ASWVAGITGACHHARHEWNFKC
5492	10989	A	5817	37	2496	
5493	10990	A	5818	2	1814	
5494	10991	A	5819	1	394	
5495	10992	A	5820	2	1785	QLFACVPKTSPPATVISSVTSTCSSL PSVSSAPITSGQAPTTFLPASTSQAQ LSSQKMESFSAVPPTKEKVSTQDQP MANLCTPSSTANSCSSASNTPGAP ETHPSSPTPTSSNTQEEAQSSVSD LSPMSMPFASNSEPAPLTLTSPRMV AADNQDTSNLPQLAVPAPRVSHRM QPRGSFYSMVPNATIHQDPQSIFVT NPVTLTPPQGPAAVQLSSAVNIMN GSQM HINPANKSLPPTFGPATLFNH FSSLFDSSQVPANQGWGDGPLSSRV ATDASFTVQSAFLGNSVLGHLENM HPDNSKAPGFRPPSQRVSTSPVGLP SIDPSC\SSPSSSSAPL\ASFSGIPGNQ GFFLQGP\APVGGLLSFNQRHF/SFP HPW\TSASNCDSPISVSSGSSSPLS ATS\APPTLG\QPKGSQCQSRIKGY LPPIGTERLARILQGGSV AQAPAG\T SFVAPVGHSGVWSFGVNAV\EGLAS GWSQSVMG\NHPMAFN NFSGPKAH FSQHQP MERDDSGMVAPSNIFHQP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MASGFVDFSKGLPISMYGGTIIPSHP QLADVPGGPLFNGLHNPDPAWNPM IKVIQNSTECTDAQQVKWA
5496	10993	A	5821	3	125	
5497	10994	A	5822	3448	3831	KNRFCSGVSSNSKSNNSCVYVYIDR DIDTHTYIHIHTNICIHILFFFFETES HALSPRLECNGVISAHCNLHPPGASS DSPASAARVAGVTGTCHHAQLIFFF FVFLVETGFHHAAQAGSQTPDLR* S TPLGFPKC*DYRR/AAIVPGIFLLH* I R*\KVPTLLTDMRNASEYDCDFSTN KIDKEETFS*NASLNLCLLST*PYEM VTHFKGY*ILPLFFFFFLRQSL/SSVT QAGVQWHNLGSLQPLPPGFKQFSC LSLPSSWDYRYQLPRLA/NF/FVFLV ETGFHHAAQAGSQTPDLR

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-5497, a mature protein coding portion of SEQ ID NO: 1-5497, an active domain of SEQ ID NO: 1-5497, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively
25 associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - 30 (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-5497.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- 5 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample under stringent hybridization conditions with
- 10 nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the
- 15 sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

20 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

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17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- 30 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-5497, a mature protein coding portion of SEQ ID NO: 1-5497, an active domain of SEQ ID NO: 1-5497, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-5497, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 5498-10994, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-5497.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 5 28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

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(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

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INTERNATIONAL SEARCH REPORT

International application No.

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A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70; C07K 14/00

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B. FIELDS SEARCHED

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Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database EST, ID No. AW570442, SHOEMAKER et al. 'Public soybean EST project', March 2000. See sequence alignment.	1-9, 19, and 22-26
X	Database EST, ID No. BE609432, SHOEMAKER et al. 'Public soybean EST project', August 2000. See sequence alignment.	1-9, 19, and 22-26
Y	WATSON et al. Recombinant DNA. New York: Scientific American Books. 1994, especially pages 72-76.	19, and 22-26

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

Special categories of cited documents:	
A document defining the general state of the art which is not considered to be of particular relevance	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
E earlier application or patent published on or after the international filing date	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
O document referring to an oral disclosure, use, exhibition or other means	* & * document member of the same patent family
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INTERNATIONAL SEARCH REPORT

International application No.

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Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
see continuation of Box II

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9, 19, 22-26 and SEQ ID NO:1

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08656

Continuation of Box II

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Groups 1-5497 (claim(s) 1-9, 19, and 22-26), all in part, drawn to an isolated nucleic acid molecule of SEQ ID NO X, vectors, host cells containing same, and the first method of using the nucleic acid molecule to make a polypeptide, wherein X is any one of SEQ ID NOs: 1-5497. For example,

If Group 1 is elected, this correlates to SEQ ID NO:1.

Groups 5498-10994 (claim(s) 10-11, and 20-21), all in part, drawn to a polypeptide of SEQ ID NO Y, wherein Y is any one of SEQ ID NOs: 5498-10994. For example,

If Group 5498 is elected, this correlates SEQ ID NO:5498.

Groups 10995-16491 (claim(s) 12), drawn to an antibody which binds to a protein with SEQ ID NO Y encoded by a nucleic acid with SEQ ID NO X. For example,

If Group 10995 is elected, this correlates to SEQ ID NO:1, and SEQ ID NO:5498.

Groups 16492-21988 (claim(s) 13-16), drawn to methods of detecting the polynucleotide of SEQ ID NO X. For example,

If Group 16492 is elected, this correlates to SEQ ID NO:1

Groups 21989-27485 (claim(s) 17-18), drawn to methods of identifying a binding partner to a polypeptide of SEQ ID NO Y. For example,

If Group 21989 is elected, this correlates to SEQ ID NO:5498.

Groups 27486-32982 (claim(s) 27), drawn to a method for treatment by administering a polypeptide of SEQ ID NO Y. For example,

If Group 27486 is elected, this correlates to SEQ ID NO:5498.

Groups 32983-38479 (claim(s) 28), drawn to a method for treatment by administering an antibody against a protein with SEQ ID NO Y encoded by a nucleic acid with SEQ ID NO X. For example,

If Group 32983 is elected, this correlates to SEQ ID NO:1, and SEQ ID NO:5498.

The inventions listed as Groups 1-38479 do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reason:

The polynucleotides and polypeptides of each invention are unrelated, each to each other. GIBCO BRL discloses random priming nucleic acids comprising sequences that are complements of, and can hybridize to the claimed polynucleotides in claim 1 (GIBCO BRL Catalogue and Reference Guide, 1990). Such nucleic acid renders claims 1 and 2, among the others, not novel. Thus, the technical feature of the polynucleotide sequence is not special and the groups are not so linked under PCT Rule 13.1. Additionally the claimed methods produce different products and/or different results which are not coextensive and which do not share the same technical feature.

Furthermore, the claims are directed to different genes corresponding to SEQ ID NOs: 1-5497. Each of these genes are separate entities which encode different proteins with different activities, binding reactions, antibody recognition, etc. and thus each has its own special technical feature.

Thus, in summary, the inventions listed as Groups 1-38479 are not so linked under PCT Rule 13.1.